

Novel Proteins and Nucleic Acids Encoding Same

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RELATED APPLICATIONS

5 This is a request for filing a new nonprovisional application under 37 C.F.R. §1.53(b). This application claims priority to U.S.S.N. 60/274,322 filed on March 8, 2001 (Cura 590); U.S.S.N. 60/283,675 filed on April 13, 2001 (Cura 590D1); U.S.S.N. 60/338,092 filed on December 3, 2001 (Cura 590D2); U.S.S.N. 60/274,281 filed on March 8, 2001 (Cura 591);
10 U.S.S.N. 60/274,101 filed on March 8, 2001 (Cura 592); U.S.S.N. 60/325,681 filed on September 27, 2001 (Cura 592J1); U.S.S.N. 60/304,354 filed on July 10, 2001 (Cura 592I1); U.S.S.N. 60/279,995 filed on March 30, 2001 (Cura 592H1); U.S.S.N. 60/294,899 filed on May 31, 2001 (Cura 592E1); U.S.S.N. 60/287,424 filed on April 30, 2001 (Cura 592D1); U.S.S.N. 60/299,027 filed on June 18, 2001 (Cura 592D2); U.S.S.N. 60/309,198
15 filed on July 31, 2001 (Cura 592C1); U.S.S.N. 60/281,194 filed on April 4, 2001 (Cura 592A1); U.S.S.N. 60/274,194 filed on March 8, 2001 (Cura 593); U.S.S.N. 60/274,849 filed on March 9, 2001 (Cura 594); U.S.S.N. 60/330,380 filed on October 18, 2001 (Cura 594C1); U.S.S.N. 60/275,235 filed on March 12, 2001 (Cura 595); U.S.S.N. 60/288,342 filed on May 3, 2001 (Cura 595J1); U.S.S.N. 60/275,578 filed on March 13, 2001 (Cura 596); U.S.S.N. 60/291,240 filed on May 16, 2001 (Cura 596I1); U.S.S.N. 60/294,485 filed on May 30, 2001 (Cura 596B1); U.S.S.N. 60/299,310 filed on June 19, 2001 (Cura 596A1); U.S.S.N. 60/275,579 filed on March 13, 2001 (Cura 597); U.S.S.N. 60/275,601 filed on March 13, 2001 (Cura 598); U.S.S.N. 60/276,000 filed on March 14, 2001 (Cura 599); U.S.S.N. 60/280,900 filed on April 2, 2001 (Cura 599E1); U.S.S.N. 60/276,776 filed on March 16, 2001 (Cura 600); U.S.S.N. 60/294,889 filed on May 31, 2001 (Cura 600G1); U.S.S.N. 60/318,770 filed on September 12, 2001 (Cura 600E1); U.S.S.N. 60/276,994 filed on March 19, 2001 (Cura 604); U.S.S.N. 60/277,338 filed on March 20, 2001 (Cura 607); U.S.S.N. 60/325,430 filed on September 27, 2001 (Cura 607J1); U.S.S.N. 60/332,094 filed on November 21, 2001 (Cura 607C1); U.S.S.N. 60/299,303 filed on June 19, 2001 (Cura 607B1); U.S.S.N. 60/288,066 filed on May 2, 2001 (Cura 607A1); U.S.S.N. 60/277,321 filed on March 20, 2001 (Cura 608); U.S.S.N. 60/280,822 filed on April 2, 2001 (Cura 608A); U.S.S.N. 60/277,239 filed on March 20, 2001 (Cura 609); U.S.S.N. 60/277,327 filed on March 20, 2001 (Cura 610); U.S.S.N. 60/277,791 filed on March 21, 2001 (Cura 611); U.S.S.N. 60/333,184 filed on November 14, 2001 (Cura 611H1); U.S.S.N. 60/277,833 filed on March 22, 2001 (Cura 612); U.S.S.N. 60/318,462 filed on September 10, 2001 (Cura 612J1); U.S.S.N. 60/288,528 filed on May 3, 2001 (Cura 612A1); U.S.S.N.

60/278,152 filed on March 23, 2001 (Cura 613); U.S.S.N. 60/332,272 filed on November 14, 2001 (Cura 613D1); U.S.S.N. 60/278,894 filed on March 26, 2001 (Cura 614); U.S.S.N. 60/312,903 filed on August 16, 2001 (Cura 614C1); U.S.S.N. 60/333,272 filed on November 14, 2001 (Cura 614C2); U.S.S.N. 60/279,036 filed on March 27, 2001 (Cura 615); U.S.S.N. 60/332,172 filed on November 14, 2001 (Cura 615I1); U.S.S.N. 60/337,426 filed on December 3, 2001 (Cura 615I2); U.S.S.N. 60/278,999 filed on March 27, 2001 (Cura 616); U.S.S.N. 60/279,344 filed on March 28, 2001 (Cura 617); U.S.S.N. 60/332,271 filed on November 14, 2001 (Cura 617J1); U.S.S.N. 60/291,099 filed on May 16, 2001 (Cura 617H1); U.S.S.N. 60/291,190 filed on May 15, 2001 (Cura 617E1); U.S.S.N. 60/280,233 filed on March 30, 2001 (Cura 618); U.S.S.N. 60/280,802 filed on April 2, 2001 (Cura 621); U.S.S.N. 60/335,301 filed on October 31, 2001 (Cura 621F1); U.S.S.N. 60/337,185 filed on December 4, 2001 (Cura 621D1); and U.S.S.N. 60/345,705 filed on January 3, 2002 (Cura 621B1).

Field of the Invention

The present invention relates to novel polypeptides that are targets of small molecule drugs and that have properties related to stimulation of biochemical or physiological responses in a cell, a tissue, an organ or an organism. More particularly, the novel polypeptides are gene products of novel genes, or are specified biologically active fragments or derivatives thereof. Methods of use encompass diagnostic and prognostic assay procedures as well as methods of treating diverse pathological conditions. The present invention discloses novel associations of proteins and polypeptides and the nucleic acids that encode them with various diseases or pathologies. The proteins and related proteins that are similar to them, are encoded by a cDNA and/or by genomic DNA. The proteins, polypeptides and their cognate nucleic acids were identified by Curagen Corporation in certain cases. The XYZase-encoded protein and any variants, thereof, are suitable as diagnostic markers, targets for an antibody therapeutic and targets for small molecule drugs. As such the current invention embodies the use of recombinantly expressed and/or endogenously expressed protein in various screens to identify such therapeutic antibodies and/or therapeutic small molecules.

Signaling proteins may be classified as endocrine effectors, paracrine effectors or autocrine effectors. Endocrine effectors are signaling molecules secreted by a given organ into the circulatory system, which are then transported to a distant target organ or tissue. The target cells include the receptors for the endocrine effector, and when the endocrine effector binds, a signaling cascade is induced. Paracrine effectors involve secreting cells and receptor cells in close proximity to each other, for example two different classes of cells in the same tissue or organ. One class of cells secretes the paracrine effector, which then reaches the second class of cells, for example by diffusion through the extracellular fluid. The second class of cells contains the receptors for the paracrine effector; binding of the effector results in induction of the signaling cascade that elicits the corresponding biochemical or physiological effect. Autocrine effectors are highly analogous to paracrine effectors, except that the same cell type that secretes the autocrine effector also contains the receptor. Thus the autocrine effector binds to receptors on the same cell, or on identical neighboring cells. The binding process then elicits the characteristic biochemical or physiological effect.

30 Many pathological conditions involve dysregulation of expression of important effector proteins. In certain classes of pathologies the dysregulation is manifested as diminished or suppressed level of synthesis and secretion protein effectors. In a clinical setting a subject may be suspected of suffering from a condition brought on by diminished or suppressed levels of a protein effector of interest. Therefore there is a need to be able to

In many cases the objective of such screening assays is to identify small molecule candidates; this is commonly approached by the use of combinatorial methodologies to develop the population of substances to be tested. The implementation of high throughput screening methodologies is advantageous when working with large, combinatorial libraries of compounds.

It is an objective of this invention to provide at least one target biopolymer that is intended to serve as the macromolecular component in a screening assay for identifying candidate pharmaceutical agents.

It is another objective of the present invention to provide screening assays that positively identify candidate pharmaceutical agents from among a combinatorial library of low molecular weight substances or compounds.

It is still a further objective of this invention to employ the candidate pharmaceutical agents in any of a variety of in vitro, ex vivo and in vivo assays in order to identify pharmaceutical agents with advantageous therapeutic applications in the treatment of a disease, pathology, or abnormal state or condition in a mammal.

Summary Of The Invention

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "NOVX" nucleic acid, which represents the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or polypeptide sequences, which represents the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

In one aspect, the invention provides an isolated polypeptide comprising a mature form of a NOVX amino acid. One example is a variant of a mature form of a NOVX amino acid sequence, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed. The amino acid can be, for example, a NOVX amino acid sequence or a variant of a NOVX amino acid sequence, wherein any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed. The invention also includes fragments of any of these. In another aspect, the invention also includes an

isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof.

Also included in the invention is a NOVX polypeptide that is a naturally occurring allelic variant of a NOVX sequence. In one embodiment, the allelic variant includes an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide from a NOVX nucleic acid sequence. In another embodiment, the NOVX polypeptide is a variant polypeptide described therein, wherein any amino acid specified in the chosen sequence is changed to provide a conservative substitution. In one embodiment, the invention discloses a method for determining the presence or amount of the NOVX polypeptide in a sample. The method involves the steps of: providing a sample; introducing the sample to an antibody that binds immunospecifically to the polypeptide; and determining the presence or amount of antibody bound to the NOVX polypeptide, thereby determining the presence or amount of the NOVX polypeptide in the sample. In another embodiment, the invention provides a method for determining the presence of or predisposition to a disease associated with altered levels of a NOVX polypeptide in a mammalian subject. This method involves the steps of: measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and comparing the amount of the polypeptide in the sample of the first step to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, the disease, wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

In a further embodiment, the invention includes a method of identifying an agent that binds to a NOVX polypeptide. This method involves the steps of: introducing the polypeptide to the agent; and determining whether the agent binds to the polypeptide. In various embodiments, the agent is a cellular receptor or a downstream effector.

In another aspect, the invention provides a method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of a NOVX polypeptide. The method involves the steps of: providing a cell expressing the NOVX polypeptide and having a property or function ascribable to the polypeptide; contacting the cell with a composition comprising a candidate substance; and determining whether the substance alters the property or function ascribable to the polypeptide; whereby, if an alteration observed in the presence of the substance is not observed when the cell is contacted with a

composition devoid of the substance, the substance is identified as a potential therapeutic agent. In another aspect, the invention describes a method for screening for a modulator of activity or of latency or predisposition to a pathology associated with the NOVX polypeptide. This method involves the following steps: administering a test compound to a test animal at increased risk for a pathology associated with the NOVX polypeptide, wherein the test animal recombinantly expresses the NOVX polypeptide. This method involves the steps of measuring the activity of the NOVX polypeptide in the test animal after administering the compound of step; and comparing the activity of the protein in the test animal with the activity of the NOVX polypeptide in a control animal not administered the polypeptide, wherein a change in the activity of the NOVX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of, or predisposition to, a pathology associated with the NOVX polypeptide. In one embodiment, the test animal is a recombinant test animal that expresses a test protein transgene or expresses the transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein the promoter is not the native gene promoter of the transgene. In another aspect, the invention includes a method for modulating the activity of the NOVX polypeptide, the method comprising introducing a cell sample expressing the NOVX polypeptide with a compound that binds to the polypeptide in an amount sufficient to modulate the activity of the polypeptide.

The invention also includes an isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof. In a preferred embodiment, the nucleic acid molecule comprises the nucleotide sequence of a naturally occurring allelic nucleic acid variant. In another embodiment, the nucleic acid encodes a variant polypeptide, wherein the variant polypeptide has the polypeptide sequence of a naturally occurring polypeptide variant. In another embodiment, the nucleic acid molecule differs by a single nucleotide from a NOVX nucleic acid sequence. In one embodiment, the NOVX nucleic acid molecule hybridizes under stringent conditions to the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement of the nucleotide sequence. In another aspect, the invention provides a vector or a cell expressing a NOVX nucleotide sequence.

In one embodiment, the invention discloses a method for modulating the activity of a NOVX polypeptide. The method includes the steps of: introducing a cell sample expressing the NOVX polypeptide with a compound that binds to the polypeptide in an amount sufficient to modulate the activity of the polypeptide. In another embodiment, the

invention includes an isolated NOVX nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising a NOVX amino acid sequence or a variant of a mature form of the NOVX amino acid sequence, wherein any amino acid in the mature form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed. In another embodiment, the invention includes an amino acid sequence that is a variant of the NOVX amino acid sequence, in which any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed.

10 In one embodiment, the invention discloses a NOVX nucleic acid fragment encoding at least a portion of a NOVX polypeptide or any variant of the polypeptide, wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed. In another embodiment, the invention includes the complement of any of the NOVX
15 nucleic acid molecules or a naturally occurring allelic nucleic acid variant. In another embodiment, the invention discloses a NOVX nucleic acid molecule that encodes a variant polypeptide, wherein the variant polypeptide has the polypeptide sequence of a naturally occurring polypeptide variant. In another embodiment, the invention discloses a NOVX nucleic acid, wherein the nucleic acid molecule differs by a single nucleotide from a
20 NOVX nucleic acid sequence.

In another aspect, the invention includes a NOVX nucleic acid, wherein one or more nucleotides in the NOVX nucleotide sequence is changed to a different nucleotide provided that no more than 15% of the nucleotides are so changed. In one embodiment, the invention discloses a nucleic acid fragment of the NOVX nucleotide sequence and a
25 nucleic acid fragment wherein one or more nucleotides in the NOVX nucleotide sequence is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed. In another embodiment, the invention includes a nucleic acid molecule wherein the nucleic acid molecule hybridizes under stringent conditions to a NOVX nucleotide sequence or a
30 complement of the NOVX nucleotide sequence. In one embodiment, the invention includes a nucleic acid molecule, wherein the sequence is changed such that no more than 15% of the nucleotides in the coding sequence differ from the NOVX nucleotide sequence or a fragment thereof.

In a further aspect, the invention includes a method for determining the presence or amount of the NOVX nucleic acid in a sample. The method involves the steps of: providing the sample; introducing the sample to a probe that binds to the nucleic acid molecule; and determining the presence or amount of the probe bound to the NOVX nucleic acid molecule, thereby determining the presence or amount of the NOVX nucleic acid molecule in the sample. In one embodiment, the presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

In another aspect, the invention discloses a method for determining the presence of or predisposition to a disease associated with altered levels of the NOVX nucleic acid molecule of in a first mammalian subject. The method involves the steps of: measuring the amount of NOVX nucleic acid in a sample from the first mammalian subject; and comparing the amount of the nucleic acid in the sample of step (a) to the amount of NOVX nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease; wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Detailed Description Of The Invention

The present invention provides novel nucleotides and polypeptides encoded thereby. Included in the invention are the novel nucleic acid sequences, their encoded polypeptides, antibodies, and other related compounds. The sequences are collectively

referred to herein as "NOVX nucleic acids" or "NOVX polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table 1 provides a summary of the NOVX nucleic acids and their encoded polypeptides.

TABLE 1. Sequences and Corresponding SEQ ID Numbers

NOVX No.	Internal Acc. No.	Nucleic Acid SEQ ID NO.	Amino Acid SEQ ID NO.	Homology
1a	CG58522-01	1	2	human platelet activating factor acetylhydrolase
2a	CG58520-01	3	4	GABA(A) receptor
2b	CG58520-02	5	6	GABA(A) receptor
2c	CG58520-03	7	8	GABA(A) receptor
3a	CG58518-01	9	10	GABA(A) receptor
4a	CG58516-01	11	12	Beta transducin
5a	CG58473-01	13	14	Protein kinase
6a	CG58470-01	15	16	UDP-N-acetylhexosamine pyrophosphorylase
7a	CG58593-01	17	18	ubiquitin 52 like
8a	CG57871-01	19	20	tousled like kinase like
9a	CG58590-01	21	22	guanylate kinase like
9b	CG58590-02	23	24	guanylate kinase like
10a	CG58572-01	25	26	glucosamine phosphate N acetyltransferase like
10b	CG58572-02	27	28	glucosamine phosphate N acetyltransferase like
11a	CG58564-01	29	30	Protein tyrosine phosphatase like
11b	CG58564-02	31	32	Protein tyrosine phosphatase like
11c	CG58564-03	33	34	Dual-Specificity phosphatase like
11d	CG58564-04	35	36	Dual-Specificity phosphatase like
12a	CG57819-01	37	38	RPGR interacting protein 1 like
13a	CG57789-01	39	40	RAS like protein RRP22 like
13b	CG57789-02	41	42	RAS like protein RRP22 like
14a	CG57758-01	43	44	sodium/lithium dependent dicarboxylate transporter like
14b	CG57758-02	45	46	sodium/lithium

				dependent dicarboxylate transporter like
14c	CG57758-03	47	48	sodium/lithium dependent dicarboxylate transporter like
14d	CG57758-04	49	50	sodium/lithium dependent dicarboxylate transporter like
14e	CG57758-05	51	52	sodium/lithium dependent dicarboxylate transporter like
15a	CG57732-01	53	54	Ca 2+ calmodulin dependent protein kinase IV kinase like
15b	CG57732-02	55	56	Ca 2+ calmodulin dependent protein kinase IV kinase like
15c	CG57732-03	57	58	Ca 2+ calmodulin dependent protein kinase IV kinase like
16a	CG57709-01	59	60	TCE2 like
17a	CG57700-01	61	62	hydroxyacylglutathione hydrolase like
17b	CG57700-02	63	64	hydroxyacylglutathione hydrolase like
17c	CG57700-03	65	66	hydroxyacylglutathione hydrolase like
17d	CG57700-04	67	68	hydroxyacylglutathione hydrolase like
18a	CG58553-01	69	70	vasopressin receptor like
19a	CG58626-01	71	72	phosphatidic acid preferring phospholipase A1 like
20a	CG57597-01	73	74	hypothetical protein like
21a	CG57804-01	75	76	Talin like
22a	CG57551-01	77	78	NAC-1 like
23a	CG57411-01	79	80	Kelch like
24a	CG57399-01	81	82	phospholipase ADRAB-B precursor like
24b	CG57399-02	83	84	phospholipase ADRAB-B precursor like
24c	CG57399-03	85	86	phospholipase ADRAB-B precursor like
25a	CG59311-01	87	88	acyl-coenzyme A thioester hydrolase

25b	CG59311-02	89	90	peroxisomal acyl-coenzyme A thioester hydrolase like
25c	CG59311-03	91	92	peroxisomal acyl-coenzyme A thioester hydrolase like
26a	CG59309-01	93	94	acyl-coenzyme A thioester hydrolase
27a	CG57364-01	95	96	CG6896
28a	CG59348-01	97	98	cytoplasmic protein (patent calls this Cyclin L-like)
29a	CG59245-01	99	100	glucose 6-phosphatase
29b	CG59245-02	101	102	glucose 6-phosphatase
30a	CG59241-01	103	104	Amiloride-sensitive sodium channel
31a	CG58602-01	105	106	FAD binding domain containing protein
32a	CG58468-01	107	108	Serum Amyloid Protein
33a	CG58183-01	109	110	N-Methyl-D-Aspartate receptor
34a	CG59315-01	111	112	Connexin
35a	CG59203-01	113	114	lysozyme C
35b	CG59203-02	115	116	lysozyme C
36a	CG58662-01	117	118	cytoplasmic protein
36b	CG58662-02	119	120	cytoplasmic protein
37a	CG58584-01	121	122	40S ribosomal protein S29 like
38a	CG58538-01	123	124	Histone deacetylase complex protein 66 like
39a	CG59371-01	125	126	expressed cytoplasmic protein like
40a	CG59346-01	127	128	cortactin binding protein 1 like
41a	CG57814-01	129	130	Basic I 19 like homo sapiens
41b	CG57814-02	131	132	Basic I 19 like homo sapiens
42a	CG59327-01	133	134	Monocarboxylate transporter 1 like
43a	CG59494-01	135	136	myelin P2 like
44a	CG59432-01	137	138	chloride channel like
44b	CG59432-02	139	140	chloride channel like
45a	CG59394-01	141	142	GPCR like
46a	CG59383-01	143	144	D6MM5E PROTEIN like
46b	CG59383-02	145	146	D6MM5E PROTEIN like
47a	CG58526-01	147	148	scramblase like
48a	CG57851-01	149	150	sulfotransferase like
49a	CG59377-01	151	152	epsin like
50a	CG59258-01	153	154	transcriptional activator like
51a	CG59492-01	155	156	Myosin Head (Motor

				Domain) like
52a	CG59564-01	157	158	Sorting nexin 6 like
53a	CG59553-01	159	160	Secretory protein SEC8 like
54a	CG59545-01	161	162	Placental protein 13 like
55a	CG59435-01	163	164	Nedd-1 like
55b	CG59435-02	165	166	Nedd-1 like
56a	CG59439-01	167	168	Xenobiotic/medium-chain fatty acid:CoA ligase form XL-III like
56b	CG59439-02	169	170	Xenobiotic/medium-chain fatty acid:CoA ligase form XL-III like
57a	CG59354-01	171	172	phosducin like
57b	CG59354-02	173	174	phosducin like
57c	CG59354-03	175	176	phosducin like
58a	CG59319-01	177	178	phosducin like
58b	CG59319-02	179	180	phosducin like
59a	CG59576-01	181	182	GPCR like
60a	CG59557-01	183	184	GPCR like
61a	CG59555-01	185	186	GPCR like
62a	CG59551-01	187	188	GPCR like
63a	CG59540-01	189	190	GPCR like
64a	CG59280-01	191	192	GPCR like
64b	CG59280-02	193	194	GPCR like
65a	CG59568-01	195	196	GPCR like
66a	CG59224-01	197	198	GPCR like
67a	CG59222-01	199	200	GPCR like
68a	CG59220-01	201	202	GPCR like
69a	CG59218-01	203	204	GPCR like
70a	CG59216-01	205	206	GPCR like
71a	CG59214-01	207	208	GPCR like
72a	CG59211-01	209	210	GPCR like
73a	CG59276-01	211	212	Dihydroorotate dehydrogenase like
74a	CG59268-01	213	214	monooxygenase like
75a	CG59549-01	215	216	H326 like (cytoplasmic protein with WD repeat domain)
76a	CG59641-01	217	218	Acetyl-CoA Carboxylase 2 like
77a	CG59630-01	219	220	Midnolin like
78a	CG59561-01	221	222	ACYL COENZYME A THIOESTER HYDROLASE like
79a	CG59452-01	223	224	CELL PROLIFERATION RELATED PROTEIN CAP like
80a	CG59572-01	225	226	Pseudouridine Synthase 3 like
80b	CG59572-02	227	228	Pseudouridine Synthase 3 like

81a	CG59522-01	229	230	Myosin like
82a	CG59520-01	231	232	Farnesyl-pyrophosphate synthetase like
83a	CG59758-01	233	234	UBIQUITIN like
83b	CG59758-02	235	236	UBIQUITIN like
84a	CG59586-01	237	238	glucokinase like
85a	CG59704-01	239	240	serine/threonine kinase like
86a	CG59628-01	241	242	Short-chain dehydrogenase like
87a	CG59516-01	243	244	Calponin like
87b	CG59516-02	245	246	Calponin like
88a	CG59671-02	247	248	acyl-coenzyme A thioester hydrolase
89a	CG56870-01	249	250	NDRG3 like
89b	CG56870-02	251	252	NDRG3 like
89c	CG56870-03	253	254	NDRG3 like
89d	CG56870-04	255	256	NDRG3 like
89e	CG56870-05	257	258	NDRG3 like
90a	CG59764-01	259	260	Ferritin like
91a	CG59710-01	261	262	P14 like
92a	CG59754-02	263	264	Downs syndrome cell adhesion molecule like
92b	CG59754-01	265	266	Downs syndrome cell adhesion molecule like
93a	CG59800-01	267	268	HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-3B like
94a	CG59761-01	269	270	AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) like
95a	CG59756-01	271	272	JUNCTOPHILIN TYPE 2 like
96a	CG59708-01	273	274	Ubiquitin carboxyl-terminal hydrolase 21 like
96b	CG59708-02	275	276	Ubiquitin carboxyl-terminal hydrolase 21 like
96c	CG59708-03	277	278	Ubiquitin carboxyl-terminal hydrolase 21 like
97a	CG59559-01	279	280	BA12M19.1.3 like
98a	CG59669-01	281	282	carbonyl reductase (called NADPH-dependent carbonyl reductase-like in patent)
99a	CG58624-01	283	284	metal transporter
100a	CG59679-01	285	286	carbonyl reductase

101a	CG59644-01	287	288	CG12091 (putative protein phosphatase)
102a	CG59662-01	289	290	Cyclophilin
103a	CG59773-01	291	292	Myomegalin
103b	CG59773-02	293	294	Myomegalin
103c	CG59773-03	295	296	Myomegalin
104a	CG57460-01	297	298	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE like
105a	CG57464-01	299	300	N-ACETYLTRANSFERASE like
106a	CG57466-01	301	302	Acetylglucosaminyltransferase like
107a	CG57468-01	303	304	ABC transporter like homo sapiens
108a	CG59609-01	305	306	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A like
109a	CG59613-01	307	308	Proliferating cell nuclear antigen like
110a	CG59619-01	309	310	CYTOPLASMIC ACTIN 2 like
111a	CG59621-01	311	312	SELENOPHOSPHATASE SYNTHETASE like
112a	CG59625-01	313	314	glucose transporter like
113a	CG59887-01	315	316	Amino Acid/Metabolite Permease like
113b	CG59887-02	317	318	Amino Acid/Metabolite Permease like
114a	CG59861-01	319	320	RIBULOSE-5-PHOSPHATE-EPIMERASE like
114b	CG59861-02	321	322	RIBULOSE-5-PHOSPHATE-EPIMERASE like
115a	CG59857-01	323	324	Rhotekin like homo sapiens
116a	CG59855-01	325	326	ATP SYNTHASE SUBUNIT C like
116b	CG59855-02	327	328	ATP SYNTHASE SUBUNIT C like
117a	CG59807-01	329	330	Zinc finger like
118a	CG59805-01	331	332	Zinc finger like
119a	CG59928-01	333	334	Universal Stress (USP) Domain Containing Protein like
120a	CG59947-01	335	336	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) like
121a	CG59938-01	337	338	arylsulfatase like homo sapiens
122a	CG59746-01	339	340	ubiquitin-specific

				processing protease like homo sapiens
123a	CG88613-01	341	342	INOSITOL 1,4,5- TRISPHOSPHATE 3- KINASE ISOENZYME like
124a	CG59993-01	343	344	synaptotagmin II like
124b	CG59993-02	345	346	synaptotagmin II like
125a	CG59991-01	347	348	ooplasm specific protein like
126a	CG59987-01	349	350	GTP-RHO binding protein 1 (rhopilin) like
126b	CG59987-02	351	352	GTP-RHO binding protein 1 (rhopilin) like
127a	CG59971-01	353	354	Leucine rich repeat (LRR) like
127b	CG59971-02	355	356	Leucine rich repeat (LRR) like

Table 1 indicates homology of NOVX nucleic acids to known protein families. Thus, the nucleic acids and polypeptides, antibodies and related compounds according to the invention corresponding to a NOVX as identified in column 1 of Table 1 will be useful in therapeutic and diagnostic applications implicated in, for example, pathologies and disorders associated with the known protein families identified in column 5 of Table 1.

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

Consistent with other known members of the family of proteins, identified in column 5 of Table 1, the NOVX polypeptides of the present invention show homology to, and contain domains that are characteristic of, other members of such protein families. Details of the sequence relatedness and domain analysis for each NOVX are presented in Example A.

The NOVX nucleic acids and polypeptides can also be used to screen for molecules, which inhibit or enhance NOVX activity or function. Specifically, the nucleic acids and polypeptides according to the invention may be used as targets for the

identification of small molecules that modulate or inhibit diseases associated with the protein families listed in Table 1.

The NOVX nucleic acids and polypeptides are also useful for detecting specific cell types. Details of the expression analysis for each NOVX are presented in Example C.

5 Accordingly, the NOVX nucleic acids, polypeptides, antibodies and related compounds according to the invention will have diagnostic and therapeutic applications in the detection of a variety of diseases with differential expression in normal vs. diseased tissues, e.g. a variety of cancers.

Additional utilities for NOVX nucleic acids and polypeptides according to the
10 invention are disclosed herein.

The present invention is based on the identification of biological macromolecules differentially modulated in a pathologic state, disease, or an abnormal condition or state. Among the pathologies or diseases of present interest include metabolic diseases including those related to endocrinologic disorders, cancers, various tumors and neoplasias, inflammatory disorders, central nervous system disorders, and similar abnormal conditions or states. In very significant embodiments of the present invention, the biological macromolecules implicated in the pathologies and conditions are proteins and polypeptides, and in such cases the present invention is related as well to the nucleic acids that encode them. Methods that may be employed to identify relevant biological macromolecules include any procedures that detect differential expression of nucleic acids encoding proteins and polypeptides associated with the disorder, as well as procedures that detect the respective proteins and polypeptides themselves. Significant methods that have been employed by the present inventors, include GeneCalling ® technology and SeqCalling TM technology, disclosed respectively, in U. S. Patent No. 5,871,697, and in U. S. Ser. No. 09/417,386, filed Oct. 13, 1999, each of which is incorporated herein by reference in its entirety. GeneCalling ® is also described in Shimkets, et al., "Gene expression analysis by transcript profiling coupled to a gene database query" Nature Biotechnology 17:198-803 (1999).

The invention provides polypeptides and nucleotides encoded thereby that have been identified as having novel associations with a disease or pathology, or an abnormal state or condition, in a mammal. The present invention further identifies a set of proteins and polypeptides, including naturally occurring polypeptides, precursor forms or proproteins, or mature forms of the polypeptides or proteins, which are implicated as targets for therapeutic agents in the treatment of various diseases, pathologies, abnormal

states and conditions. A target may be employed in any of a variety of screening methodologies in order to identify candidate therapeutic agents which interact with the target and in so doing exert a desired or favorable effect. The candidate therapeutic agent is identified by screening a large collection of substances or compounds in an important embodiment of the invention. Such a collection may comprise a combinatorial library of substances or compounds in which, in at least one subset of substances or compounds, the individual members are related to each other by simple structural variations based on a particular canonical or basic chemical structure. The variations may include, by way of nonlimiting example, changes in length or identity of a basic framework of bonded atoms; changes in number, composition and disposition of ringed structures, bridge structures, alicyclic rings, and aromatic rings; and changes in pendent or substituents atoms or groups that are bonded at particular positions to the basic framework of bonded atoms or to the ringed structures, the bridge structures, the alicyclic structures, or the aromatic structures.

A polypeptide or protein described herein, and that serves as a target in the screening procedure, includes the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, e.g., the full-length gene product, encoded by the corresponding gene. The naturally occurring polypeptide also includes the polypeptide, precursor or proprotein encoded by an open reading frame described herein. A "mature" form of a polypeptide or protein arises as a result of one or more naturally occurring processing steps as they may occur within the cell, including a host cell. The processing steps occur as the gene product arises, e.g., via cleavage of the amino-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus, a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an amino-terminal signal sequence from residue 1 to residue M is cleaved, includes the residues from residue M+1 to residue N remaining. A "mature" form of a polypeptide or protein may also arise from non-proteolytic post-translational modification. Such non-proteolytic processes include, e.g., glycosylation, myristylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or the combination of any of them.

As used herein, "identical" residues correspond to those residues in a comparison between two sequences where the equivalent nucleotide base or amino acid residue in an

alignment of two sequences is the same residue. Residues are alternatively described as “similar” or “positive” when the comparisons between two sequences in an alignment show that residues in an equivalent position in a comparison are either the same amino acid or a conserved amino acid as defined below.

5 As used herein, a “chemical composition” relates to a composition including at least one compound that is either synthesized or extracted from a natural source. A chemical compound may be the product of a defined synthetic procedure. Such a synthesized compound is understood herein to have defined properties in terms of molecular formula, molecular structure relating the association of bonded atoms to each other, physical
10 properties such as chromatographic or spectroscopic characterizations, and the like. A compound extracted from a natural source is advantageously analyzed by chemical and physical methods in order to provide a representation of its defined properties, including its molecular formula, molecular structure relating the association of bonded atoms to each other, physical properties such as chromatographic or spectroscopic characterizations, and
15 the like.

 As used herein, a “candidate therapeutic agent” is a chemical compound that includes at least one substance shown to bind to a target biopolymer. In important embodiments of the invention, the target biopolymer is a protein or polypeptide, a nucleic acid, a polysaccharide or proteoglycan, or a lipid such as a complex lipid. The method of
20 identifying compounds that bind to the target effectively eliminates compounds with little or no binding affinity, thereby increasing the potential that the identified chemical compound may have beneficial therapeutic applications. In cases where the “candidate therapeutic agent” is a mixture of more than one chemical compound, subsequent screening procedures may be carried out to identify the particular substance in the mixture that is the
25 binding compound, and that is to be identified as a candidate therapeutic agent.

 As used herein, a “pharmaceutical agent” is provided by screening a candidate therapeutic agent using models for a disease state or pathology in order to identify a candidate exerting a desired or beneficial therapeutic effect with relation to the disease or pathology. Such a candidate that successfully provides such an effect is termed a
30 pharmaceutical agent herein. Nonlimiting examples of model systems that may be used in such screens include particular cell lines, cultured cells, tissue preparations, whole tissues, organ preparations, intact organs, and nonhuman mammals. Screens employing at least one system, and preferably more than one system, may be employed in order to identify a

pharmaceutical agent. Any pharmaceutical agent so identified may be pursued in further investigation using human subjects.

NOVX Nucleic Acids and Polypeptides

NOVX clones

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

The NOVX genes and their corresponding encoded proteins are useful for preventing, treating or ameliorating medical conditions, *e.g.*, by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the NOVX genes, based on the tissues in which they are most highly expressed. Uses include developing products for the diagnosis or treatment of a variety of diseases and disorders.

The NOVX nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration *in vitro* and *in vivo* (vi) biological defense weapon.

In one specific embodiment, the invention includes an isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of

the mature form are so changed; (c) an amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 178 wherein any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; and (e) a fragment of any of (a) through (d).

In another specific embodiment, the invention includes an isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a mature form of the amino acid sequence given SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 wherein any amino acid in the mature form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed; (c) the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, in which any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; (e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 or any variant of said polypeptide wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed; and (f) the complement of any of said nucleic acid molecules.

In yet another specific embodiment, the invention includes an isolated nucleic acid molecule, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178; (b) a nucleotide sequence wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed; (c) a nucleic acid fragment of the sequence selected from the group consisting of SEQ ID NO:

2n-1, wherein n is an integer between 1 and 178; and (d) a nucleic acid fragment wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed.

One aspect of the invention pertains to isolated nucleic acid molecules that encode NOVX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify NOVX-encoding nucleic acids (*e.g.*, NOVX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of NOVX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An NOVX nucleic acid can encode a mature NOVX polypeptide. As used herein, a "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional

processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term "probes", as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated NOVX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 as a hybridization probe, NOVX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

Furthermore, oligonucleotides corresponding to NOVX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term “oligonucleotide” refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue.

Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a portion of this nucleotide sequence (e.g., a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an NOVX polypeptide). A nucleic acid molecule that is complementary to the nucleotide sequence from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is one that is sufficiently complementary to the nucleotide sequence from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 that it can hydrogen bond with little or no mismatches to the nucleotide sequence from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, thereby forming a stable duplex.

As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of

another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

A full-length NOVX clone is identified as containing an ATG translation start codon and an in-frame stop codon. Any disclosed NOVX nucleotide sequence lacking an ATG start codon therefore encodes a truncated C-terminal fragment of the respective NOVX polypeptide, and requires that the corresponding full-length cDNA extend in the 5' direction of the disclosed sequence. Any disclosed NOVX nucleotide sequence lacking an in-frame stop codon similarly encodes a truncated N-terminal fragment of the respective NOVX polypeptide, and requires that the corresponding full-length cDNA extend in the 3' direction of the disclosed sequence.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. *See e.g.*

Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of NOVX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an NOVX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human NOVX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, as well as a polypeptide possessing NOVX biological activity. Various biological activities of the NOVX proteins are described below.

An NOVX polypeptide is encoded by the open reading frame ("ORF") of an NOVX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human NOVX genes allows for the generation of probes and primers designed for use in identifying and/or cloning NOVX homologues in other cell types, *e.g.* from other tissues, as well as NOVX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide

sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178; or an anti-sense strand nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178.

5 Probes based on the human NOVX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues
10 which mis-express an NOVX protein, such as by measuring a level of an NOVX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting NOVX mRNA levels or determining whether a genomic NOVX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an NOVX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity
15 of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of NOVX" can be prepared by isolating a portion SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, that encodes a polypeptide having an NOVX biological activity (the biological activities of the NOVX proteins are described
20 below), expressing the encoded portion of NOVX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of NOVX.

NOVX Nucleic Acid and Polypeptide Variants

25 The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 due to degeneracy of the genetic code and thus encode the same NOVX proteins as that encoded by the nucleotide sequences shown in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178. In another embodiment, an isolated nucleic acid molecule of
30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

In addition to the human NOVX nucleotide sequences shown in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the
35 NOVX polypeptides may exist within a population (*e.g.*, the human population). Such

genetic polymorphism in the NOVX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an NOVX protein, preferably a vertebrate NOVX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the NOVX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the NOVX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the NOVX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding NOVX proteins from other species, and thus that have a nucleotide sequence that differs from the human SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the NOVX cDNAs of the invention can be isolated based on their homology to the human NOVX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding NOVX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures

than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. *See, e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN

MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (e.g., as employed for cross-species hybridizations). See, e.g., Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of NOVX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, thereby leading to changes in the amino acid sequences of the encoded NOVX proteins, without altering the functional ability of said NOVX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence SEQ ID NO: 2n, wherein n is an integer between 1 and 178. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the NOVX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the NOVX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity. Such NOVX proteins differ in amino acid sequence from SEQ ID NO: 2n-1, wherein n is an

integer between 1 and 178 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences SEQ ID NO: 2n, wherein n is an integer between 1 and 178. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178; more preferably at least about 70% homologous SEQ ID NO: 2n, wherein n is an integer between 1 and 178; still more preferably at least about 80% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178; even more preferably at least about 90% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178; and most preferably at least about 95% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

An isolated nucleic acid molecule encoding an NOVX protein homologous to the protein of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the NOVX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an NOVX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for NOVX biological activity to identify mutants that retain activity. Following mutagenesis

SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant NOVX protein can be assayed for (i) the ability to form protein:protein interactions with other NOVX proteins, other cell-surface proteins, or biologically-active portions thereof, (ii) complex formation between a mutant NOVX protein and an NOVX ligand; or (iii) the ability of a mutant NOVX protein to bind to an intracellular target protein or biologically-active portion thereof; (e.g. avidin proteins).

In yet another embodiment, a mutant NOVX protein can be assayed for the ability to regulate a specific biological function (e.g., regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire NOVX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an NOVX protein of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, or antisense nucleic acids complementary to an NOVX nucleic acid sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an NOVX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the NOVX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the NOVX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of NOVX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of NOVX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of NOVX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil,

5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v),
5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and
2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically
using an expression vector into which a nucleic acid has been subcloned in an antisense
5 orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense
orientation to a target nucleic acid of interest, described further in the following
subsection).

The antisense nucleic acid molecules of the invention are typically administered to
a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or
10 genomic DNA encoding an NOVX protein to thereby inhibit expression of the protein
(*e.g.*, by inhibiting transcription and/or translation). The hybridization can be by
conventional nucleotide complementarity to form a stable duplex, or, for example, in the
case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific
interactions in the major groove of the double helix. An example of a route of
15 administration of antisense nucleic acid molecules of the invention includes direct
injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to
target selected cells and then administered systemically. For example, for systemic
administration, antisense molecules can be modified such that they specifically bind to
receptors or antigens expressed on a selected cell surface (*e.g.*, by linking the antisense
20 nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or
antigens). The antisense nucleic acid molecules can also be delivered to cells using the
vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in
which the antisense nucleic acid molecule is placed under the control of a strong pol II or
pol III promoter are preferred.

25 In yet another embodiment, the antisense nucleic acid molecule of the invention is
an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific
double-stranded hybrids with complementary RNA in which, contrary to the usual β -units,
the strands run parallel to each other. *See, e.g.*, Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**:
6625-6641. The antisense nucleic acid molecule can also comprise a
30 2'-o-methylribonucleotide (*See, e.g.*, Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or
a chimeric RNA-DNA analogue (*See, e.g.*, Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330).

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave NOVX mRNA transcripts to thereby inhibit translation of NOVX mRNA. A ribozyme having specificity for an NOVX-encoding nucleic acid can be designed based upon the nucleotide sequence of an NOVX cDNA disclosed herein (*i.e.*, SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an NOVX-encoding mRNA. *See, e.g.*, U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* NOVX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. *See, e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, NOVX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the NOVX nucleic acid (*e.g.*, the NOVX promoter and/or enhancers) to form triple helical structures that prevent transcription of the NOVX gene in target cells. *See, e.g.*, Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the NOVX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. *See, e.g.*, Hyrup, *et al.*, 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural

nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, *et al.*, 1996. *supra*; Perry-O'Keefe, *et al.*, 1996. *Proc.*

5 *Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of NOVX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of NOVX can also be used, for example, in the analysis of
10 single base pair mutations in a gene (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S₁ nucleases (*See*, Hyrup, *et al.*, 1996. *supra*); or as probes or primers for DNA sequence and hybridization (*See*, Hyrup, *et al.*, 1996, *supra*; Perry-O'Keefe, *et al.*, 1996. *supra*).

In another embodiment, PNAs of NOVX can be modified, *e.g.*, to enhance their
15 stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of NOVX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the
20 DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (*see*, Hyrup, *et al.*, 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.*, 1996. *supra* and Finn, *et al.*, 1996. *Nucl Acids Res* 24: 3357-3363. For
25 example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. *See, e.g.*, Mag, *et al.*, 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule
30 with a 5' PNA segment and a 3' DNA segment. *See, e.g.*, Finn, *et al.*, 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.*, Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as

peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.*, Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.*, Krol, *et al.*, 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g.*, Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

NOVX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of NOVX polypeptides whose sequences are provided in SEQ ID NO: 2n, wherein n is an integer between 1 and 178. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178 while still encoding a protein that maintains its NOVX activities and physiological functions, or a functional fragment thereof.

In general, an NOVX variant that preserves NOVX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated NOVX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-NOVX antibodies. In one embodiment, native NOVX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, NOVX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an NOVX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the NOVX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language

5 "substantially free of cellular material" includes preparations of NOVX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of NOVX proteins having less than about 30% (by dry weight) of non-NOVX proteins (also referred to herein as a "contaminating protein"), more

10 preferably less than about 20% of non-NOVX proteins, still more preferably less than about 10% of non-NOVX proteins, and most preferably less than about 5% of non-NOVX proteins. When the NOVX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably

15 less than about 5% of the volume of the NOVX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one

20 embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins having less than about 30% (by dry weight) of chemical precursors or non-NOVX chemicals, more preferably less than about 20% chemical precursors or non-NOVX chemicals, still more preferably less than about 10% chemical precursors or non-NOVX chemicals, and most preferably less than about 5% chemical precursors or non-NOVX chemicals.

25 Biologically-active portions of NOVX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the NOVX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178) that include fewer amino acids than the full-length NOVX proteins, and exhibit at least one activity of an NOVX protein. Typically, biologically-

30 active portions comprise a domain or motif with at least one activity of the NOVX protein. A biologically-active portion of an NOVX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native NOVX protein.

In an embodiment, the NOVX protein has an amino acid sequence shown SEQ ID NO: 2n, wherein n is an integer between 1 and 178. In other embodiments, the NOVX protein is substantially homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178, and retains the functional activity of the protein of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the NOVX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NO: 2n, wherein n is an integer between 1 and 178, and retains the functional activity of the NOVX proteins of SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

15 **Determining Homology Between Two or More Sequences**

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. *See*, Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

15 **Chimeric and Fusion Proteins**

The invention also provides NOVX chimeric or fusion proteins. As used herein, an NOVX "chimeric protein" or "fusion protein" comprises an NOVX polypeptide operatively-linked to a non-NOVX polypeptide. An "NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an NOVX protein SEQ ID NO: 2n, wherein n is an integer between 1 and 178, whereas a "non-NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the NOVX protein, *e.g.*, a protein that is different from the NOVX protein and that is derived from the same or a different organism. Within an NOVX fusion protein the NOVX polypeptide can correspond to all or a portion of an NOVX protein. In one embodiment, an NOVX fusion protein comprises at least one biologically-active portion of an NOVX protein. In another embodiment, an NOVX fusion protein comprises at least two biologically-active portions of an NOVX protein. In yet another embodiment, an NOVX fusion protein comprises at least three biologically-active portions of an NOVX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the NOVX polypeptide and the non-NOVX polypeptide are fused in-frame with one another. The non-NOVX polypeptide can be fused to the N-terminus or C-terminus of the NOVX polypeptide.

In one embodiment, the fusion protein is a GST-NOVX fusion protein in which the NOVX sequences are fused to the C-terminus of the GST (glutathione S-transferase)

In another embodiment, the fusion protein is an NOVX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of NOVX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an NOVX-immunoglobulin fusion protein in which the NOVX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The NOVX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an NOVX ligand and an NOVX protein on the surface of a cell, to thereby suppress NOVX-mediated signal transduction *in vivo*. The NOVX-immunoglobulin fusion proteins can be used to affect the bioavailability of an NOVX cognate ligand. Inhibition of the NOVX ligand/NOVX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the NOVX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-NOVX antibodies in a subject, to purify NOVX ligands, and in screening assays to identify molecules that inhibit the interaction of NOVX with an NOVX ligand.

An NOVX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.*, Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An NOVX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the NOVX protein.

NOVX Agonists and Antagonists

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The invention also pertains to variants of the NOVX proteins that function as either
5 NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists. Variants of the NOVX protein
can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the NOVX
protein). An agonist of the NOVX protein can retain substantially the same, or a subset of,
the biological activities of the naturally occurring form of the NOVX protein. An
antagonist of the NOVX protein can inhibit one or more of the activities of the naturally
10 occurring form of the NOVX protein by, for example, competitively binding to a
downstream or upstream member of a cellular signaling cascade which includes the NOVX
protein. Thus, specific biological effects can be elicited by treatment with a variant of
limited function. In one embodiment, treatment of a subject with a variant having a subset
of the biological activities of the naturally occurring form of the protein has fewer side
15 effects in a subject relative to treatment with the naturally occurring form of the NOVX
proteins.

Variants of the NOVX proteins that function as either NOVX agonists (*i.e.*,
mimetics) or as NOVX antagonists can be identified by screening combinatorial libraries of
mutants (*e.g.*, truncation mutants) of the NOVX proteins for NOVX protein agonist or
20 antagonist activity. In one embodiment, a variegated library of NOVX variants is
generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a
variegated gene library. A variegated library of NOVX variants can be produced by, for
example, enzymatically ligating a mixture of synthetic oligonucleotides into gene
sequences such that a degenerate set of potential NOVX sequences is expressible as
25 individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage
display) containing the set of NOVX sequences therein. There are a variety of methods
which can be used to produce libraries of potential NOVX variants from a degenerate
oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be
performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an
30 appropriate expression vector. Use of a degenerate set of genes allows for the provision, in
one mixture, of all of the sequences encoding the desired set of potential NOVX sequences.
Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See*,
e.g., Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323;
Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the NOVX protein coding sequences can be used to generate a variegated population of NOVX fragments for screening and subsequent selection of variants of an NOVX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an NOVX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S_1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the NOVX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of NOVX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify NOVX variants. *See, e.g., Arkin and Yourvan, 1992. Proc. Natl. Acad. Sci. USA 89: 7811-7815; Delgrave, et al., 1993. Protein Engineering 6:327-331.*

NOVX Antibodies

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single

chain, F_{ab}, F_{ab}' and F_{(ab)2} fragments, and an F_{ab} expression library. In general, antibody molecules obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated protein of the invention intended to serve as an antigen, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of NOVX that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human NOVX protein sequence will indicate which regions of a NOVX polypeptide are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety. Antibodies that are specific for one or more domains within an

antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that
5 immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor
10 Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g.,
15 rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may
20 be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete
25 and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose
30 dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide

primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D.

- 5 Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8
(April 17, 2000), pp. 25-28).

Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium

for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a

5 medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is
15 determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). It is an objective, especially important in therapeutic
20 applications of monoclonal antibodies, to identify antibodies having a high degree of specificity and a high binding affinity for the target antigen.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods (Goding, 1986). Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium
25 and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel
30 electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding

the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce

immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will

comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5 Human Antibodies

Fully human antibodies essentially relate to antibody molecules in which the entire sequence of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al, (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light

immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_(ab)2 fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_(ab)2 fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least

part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well

as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted
5 cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include
10 iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector
15 function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992).
20 Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al.,
25 Anti-Cancer Drug Design, 3: 219-230 (1989).

Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an
30 enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A

chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the
 5 tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as
 10 dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin
 15 can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such
 20 streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

25 **Immunoliposomes**

The antibodies disclosed herein can also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang et al.,
Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545.
 30 Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the

antibody of the present invention can be conjugated to the liposomes as described in Martin et al., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., J. National Cancer Inst., 81(19): 1484 (1989).

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Diagnostic Applications of Antibodies Directed Against the Proteins of the Invention

Antibodies directed against a protein of the invention may be used in methods known within the art relating to the localization and/or quantitation of the protein (e.g., for use in measuring levels of the protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies against the proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antigen binding domain, are utilized as pharmacologically-active compounds (see below).

An antibody specific for a protein of the invention can be used to isolate the protein by standard techniques, such as immunoaffinity chromatography or immunoprecipitation. Such an antibody can facilitate the purification of the natural protein antigen from cells and of recombinantly produced antigen expressed in host cells. Moreover, such an antibody can be used to detect the antigenic protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the antigenic protein.

Antibodies directed against the protein can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Antibodies of the invention, including polyclonal, monoclonal, humanized and fully human antibodies, may be used as therapeutic agents. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high specificity and high affinity for its target antigen, is administered to the subject and will generally have an effect due to its binding with the target. Such an effect may be one of two kinds, depending on the specific nature of the interaction between the given antibody molecule and the target antigen in question. In the first instance, administration of the antibody may abrogate or inhibit the binding of the target with an endogenous ligand to which it naturally binds. In this case, the antibody binds to the target and masks a binding site of the naturally occurring ligand, wherein the ligand serves as an effector molecule. Thus the receptor mediates a signal transduction pathway for which the ligand is responsible.

Alternatively, the effect may be one in which the antibody elicits a physiological result by virtue of binding to an effector binding site on the target molecule. In this case the target, a receptor having an endogenous ligand which may be absent or defective in the disease or pathology, binds the antibody as a surrogate effector ligand, initiating a receptor-based signal transduction event by the receptor.

A therapeutically effective amount of an antibody of the invention relates generally to the amount needed to achieve a therapeutic objective. As noted above, this may be a binding interaction between the antibody and its target antigen that, in certain cases, interferes with the functioning of the target, and in other cases, promotes a physiological response. The amount required to be administered will furthermore depend on the binding affinity of the antibody for its specific antigen, and will also depend on the rate at which an administered antibody is depleted from the free volume other subject to which it is administered. Common ranges for therapeutically effective dosing of an antibody or antibody fragment of the invention may be, by way of nonlimiting example, from about 0.1 mg/kg body weight to about 50 mg/kg body weight. Common dosing frequencies may range, for example, from twice daily to once a week.

Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a protein of the invention, as well as other molecules identified by the screening assays disclosed herein, can be administered for the treatment of various disorders in the form of pharmaceutical compositions. Principles and

If the antigenic protein is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients can also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions.

The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S.

Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

ELISA Assay

An agent for detecting an analyte protein is an antibody capable of binding to an analyte protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., F_{ab} or $F_{(ab)2}$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. Included within the usage of the term "biological sample", therefore, is blood and a fraction or component of blood including blood serum, blood plasma, or lymph. That is, the detection method of the invention can be used to detect an analyte mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of an analyte mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an analyte protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an analyte genomic DNA include Southern hybridizations. Procedures for conducting immunoassays are described, for example in "ELISA: Theory and Practice: Methods in Molecular Biology", Vol. 42, J. R. Crowther (Ed.) Human Press, Totowa, NJ, 1995; "Immunoassay", E. Diamandis and T. Christopoulos, Academic Press, Inc., San Diego, CA, 1996; and "Practice and Theory of Enzyme Immunoassays", P. Tijssen, Elsevier Science Publishers, Amsterdam, 1985. Furthermore, *in vivo* techniques for detection of an analyte protein include introducing into a subject a labeled anti-analyte protein antibody.

For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

NOVX Recombinant Expression Vectors and Host Cells

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Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an NOVX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

25 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., NOVX proteins, mutant forms of NOVX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of NOVX proteins in prokaryotic or eukaryotic cells. For example, NOVX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5

(Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION

5 TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. *See, e.g.*, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN
10 ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (*see, e.g.*, Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis
15 techniques.

In another embodiment, the NOVX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen
20 Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.). Alternatively, NOVX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

25 In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For
30 example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, *e.g.*, Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to NOVX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.,* Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms

refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

5 A host cell can be any prokaryotic or eukaryotic cell. For example, NOVX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

10 Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found
15 in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

20 For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell
25 on the same vector as that encoding NOVX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

30 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) NOVX protein. Accordingly, the invention further provides methods for producing NOVX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding NOVX protein has been introduced) in a suitable

medium such that NOVX protein is produced. In another embodiment, the method further comprises isolating NOVX protein from the medium or the host cell.

Transgenic NOVX Animals

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The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which NOVX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous NOVX sequences have been introduced into their genome or homologous recombinant animals in which endogenous NOVX sequences have been altered. Such animals are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous NOVX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing NOVX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human NOVX cDNA sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human NOVX gene, such as a mouse NOVX gene, can be isolated based on hybridization to the human NOVX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be

operably-linked to the NOVX transgene to direct expression of NOVX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the NOVX transgene in its genome and/or expression of NOVX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding NOVX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an NOVX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the NOVX gene. The NOVX gene can be a human gene (*e.g.*, the cDNA of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178), but more preferably, is a non-human homologue of a human NOVX gene. For example, a mouse homologue of human NOVX gene of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 can be used to construct a homologous recombination vector suitable for altering an endogenous NOVX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous NOVX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous NOVX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous NOVX protein). In the homologous recombination vector, the altered portion of the NOVX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the NOVX gene to allow for homologous recombination to occur between the exogenous NOVX gene carried by the vector and an endogenous NOVX gene in an embryonic stem cell. The additional flanking NOVX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g.*, Thomas, *et al.*, 1987. *Cell* 51: 503 for a description of homologous

5 The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See, e.g., Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; 15 and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, *See, e.g., Lakso, et al., 1992. Proc. Natl. Acad. Sci. USA* 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae*. *See, O'Gorman, et al., 1991. Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.*

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animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (*e.g.*, the somatic cell) is isolated.

Pharmaceutical Compositions

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The NOVX nucleic acid molecules, NOVX proteins, and anti-NOVX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the

10 nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical

15 Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any

20 conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include

25 parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl

30 alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or

35 multiple dose vials made of glass or plastic.

20 Sterile injectable solutions can be prepared by incorporating the active compound
(*e.g.*, an NOVX protein or anti-NOVX antibody) in the required amount in an appropriate
solvent with one or a combination of ingredients enumerated above, as required, followed
by filtered sterilization. Generally, dispersions are prepared by incorporating the active
compound into a sterile vehicle that contains a basic dispersion medium and the required
25 other ingredients from those enumerated above. In the case of sterile powders for the
preparation of sterile injectable solutions, methods of preparation are vacuum drying and
freeze-drying that yields a powder of the active ingredient plus any additional desired
ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible

binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be

treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express NOVX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect NOVX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an NOVX gene, and to modulate NOVX activity, as described further, below. In addition, the NOVX proteins can be used to screen drugs or compounds that modulate the NOVX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of NOVX protein or production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-NOVX antibodies of the invention can be used to detect and isolate NOVX proteins and modulate NOVX activity. In yet a further aspect, the invention can be used in methods

and modulate NOX activity. In yet a further aspect, the invention can be used in methods

to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

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Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, 10 peptidomimetics, small molecules or other drugs) that bind to NOVX proteins or have a stimulatory or inhibitory effect on, *e.g.*, NOVX protein expression or NOVX protein activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test 15 compounds which bind to or modulate the activity of the membrane-bound form of an NOVX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring 20 deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. *See, e.g.*, Lam, 1997. *Anticancer Drug Design* 12: 145.

25 A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.*, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can 30 be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed.*

Engl. 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an NOVX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the NOVX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the NOVX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the NOVX protein or

biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule. As used herein, a "target molecule" is a molecule with which an NOVX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an NOVX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An NOVX target molecule can be a non-NOVX molecule or an NOVX protein or polypeptide of the invention. In one embodiment, an NOVX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound NOVX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with NOVX.

Determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an NOVX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the NOVX protein or biologically-active portion thereof. Binding of the test compound to the NOVX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to

interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX or biologically-active portion thereof as compared to the known compound.

- 5 In still another embodiment, an assay is a cell-free assay comprising contacting NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX can be accomplished, for example, by
- 10 determining the ability of the NOVX protein to bind to an NOVX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of NOVX protein can be accomplished by determining the ability of the NOVX protein further modulate an NOVX target molecule. For example, the catalytic/enzymatic activity
- 15 of the target molecule on an appropriate substrate can be determined as described, *supra*.

- In yet another embodiment, the cell-free assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein
- 20 determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the NOVX protein to preferentially bind to or modulate the activity of an NOVX target molecule.

- The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the
- 25 membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of NOVX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®],
- 30 Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

 In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either NOVX protein or its target molecule to facilitate

5 reactants. Examples of such vessels include microtiter plates, test tubes, and
micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a
domain that allows one or both of the proteins to be bound to a matrix. For example, GST-
NOVX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione
sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter
10 plates, that are then combined with the test compound or the test compound and either the
non-adsorbed target protein or NOVX protein, and the mixture is incubated under
conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and
pH). Following incubation, the beads or microtiter plate wells are washed to remove any
unbound components, the matrix immobilized in the case of beads, complex determined
15 either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes
can be dissociated from the matrix, and the level of NOVX protein binding or activity
determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the NOVX protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated NOVX protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with NOVX protein or target molecules, but which do not interfere with binding of the NOVX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or NOVX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the NOVX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the NOVX protein or target molecule.

In another embodiment, modulators of NOVX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of NOVX mRNA or protein in the cell is determined. The level of expression of NOVX

mRNA or protein in the presence of the candidate compound is compared to the level of expression of NOVX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of NOVX mRNA or protein expression based upon this comparison. For example, when expression of NOVX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of NOVX mRNA or protein expression. Alternatively, when expression of NOVX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of NOVX mRNA or protein expression. The level of NOVX mRNA or protein expression in the cells can be determined by methods described herein for detecting NOVX mRNA or protein.

In yet another aspect of the invention, the NOVX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with NOVX ("NOVX-binding proteins" or "NOVX-bp") and modulate NOVX activity. Such NOVX-binding proteins are also likely to be involved in the propagation of signals by the NOVX proteins as, for example, upstream or downstream elements of the NOVX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for NOVX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an NOVX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with NOVX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

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Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

10

Chromosome Mapping

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Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the NOVX sequences, SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments or derivatives thereof, can be used to map the location of the NOVX genes, respectively, on a chromosome. The mapping of the NOVX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

20

Briefly, NOVX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the NOVX sequences. Computer analysis of the NOVX sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the NOVX sequences will yield an amplified fragment.

25

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (e.g., human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human

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chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. See, e.g., D'Eustachio, *et al.*, 1983. *Science* 220: 919-924. Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human
5 chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the NOVX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific
10 chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes
15 can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection.
20 Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, see, Verma, *et al.*, HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for
25 marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical
30 position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, e.g., in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through

linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the NOVX gene, can be determined. If a
5 mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence.
10 Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

The NOVX sequences of the invention can also be used to identify individuals from
15 minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

20 Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the NOVX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

25 Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The NOVX sequences of the invention uniquely represent portions of the human genome. Allelic
30 variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining NOVX protein and/or nucleic acid expression as well as NOVX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant NOVX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. For example, mutations in an NOVX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with NOVX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining NOVX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the

genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX in clinical trials.

5 These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of NOVX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting NOVX protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes NOVX protein such that the presence of NOVX is detected in the biological sample. An agent for detecting NOVX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to NOVX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length NOVX nucleic acid, such as the nucleic acid of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to NOVX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting NOVX protein is an antibody capable of binding to NOVX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect NOVX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of NOVX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of NOVX

protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of NOVX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of NOVX protein include introducing into a subject a labeled anti-NOVX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting NOVX protein, mRNA, or genomic DNA, such that the presence of NOVX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of NOVX protein, mRNA or genomic DNA in the control sample with the presence of NOVX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of NOVX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting NOVX protein or mRNA in a biological sample; means for determining the amount of NOVX in the sample; and means for comparing the amount of NOVX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect NOVX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant NOVX expression or activity in which a test sample is obtained from a subject and NOVX protein or nucleic

acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample
5 can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant NOVX expression or activity. For
10 example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant NOVX expression or activity in which a test sample is obtained and NOVX protein or nucleic acid is detected (*e.g.*, wherein the presence of NOVX protein or nucleic
15 acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant NOVX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an NOVX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various
20 embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an NOVX-protein, or the misexpression of the NOVX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (i) a deletion of one or more nucleotides from an NOVX gene;
25 (ii) an addition of one or more nucleotides to an NOVX gene; (iii) a substitution of one or more nucleotides of an NOVX gene, (iv) a chromosomal rearrangement of an NOVX gene; (v) an alteration in the level of a messenger RNA transcript of an NOVX gene, (vi) aberrant modification of an NOVX gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an
30 NOVX gene, (viii) a non-wild-type level of an NOVX protein, (ix) allelic loss of an NOVX gene, and (x) inappropriate post-translational modification of an NOVX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an NOVX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.*, Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the NOVX-gene (*see*, Abravaya, *et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an NOVX gene under conditions such that hybridization and amplification of the NOVX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (*see*, Guatelli, *et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see*, Kwoh, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Q β Replicase (*see*, Lizardi, *et al.*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an NOVX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in NOVX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotide probes. *See, e.g.*, Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in NOVX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the NOVX gene and detect mutations by comparing the sequence of the sample NOVX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (see, e.g., Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (see, e.g., PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the NOVX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. *See, e.g., Myers, et al., 1985. Science 230: 1242.* In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type NOVX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁ nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with

hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. *See, e.g.,* Cotton, *et al.*, 1988. *Proc. Natl. Acad. Sci. USA* 85: 4397; Saleeba, *et al.*, 1992. *Methods Enzymol.* 217: 286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in NOVX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. *See, e.g.,* Hsu, *et al.*, 1994. *Carcinogenesis* 15: 1657-1662. According to an exemplary embodiment, a probe based on an NOVX sequence, *e.g.*, a wild-type NOVX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. *See, e.g.,* U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in NOVX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g.,* Orita, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton, 1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79. Single-stranded DNA fragments of sample and control NOVX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g.,* Keen, *et al.*, 1991. *Trends Genet.* 7: 5.

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g.,* Myers, *et al.*, 1985. *Nature* 313: 495.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which NOVX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

5

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on NOVX activity (*e.g.*, NOVX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited

enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome PREGNANCY ZONE PROTEIN PRECURSOR enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification. Thus, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an NOVX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials.

For example, the effectiveness of an agent determined by a screening assay as described herein to increase NOVX gene expression, protein levels, or upregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting decreased NOVX gene expression, protein levels, or downregulated NOVX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease NOVX gene expression, protein levels, or downregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting increased NOVX gene expression, protein levels, or upregulated NOVX activity. In such clinical trials, the expression or activity of NOVX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including NOVX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates NOVX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of NOVX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of NOVX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of an NOVX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the pre-administration sample with the NOVX protein, mRNA, or genomic DNA in the post administration sample or

samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of NOVX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of NOVX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant NOVX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Osteodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (i) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to an aforementioned peptide; (iii) nucleic acids encoding an aforementioned peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous

- 5 Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, 10 derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (e.g., by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (e.g., Northern assays, dot blots, *in situ* hybridization, and the like).

20 Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant NOVX expression or activity, by administering to the subject an agent that modulates NOVX expression or at least one NOVX activity. Subjects at risk for a disease that is caused or contributed to by aberrant NOVX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the NOVX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression.

30 Depending upon the type of NOVX aberrancy, for example, an NOVX agonist or NOVX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The NOVX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

As an example, a cDNA encoding the NOVX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

Both the novel nucleic acid encoding the NOVX protein, and the NOVX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies, which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

Sequence Analyses

The sequence of NOVX was derived by laboratory cloning of cDNA fragments, by *in silico* prediction of the sequence. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, were cloned. *In silico* prediction was

based on sequences available in CuraGen's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

- 5 The laboratory cloning was performed using one or more of the methods summarized below:

SeqCalling™Technology: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue,
10 primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen Corporation's SeqCalling technology which is disclosed in full in U. S. Ser. Nos.
15 09/417,386 filed Oct. 13, 1999, and 09/614,505 filed July 11, 2000. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatics programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as
20 components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

 Variant sequences are also included in this application. A variant sequence can
25 include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide
30 or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the

genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

Presented information includes that associated with genomic clones, public genes and ESTs sharing sequence identity with the disclosed sequence and CuraGen Corporation's Electronic Northern bioinformatic tool.

Examples

Example A: Sequence related information

The NOV1 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 1A.

Table 1A. NOV1 Sequence Analysis			
	SEQ ID NO: 1	711 bp	
NOV1a, CG58522-01 DNA Sequence	<div>TGCAGAATGAACCAAGGAGACTCAAACCCAGCAGCTACTCCGCATGCGGCAGAAGACA TTCAAGGAGATGACAGATGGATGTGTGTCAGCACAAACAGATTGTTTGGACTGTAAAGA CAAACAGCCTGATGTACCATTTGCGGGAGGCTCCGTGGTGCACTTACTGCAGCCATAT GAGATATGGCGAGAGCTTTTTCCCCACTTCATGCACTGAATTTGGAACCTGGGGGAG ATACAACAAGACATGTTTTGTGGAGACTAAAGAGCGGAGAACTGGGGAATACTAAGCC TAAGGTCAATTGTTTTCTGGCTAGGAAGAAAACAACCATGAAAATATGGCAGAAGAGGTA GCAGGTGGTATGGCGGCCATCGTACAACCTTATCAACAAGGCAGCCACAGGCCAAAA TCATTGTATTGATCTGTTACCTCAAGGTGAGAAACCCAACCTTTGAGGCAAAAGAA CGCCAAGGTGAACCCACTCGTCAAGATTTGCTGCTGAAACTTACCAACGTGCAGCTC CTGGATACTGACAGGGGTTTTCGTGCACTCCGACCGTGCCATCTCTGCCACGACATGT TTGATTTTCTGCATTTGACAGGAGGTGGCTACTCAAAGGTCTGCAAACCTTGAATGA ACTGATCATGCAGTTGTTGGAGGAAACACCTGAGGAGAAACAAACCACCATTCGCTGA CTGGCTCCCATGAGT</div>		
	ORF Start: ATG at 7	ORF Stop: TGA at 694	
	SEQ ID NO: 2	229 aa	MW at 25656.2kD
NOV1a, CG58522-01 Protein Sequence	<div>MNQGDSNPAATPHAAEDIQGDDRWCQHNRFVLDCKDKQPDVPFAGGSVVQLLPYEI WRELFSPHALNFGTGGDTTRHVLWRLKSGELGNTKPKVIVFWLGRNNHENMAEEVAG GMAAIVQLINTRPQAKIIIVFDLLPQGEKPNPLRQKNKVNPLVKISLLKLTNVQLLD TDRGFVHSDRAISCHDMFDLHLTGGSYSKVCKPLNELINQLEETPEEKQTTIA</div>		

Further analysis of the NOV1a protein yielded the following properties shown in Table 1B.

Table 1B. Protein Sequence Properties NOV1a	
Psort analysis:	0.6500 probability located in cytoplasm; 0.2340 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV1a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 1C.

Table 1C. Geneseq Results for NOV1a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB49433	Human beta platelet activating factor acetylhydrolase - Homo sapiens, 229 aa. [US6146868-A, 14-NOV-2000]	1..229 1..229	196/229 (85%) 209/229 (90%)	e-114
AAB49432	Rat beta platelet activating factor acetylhydrolase - Rattus norvegicus, 229 aa. [US6146868-A, 14-NOV-2000]	1..229 1..229	195/229 (85%) 208/229 (90%)	e-114
AAB49434	Murine beta platelet activating factor acetylhydrolase - Mus musculus, 229 aa. [US6146868-A, 14-NOV-2000]	1..229 1..229	192/229 (83%) 205/229 (88%)	e-111
AAB49436	Bovine gamma platelet activating factor acetylhydrolase - Bos taurus, 232 aa. [US6146868-A, 14-NOV-2000]	4..219 3..218	124/216 (57%) 165/216 (75%)	5e-74
AAB49435	Human gamma platelet activating factor acetylhydrolase - Homo sapiens, 231 aa. [US6146868-A, 14-NOV-2000]	4..219 3..218	124/216 (57%) 164/216 (75%)	2e-73

In a BLAST search of public sequence databases, the NOV1a protein was found to have homology to the proteins shown in the BLASTP data in Table 1D.

Table 1D. Public BLASTP Results for NOV1a				
Protein Accession Number	Protein/Organism/Length	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q29459	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAFAH beta subunit) - Homo sapiens (Human), and, 229 aa.	1..229 1..229	196/229 (85%) 209/229 (90%)	e-114
O35264	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAFAH beta subunit) (Platelet-activating factor acetylhydrolase alpha 2 subunit) (PAF-AH alpha 2) - Rattus norvegicus (Rat), 229 aa.	1..229 1..229	195/229 (85%) 208/229 (90%)	e-113
Q61206	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH beta subunit) (PAFAH beta subunit) - Mus musculus (Mouse), 229 aa.	1..229 1..229	192/229 (83%) 205/229 (88%)	e-111
Q29460	Platelet-activating factor acetylhydrolase IB gamma subunit (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit) (PAF-AH gamma subunit) (PAFAH gamma subunit) - Bos taurus (Bovine), 232 aa.	4..219 3..218	125/216 (57%) 165/216 (75%)	8e-74
Q15102	Platelet-activating factor acetylhydrolase IB gamma subunit (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit) (PAF-AH gamma subunit) (PAFAH gamma subunit) - Homo sapiens (Human), 231 aa.	4..219 3..218	124/216 (57%) 164/216 (75%)	7e-73

PFam analysis predicts that the NOV1a protein contains the domains shown in the Table 1E.

Table 1E. Domain Analysis of NOV1a			
Pfam Domain	NOV1a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PAF-AH: domain 1 of 1	7..221	150/215 (70%) 186/215 (87%)	6e-147

Example 2.

The NOV2 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 2A.

Table 2A. NOV2 Sequence Analysis			
	SEQ ID NO: 3	1457 bp	
NOV2a, CG58520-01 DNA Sequence	CGATTCCGATGGGTCTTTGAAAGCTTTTCTCTTCCCTTTTCTTCTGCGGAGTCA AAGTAGAGGGGTGAGGTGGTCTTCTGTGTTACTGACCTGCAATTGGGAAACGTTGAT AAGGCAGATGATGAAGATGATGAGGATTTAACGGTGAACAAAACCTGGGTCTTGGCCC CAAAAATTCATGAAGGAGATATCACACAAATCTGAATTCATTGCTTCAAGGCTATGA CAATAAACTTCGTCCAGATATAGGAGTGAGGCCACAGTAATTGAAACTGATGTTTAT GTAAACAGCATTGGACCAGTTGATCCAATTAATATGGAATATACAATAGATATAATT TTGCCCAAACCTGGTTTGACAGTCGTTTAAAATTCATAGTACCATGAAAGTGCTTAT GCTTAAACAGTAATATGGTTGGAAAAATTTGGATTCTGACACTTTCTTCAGAAACTCA AGAAAATCTGATGCTCACTGGATAACAACCTCTAATCGTCTGCTCGAATTTGGAATG ATGGACGAGTTCTGTATACTCTAAGGAGATTGACAATTAATGCAGAATGTTATCTTCA GCTTCATAACTTTCCCATGGATGAACATTCTGTCCACTGGAATTTTCAAGCTTCTCT ATAGATGGATACCTTAAAAATGAAATTGAGTTATCAATGGAAGCGAAGTTCTGTGGAA GTGGCGCACACAAGATCCGGAGATTATATCAGTTTGCAATTTGAGGGTTACGGAACCT AACTGAAATCACTCACACGATCTCTGGGGATTATGTTATCATGACAATTTTTTTTGAC CTGAGCAGAAGAATGGGATATTTCACTATTCAAGCTTCAATCCATGCATTCTGTGACAG TTGTTCTTTCTGGGTGTCCTTTTGGATCAATAAAGATGCAGTGCCTGCAAGAACATC GTTGGGTATGACATCTATAGGTATCACTACAGTTCTGACTATGACAACCTCGAGTACA ATTGCCAGGAAGTCTTTACCTAAGGTTTCTTATGTGACTGCGATGGATCTCTTGTGTT CTGTTTGTTTCATTTTGTGTTTTCAGCCTTGATGGAATATGGAACCTTGCATTTAT TACCAGCAACCAAAAGGAAAGACTGCTACTAAAGACAGAAGCTAAAAATAAAGCC TCGACTCTGGTCTCCATCTGGATCCACTCTGATTCCAATGAATAATATTTCTGTGCG CGCAAGAAGATGATTATGGGTATCAGTGTTTGAGGGGCAAGATTTGTGCCAGGTTCTT CTGTGCTTTGAAGACTGCAGAACAGGATCTTGGAGGGAAGGAAGGATACACATACGC ATTGCCAAAATTGACTCTTATTCTAGAATATTTTTCCCAACCGCTTTTGCCCTGTTCA ACTTGGTTTATTGGGTGGCTATCTTTACTTATAAAATCTACTTCATAGAACAAAATC AAAAGAA		
	ORF Start: ATG at 9	ORF Stop: TAA at 1425	
	SEQ ID NO: 4	472 aa	MW at 54100.9kD
NOV2a, CG58520-01 Protein Sequence	MGPLKAFLESPFLLRSGVRVLFLLTLHLGNVDKADDEDLTVNKTWVLAPKI HEGDI TQILNSLLQGYDNKLRPDIGVRPTVIE TDVVNSIGPVDPINMEYTTIDI IFAQ TWFDSRLKFNSTMKVLM LNSNMVGKIWIPTFFRNSRKSADHWITTPNRLRLIWNDR VLYTLRRLTINAE CYLQLHNFPMDEHSCPLEFSSFSIDGYPKNEIELSMEAKFCGSGR HKIRRLYQFAFVGLRNSTEIHTHTISGDYVIMTIFDLSRRMGYFTIQTYIPCIILTVVL SWVSFWINKDAVPARTSLGMTSIGITTVLMTTLSTIARKSLPKVSYVTAMDLFVSVC FIFVFAALMEYGLTHYFTSNQKGKTATKDRKLKNKASTPGLHPGSTLIPMNNISVPQE DDYGYQCLEGGKDCASFCCFEDCRGTSWREGRIHIRIAKIDSYSRIFFPTAFALPNLV YWVGYYLYL		
	SEQ ID NO: 5	1521 bp	
NOV2b, CG58520-02 DNA Sequence	CAACCAAGAGGCAAGAGGCGAGAGAAGGAAAAAAAAAAGCGATGAGTTCGCCAAAT ATATGGAGCACAGGAAGCTCAGTCTACTCGACTCTGTATTTTACAGAAAATGACGG TGTGGATTCTGCTCTGCTGTGCTCTACCTGGCTTCACTAGCCAGAAATCTGATGA TGACTATGAAGATTATGCTTCTAACAAAACATGGGTCTTGACTCCAAAAGTTCTGTAG GGTGATGTCAGTGCATCTTAAACAACCTGCTGGAAGGATATGACAATAAACTTCGGC CTGATATAGGAGTGAAGCCAACGTTAATTCACACAGACATGTATGTGAATAGCATTGG TCCAGTGAACGCTATCAATATGGAATACACTATTGATATATTTTTTGGCGAAACGTGG TATGACAGACGTTTGAAATTTAAACAGCACCATTAAAGTCTCCGATTGAACAGCAAC		

	TGGTGGGGAAAACTCGGATTCAGACACTTTCTTCAGAAATCCAAAAAGCTGATGC ACACTGGATCACCACCCCAACAGGATGCTGAGAAATTTGGAATGATGGTCGAGTGCTC TACACCCCTAAGGTTGACAAATTGATGCTGAGTGCCAATTACAATTGCACAACTTTCCAA TGGATGAACACTCCTGCCCTTGGAGTTCTCCAGTTATGGCTATCCACGTGAAGAAAT TGTTTTATCAATGGAAGCGAAGTTCTGTTGAAGTGGGCGACACAAGATCCTGGAGGCTT TATCAATTCTCATTGTTGGTCTAAGAAAATACCACCGAAGTAGTGAAGACAACCTCCG GAGATTATGTGGTCATGTCTGTCTACTTTGATCTGAGCAGAAGATGGGATACCTTTAC CATCCAGACCTATATCCCTGCACACTCATTGTCGTCTTATCCTGGGTGTCTTTCTGG ATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCAGTCTGTCTGACAA TGACCACCCTCAGCACCATTGCCCGGAAATCGCTCCCCAAGGTCCTTATGTCTCACAG GATGGATCTCTTTGTATCTGTTTGTTCATCTTTGTCTTCTGCTCTGGTGGAGTAT GGCACCTTGCAATTTTGTGTCAGCAACCCGGAACCAAGCAAGGACAAAGATAAAAAAGA AGAAAAACCTCTTCTTCGGATGTTTTCTTCAAGGCCCTACCATTGATATCCGCC AAGATCAGCAACCATTCAAATGAATAATGCTACACACCTTCAAGAGAGAGATGAAGAG TACGGCTATGAGTGTCTGGACGGCAAGGACTGTGCCAGTTTTTCTGCTGTTTTGAAG ATTGTGCAACAGGAGCTTGGAGACATGGGAGGATACATATCCGATTGCCAAAATGGA CTCCTATGCTCGGATCTTCTTCCCCACTGCCTTCTGCCTGTTTAACTCTGGTCTATTGG GTCTCTACCTCTACCTGTGAGGAGGTATGGGTTTTACTGATATGGTTCTTATTCACT GAGTCTCATGGAG		
	ORF Start: ATG at 44		ORF Stop: TGA at 1469
	SEQ ID NO: 6	475 aa	MW at 55184.9kD
NOV2b, CG58520-02 Protein Sequence	MSSPNIWSTGSSVYSTPVFSQKMTVWILLLSLYPGFTSQKSDDDYEDYASNKTWILT PKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYITIDIF FAQTWYDRRLKFNSTIKVLRNLSNMVGKIWIPTFFRNSKKADAHWITPNRMLRIWN DGRVLYTLRLTIDAECQLQHNFPMDHEHSCPLEFSSYGYPREEIVYQWRSSVEVGD RSWRLYQFSFVGLRNTTEVVKTTSGDYVVMVSVYFDLSRRMGYFTIQTYIPCTLI VVLVSVFWINKDAVPARTSLGITTVLMTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFS ALVEYGTLLHYFVSNRKP SKDKKKKNPLLRMFSPKAPTIDIRPSATIQMNRATHLQ ERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMSYARIFPPTAFCLF NLVYWVSYLYL		
	SEQ ID NO: 7	1455 bp	
NOV2c, CG58520-03 DNA Sequence	TAGTGACGACACGTAAGGCGATTCCGATGGGTCCTTTGAAAGCTTTTCTCTTCT CCCCCTTTCTCTCGCGAGTCAAAGTAGAGGGGTGAGGTTGGTCTTCTGTTACTGAC CCTGCATTGGGAACTGGGTTGATAAGGCAGATGATGAAGATGATGAGGATTTAACG GTGAACAAACCTGGGCTTGGCCCCAAAATTTCATGAAGGAGATATCACACAAATTC TGAATTCATTGCTTCAAGGCTATGACAATAAATTCGTCAGATATAGGAGTGAGGCC CACAGTAATTGAACTGATGTTTATGTAAACAGCATTTGACCAGTTGATCCAATTAAT ATGGAATATACAAATAGATATAATTTTGGCCAAACCTGGTTTGACAGTCGTTTAAAT TCAATAGTACCATGAAAGTGCTTATGCTTAACAGTAATATGGTTGGAAAAATTTGGAT TCCTGACACTTTCTTCAGAACTCAAGAAATCTGATGCTCACTGGATAACAACCTCCT AATCGTCTGCTTCAATTTGGAATGATGGACGAGTTCTGTATACTCTAAGGTTGACAA TTAATGCAGAATGTTATCTTCAGCTTCAATCTTCCATGGATGAACATTCTGTGCC ACTGGAATTTTCAAGCGATGGATACCTAAATGAAATGAAATGAGTATAGTGGAAAAAG CCCTCCGTAGAAGTGGCTGATCCTAAATACTGGAGATTATATCAGTTTGCATTGTGAT GGTTACGGAACCTCAACTGAAATCACTCACAGCATCTCTGGTGATTATGTTATCATGAC AATTTTTTTGACCTGAGCAGAAGATGGGATATTACACTATTAGACTCACTCAATCCA TGCAATCTGACAGTTGTTCTTTCTTGGGTGTCTTTTGGATCAATAAAGATGCAGTGC CTGCAAGAACATCGTTGGGTATCACTACAGTTCTGACTATGACAACCTGAGTACAAT TGCCAGGAAGTCTTTACCTAAGGTTTCTTATGTGACTGCGATGGATCTCTTGTGTTCT GTTTGTTTCATTTTTGTTTTTGCAGCCTTGATGGAATATGGAACCTTGCAATTTTTC CCAGCAACCAAGGAAAGACTGCTACTAAAGACAGAAAGCTAAAAAATAAGCCCTC GGTAACCTCTGGTCTCCATCTGGATCCACTCTGATTCCAATGAATAATATTCTGTG CCGCAAGAAGATGATTATGGGTATCAGTGTGGAGGGCAAGATTGTGCCAGCTTCT TCTGTGCTTTGAAGACTGCAGAACAGGATCTTGGAGGGAAGGAAGGATACACATAGC CATTGCCAAAATTGACTCTTATTCTAGAATATTTTCCCAACCGCTTTTGCCTGTTC AACTTGGTTTATTGGGTGGCTATCTTTACTTATAAAATCTACTTCATAAGCAAAAT CAAAA		
	ORF Start: ATG at 31		ORF Stop: TAA at 1426
	SEQ ID NO: 8	465 aa	MW at 53597.3kD
NOV2c, CG58520-03 Protein Sequence	MGPLKAFLFSPFLLRSQSRGVRLVFLLLTLHLGNWVDKADDEDDELTVNKTWVLAPK IHEGDIITQLNSLLQGYDNKLRPDIGVRPTVIEDVYVNSIGPVDPINMEYITIDIFA QTWFSRLKFNSTMVLMNLSNMVGKIWIPTFFRNSRKSDAHWITPNRMLRIWINDG RVLYTLRLTINAECYLQHNFPMDHEHSCPLEFSSDGYPKNEIEYKWKPKSVEVADPKY WRLYQAFVGLRNSTETHTISGDYVIMTIFFDLSRRMGYFTIQTYIPCTLI VVLVSVFWINKDAVPARTSLGITTVLMTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAAL MEYGTLLHYFTSNQKGTATKDRKLKNKASVTPGLHPGSTLIPMNNISVPQEDDYGQC LEGKDCASFFCCFEDCRTGWSWREGRIHIRIAKIDSYSRIFPPTAFALFNLVYWVGYLY L		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 2B.

Table 2B. Comparison of NOV2a against NOV2b through NOV2c.

Further analysis of the NOV2a protein yielded the following properties shown in Table 2C.

Table 2C. Protein Sequence Properties NOV2a

5 A search of the NOV2a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 2D.

Table 2D. Geneseq Results for NOV2a

AAR83968	GABA-A receptor gamma-3 subunit - Homo sapiens, 467 aa. [WO9529234-A1, 02-NOV-1995]	24..472 5..467	300/472 (63%) 356/472 (74%)	e-169
AAW59048	GABA-A receptor epsilon subunit related protein - Mammalia, 506 aa. [DE19644501-A1, 30-APR-1998]	62..472 70..506	193/448 (43%) 274/448 (61%)	e-102
AAW61045	Human GABA receptor epsilon subunit - Homo sapiens, 506 aa. [WO9823742-A1, 04-JUN-1998]	62..472 70..506	193/448 (43%) 274/448 (61%)	e-102

In a BLAST search of public sequence databases, the NOV2a protein was found to have homology to the proteins shown in the BLASTP data in Table 2E.

Table 2E. Public BLASTP Results for NOV2a				
Protein Accession Number	Protein/Organism/Length	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P23574	Gamma-aminobutyric-acid receptor gamma-1 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 465 aa.	1..472 1..465	426/475 (89%) 440/475 (91%)	0.0
Q9R0Y8	Gamma-aminobutyric-acid receptor gamma-1 subunit precursor (GABA(A) receptor) - Mus musculus (Mouse), 465 aa.	1..472 1..465	420/477 (88%) 434/477 (90%)	0.0
JH0824	gamma-aminobutyric acid A receptor gamma 1 chain precursor - chicken, 464 aa.	16..472 12..464	390/463 (84%) 416/463 (89%)	0.0
JH0316	gamma-aminobutyric acid A receptor gamma 2 chain alternatively spliced precursor - mouse, 466 aa.	24..472 26..466	336/451 (74%) 380/451 (83%)	0.0
P18508	Gamma-aminobutyric-acid receptor gamma-2 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 466 aa.	24..472 26..466	335/451 (74%) 379/451 (83%)	0.0

PFam analysis predicts that the NOV2a protein contains the domains shown in the Table 2F.

Table 2F. Domain Analysis of NOV2a			
Pfam Domain	NOV2a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Neur_chan_LBD: domain 1 of 1	63..273	66/271 (24%) 162/271 (60%)	2.7e-56
Cys-protease-3C: domain 1 of 1	363..369	4/7 (57%) 6/7 (86%)	5.2
Neur_chan_memb: domain 1 of 1	280..466	44/297 (15%) 164/297 (55%)	1.2e-60

Example 3.

- 5 The NOV3 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 3A.

Table 3A. NOV3 Sequence Analysis			
	SEQ ID NO: 9	1440 bp	
NOV3a, CG58518-01 DNA Sequence	GAAGAGATGGTCTCTGGCTTTCAGTTAGTCTCCTTCACCTACATCTGGATCATATTG AACCAAATGTTTGTGCTGCTTCTAACATCAAGATGACACACCAGCGGTGCTCCTCTT AATGAAACAAACCTGGAACAAGAACTAGAATGAAGAAAGATGACAGTACCAAAGCG CGGCCTCAGAAATATGAGCAACTTCTCCATATAGAGGACAACGATTTGCGAATGAGA CTGGATTTGGAGGTGAGTATTATCCTCTCAAAATTGGGTCTCCAGTGCCAGTAGGTA AGATGTCCATGTTGAAAGCATTGACAGCATTTTCAGAGACTAACATGGTAAGTTTCT ATGGGATATGACTTTACAATGACTTTTTATCTCAGGCATTACTGGAAGACGAGAGG TCTCCTTTCTAGCACAGCAAAACAAAAGCATGACATTTGATCATAGATTGACCAGAA GATCTGGGTGCTGATATCTTTTTGTCCACTCTAAAAGATCCTTCATCCATGATACA ACTATGGAGAATATCATGCTGCGCGTACACCCGTATGGAACGTCCTCCTAAGTCTC GGAGGATAACGGTTTCGGCCATGTGCTTTATGGATTTTCAGCAGGTTTCTCTTGACA TCAAAATGTTTCTCTTGAACGGAAGCGCCTACAATGAGGATGACCTAATGCTATAC TGGAAACACGGAACAAGTCTTAAATACTGAAGAACATATGTCCTTTCTCAGTTCT TCATTGAAGACTTCAGTGCATCTAGTGGATTAGCTTTCTATAGCAGCACAGGTTGGT CAATAGGCTTTTCATCAACTTTGTGCTAAGGAGGCATGTTTCTCTTTGTGCTGCA ACCTATTTCCAGCCATATTGATGGTGATGCTTTTCATGGGTTTCATTTGGATTGAC GAAGAGCTGTTCTGCAAGAGTTTCCCTGGGTGGAATCACCACAGTGTGACCATGT CACAATCATCACTGCTGTGAGCGCCTCCATGCCCGAGGTGTCTTACCTCAAGGCTGT GATGTGTACCTGTGGGTGAGTCCCTCTTTGTGTTCTGTGAGTCATTGAGTATGCA CTGTGAACTACCTCACCACAGTGAAGAGCGGAAACAATTCAAGAAGACAGGAAGGT ACAGATTTCTAGGATGTACAATATTGATGCAGTTCAAGCTATGGCCTTTGATGGTTG TACCATGACAGCGAGATTGACATGGACCAGACTTCCCTCTCTCTAAACTCAGAAGAC TCATGAGAAGAAAATCGATATGCAGCCCCAGCAGGATTCATCTCGGATAAAGAGAA AAAATCCCTAGGAGGACATGTTGGTAGAATCATTCTGGAACAACCATGTCATTGA ACCTATTCTAGGATTTTATCCCATTTGTGTATATCTTTATTTAATTT		
	ORF Start: ATG at 7	ORF Stop: TAA at 1435	
	SEQ ID NO: 10	476 aa	MW at 55285.2kD
NOV3a, CG58518-01 Protein Sequence	MVLAFQLVSFTYIWIILKPNVCAASNIKMTHQRCSSSMKQTWKQETRMKKDDSTKAR QKYEQLLHIEDNDFAMRPGFGGEYYPKIGSPVPVIGDVHVESIDSISETNMVSFFMG YDFTMTFYLRYHWKDERLSFPSTANKSMTFDHRLTRKIWVPDIFVHSKRSFIHDTTM ENIMLRVHPDGNVLLSLRRI TVSAMCFMDFSRFPLDTQNCSELESAYNEDDLMLYWK HGNKSLNTEEHMSLSQFFIEDFSASSGLAFYSTGWYNRLF INFVLRHVFFVFLQTY		

	FPAILMVMLSWVSFWIDRRVAVPARVSLGGITTVLTMSTIITAVSASMPQVSYLKAVDV YLWVSSLFVFLSVIEYAAVNYLTVEERKQFKKTGKVQISRMYNIDAVQAMAFDGCYH DSEIDMDQTSLSLNSDFMRRKSICSPSTDSSRIKRRKSLGGHVGRIILENNHVIDTY SRILFPVYIFI
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Further analysis of the NOV3a protein yielded the following properties shown in Table 3B.

Table 3B. Protein Sequence Properties NOV3a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.2400 probability located in nucleus
SignalP analysis:	Likely cleavage site between residues 25 and 26

A search of the NOV3a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 3C.

Table 3C. Geneseq Results for NOV3a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU04467	Human gamma-amino butyric acid (GABA) receptor protein #1 - Homo sapiens, 467 aa. [WO200153489-A1, 26-JUL-2001]	1..474 1..456	454/475 (95%) 454/475 (95%)	0.0
AAU04470	Human gamma-amino butyric acid (GABA) receptor protein #4 - Homo sapiens, 420 aa. [WO200153489-A1, 26-JUL-2001]	48..474 1..409	408/428 (95%) 408/428 (95%)	0.0
AAU04468	Human gamma-amino butyric acid (GABA) receptor protein #2 - Homo sapiens, 392 aa. [WO200153489-A1, 26-JUL-2001]	1..393 1..377	370/394 (93%) 370/394 (93%)	0.0
AAU04471	Human gamma-amino butyric acid (GABA) receptor protein #5 -	48..393 1..330	324/347 (93%)	e-180

	[WO200153489-A1, 26-JUL-2001]		(93%)	
AAU04469	Human gamma-amino butyric acid (GABA) receptor protein #3 - Homo sapiens, 180 aa. [WO200153489-A1, 26-JUL-2001]	1..192 1..177	176/192 (91%) 176/192 (91%)	2e-96

In a BLAST search of public sequence databases, the NOV3a protein was found to have homology to the proteins shown in the BLASTP data in Table 3D.

Table 3D. Public BLASTP Results for NOV3a				
Protein Accession Number	Protein/Organism/Length	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P50573	Gamma-aminobutyric-acid receptor rho-3 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 464 aa.	1..474 1..453	383/476 (80%) 407/476 (85%)	0.0
Q9YGQ2	GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT - Morone americana (White perch), 470 aa.	1..474 4..459	293/485 (60%) 363/485 (74%)	e-153
P50572	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 474 aa.	49..474 58..463	270/427 (63%) 317/427 (74%)	e-144
P56475	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) - Mus musculus (Mouse), 474 aa.	49..474 58..463	270/427 (63%) 317/427 (74%)	e-143
P24046	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) - Homo sapiens (Human), 473 aa.	49..474 57..462	268/427 (62%) 317/427 (73%)	e-143

PFam analysis predicts that the NOV3a protein contains the domains shown in the

5 Table 3E.

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Table 3E. Domain Analysis of NOV3a			
Pfam Domain	NOV3a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Neur_chan_LBD: domain 1 of 1	88..282	70/250 (28%) 165/250 (66%)	1.2e- 54
Neur_chan_memb: domain 1 of 1	289..475	44/292 (15%) 141/292 (48%)	7.6e- 28

Example 4.

The NOV4 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 4A.

Table 4A. NOV4 Sequence Analysis			
	SEQ ID NO: 11	1587 bp	
NOV4a, CG58516-01 DNA Sequence	GAACAGAAATGAATAAAAGTCGCTGGCAGAGTAGAAGACGACATGGGAGAAGAAGCC CCAGCAGAACCCCTTGGTTTCAGACTCCGTGATTCTGAAGACAGGTCTGACTCCCGGGC GCACAGCCCGCTCACGATTCGGCCACGGTGATGACGAGTCTCCGTCAACCTCGTCTG GCACAGCTGGGACCTCCTCTGTGCCAGAGCTACCTGGGTTTTACTTTGACCCTGAAA GAAACGCTACTTCCGCTTGCTCCCTGGACATAAACAACCTGCAACCCCTGACGAAAGA AGCATCCGGCAGAAGGAGATGGAGAGCAAGAGACTGCGGCTGCTCCAGGAAGAAGAC GACGAAAAAAGATTGCCAGGATGGGATTTAATGCATCTTCCATGCTACGAAAAAGCC GCTGGGTTTTCTCAACGTCAACCAATTACTGCCATTTAGCCACAGAGCTGCGTCTCAG TGCATGGAGAGGAAAAAGGTCAGATTCTGAAGCATGGATCCCTCGCCTTGGCAAGCG ACCGATTTAACCCTCATACTGGCAGATACCAACAGTGACCGGCTCTTTCACAGTGAACG TGTTACAGTTGGAGGCTCCAAGTATGGTATCATCAACCTGCAAAGTCTGAAGACCCCT ACGCTCAAGGTGTTCTATGCCACGAAAAACCTCCGATTCTCACCACCGGAAGGTGAAC CTTCGGTGTGCTGGGCCTCGCTGAATCACTTGGATTCCCACATTCTGCTATGCCTCA GGGACTCGCAGAGACTCCAGGCTGTGCCACCTGCTCCACAGCATCACTGTTCGTGAAT AGTCCCCACCCAGGAATAGACCGGCCTGGCATGCTCTGCAGTTTCCGGAATCCCTGGG GTGCTGTGCTGTGCCTGGTCCCTGAATATCCAAGCAAATAACTGCTTCAGTACAGG CTTGCTCTGGCGGGTCTCTGTTGACCAACGTGGTGACGGGACACCGGAGTCTCTTGG ACCAACAGTGAATGCTTTGGCCAGCAGTTTGCTCTCATGGCTCTCTGCTGTTTAAT GCTGCCGCTCTGGGGAATCTTTGCCATTGATCTGCGTTGTGGAATCAAGGCAAGG ATGGAAGGCCACCCGCTGTTTCATGATTGAGCAGTGACCTCTGTGCGGATCCTCCAA GATGAGCAATACCTGATGGCTTCAGACATGGCTGGAAGAATCAAGCTGTGGGACCTC GGACCACGAAGTGCCTAAGGCAGTACGAAGGCCACGTGAATGAGTACGCCCTACCTGC CCTGCATGTGCACAGGAGAAGGAATCCTGGTGGCAGTGGGCCAGGACTGTACACG AGAATCTGGAGCCTCCACGATGCCCGCTACTGAGAACCATAACCTCCCGTACCTCT CCTCCAAGGCCGACATTCCCAGTGTGGCCTTCTCGTCGCGGCTGGGGGGCTCCCGGG GCGCGCCGGGGCTGCTCATGGCTGTGCGGCAGGACCTTTACTGTTACTCTACAGCT ATTCTGCAGGGCAGAGCCAGAGCCATGTGGATTGACTTACGGGAGTAAAGCGTAAG TTTTTACTGCATCTAATGAGG		
	ORF Start: ATG at 9	ORF Stop: TAA at 1563	
	SEQ ID NO: 12	518 aa	MW at 57769.3kD
NOV4a, CG58516-01 Protein Sequence	MNKSRWQSRRRRHGRSHQQNPWFLRDSRSDSRRAAQAHPDHSRHGDDSPSTSSGTA GTSSVPELPGFYFDPEKKRYFRLLPGHNNCNPLTKESIRQKEMESKRRLRLQEDRRK KIARMGFNASSMLRKSQGLFNVNTNYCHLAHELRLSCMERKKVQIRSMGPSALASDRF NLILADTNSDRFLTVDVTVGSKYGIINLQSLKTPTLKVFMPRPKPPILTNRKVNTSV CWSLNLHLDHSHILLCLMGLAETPGCATLLPASLFVNSPHPGIDRPGMLCSFRI PGGA SCAWSLNIQANCFSTGLSRRVLLTNVVTGHRQSFGTNSDVLAAQGFALMAPLLFNGCR SGEIFAIDLRCGNQGGKWKATRLFHDSAVTSVRLIQDEQYLMASDMAGKIKLWDLRTT KCVRYEGHVNEYAYLPLHVHEEGILVAVGQDCYTRIWSLHDARLLRTIPSPYPASK ADIPSVAFSSRLGGSRRGAGAAHGCRAGPLLLLLQLILQGTAAQSHVDLTYSKA		

5 Further analysis of the NOV4a protein yielded the following properties shown in Table 4B.

Table 4B. Protein Sequence Properties NOV4a	
Psort analysis:	0.9600 probability located in nucleus; 0.4776 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1837 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV4a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 4C.

Table 4C. Geneseq Results for NOV4a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB11794	Human secreted protein homologue, SEQ ID NO:2164 - Homo sapiens, 500 aa. [WO200157188-A2, 09-AUG- 2001]	1..484 5..485	470/484 (97%) 471/484 (97%)	0.0
AAM79804	Human protein SEQ ID NO 3450 - Homo sapiens, 500 aa. [WO200157190-A2, 09-AUG- 2001]	1..484 5..485	470/484 (97%) 471/484 (97%)	0.0
AAM41122	Human polypeptide SEQ ID NO 6053 - Homo sapiens, 500 aa. [WO200153312-A1, 26-JUL- 2001]	1..484 5..485	470/484 (97%) 471/484 (97%)	0.0
AAG67256	Amino acid sequence of a human liver-associated gene - Homo sapiens, 489 aa. [WO200109318- A1, 08-FEB-2001]	1..484 1..474	459/484 (94%) 462/484 (94%)	0.0
AAB94587	Human protein sequence SEQ ID NO:15389 - Homo sapiens, 489 aa. [EP1074617-A2, 07-FEB- 2001]	1..484 1..474	459/484 (94%) 462/484 (94%)	0.0

In a BLAST search of public sequence databases, the NOV4a protein was found to
5 have homology to the proteins shown in the BLASTP data in Table 4D.

Table 4D. Public BLASTP Results for NOV4a

Protein Accession Number	Protein/Organism/Length	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH18979	HYPOTHETICAL 55.7 KDA PROTEIN - Homo sapiens (Human), 495 aa.	1..484 1..480	470/484 (97%) 471/484 (97%)	0.0
Q96K22	CDNA FLJ14839 FIS, CLONE OVARC1001791 - Homo sapiens (Human), 489 aa.	1..484 1..474	459/484 (94%) 462/484 (94%)	0.0
Q9Y4P5	HYPOTHETICAL 48.5 KDA PROTEIN - Homo sapiens (Human), 430 aa (fragment).	5..435 2..428	420/431 (97%) 421/431 (97%)	0.0
Q99LF7	HYPOTHETICAL 58.1 KDA PROTEIN - Mus musculus (Mouse), 519 aa.	1..484 1..481	378/485 (77%) 423/485 (86%)	0.0
Q9UF10	HYPOTHETICAL 26.0 KDA PROTEIN - Homo sapiens (Human), 234 aa (fragment).	269..483 4..217	175/215 (81%) 193/215 (89%)	4e-99

PFam analysis predicts that the NOV4a protein contains the domains shown in the Table 4E.

Table 4E. Domain Analysis of NOV4a

Pfam Domain	NOV4a Match Region	Identities/ Similarities for the Matched Region	Expect Value
WD40: domain 1 of 3	281..316	2/37 (5%) 26/37 (70%)	5.8e+02
WD40: domain 2 of 3	367..402	10/37 (27%) 27/37 (73%)	6.1
WD40: domain 3 of 3	408..446	10/39 (26%) 23/39 (59%)	13

Example 5.

The NOV5 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 5A.

Table 5A. NOV5 Sequence Analysis			
	SEQ ID NO: 13	1081 bp	
NOV5a, CG58473-01 DNA Sequence	AGGATGGCCGAGAAGGAGAACAGTTATCCCTGGCCCTATGGCAAGCAGACGGCTCCAG CCGGCCTGAGTACCCTGCTCCCGCGAGTCTCTCCCGAGGATCCCCACCGAAGCTGCGCG TGAGCTCCCGAGCTGCGCAGACCCACAGCCCGCAGCGGCCCTGGCCATGAGGTGGTGA GAGAACAGTTGTGGGAAGCGCAGCATCTTAACGCGGCCCTCTCTGGTCGACGACCTTG AGACTGGGCGTCCCTGGGCAAAGACAAGTTTGATACATGTGTACTTGGCTCGAAAGAA GACAAGCCATTTTCATCGTGGCCCTCAAGGCCCTCAAGTCTCAGATAGAGGAGGGCGTG GAGCACCAGATGCGCAGGCAGATGGAATCCAGGCCCCCTTCAGCATCCCAACATAT TGAGTCTCTACAATATTTTATGACCTGAGAAAAATCTACTGGATTCTAGAGTACGC CCCCGCCACCCCTACCCCGAGGAGCTGTACCAGGAGCTGCGAAAGAGCCCGACCTTT GACAAGAAGCCAAACAGCCACCATCACGGGGAGGTGGCAGATGCTCTGATGTACTGCC ACGGGAAGAAGGTGACTCCAGAGACATGAAGCCAGATAATCTACTCTCAGGGCTTGA GGGCGAGCTGAAAGTTGCCGACTTCGGCTGCCCTGTGCACGCCCCCTCACTGAGGAGG AAGACAAGACAAATGTGTGGCACCTGGACTACCTGTCCCAGAGACAATTGAGGGGC GCGCGCACACCGAGAAGGTGGATTGTGGTACATCGGAGCACTCGGCTATGAGCCGCT GGTGGGGAACCCACACACAATGAGGCCTATGGGCGAATCGTCAAGGTGGCCCTAAAA TTCTGGCTTCTGTGCGCAGGAGAGCCCGAGGACCTCATCTCCAAGCTGCTTAGGCATA ACCCCTCAGAACGGCTGCCCTGGCCAGGTCTCAGCCCAACCCTGGGATCCTGGCCCA TTCTCGGAGGGTTTGCCTCCCTCTGCCCATCAGTCTGTCCCCTGGTGGTCCCTGACA TTCACTCGGGGCGCTCTGTGTTGTAAAGTCTGCATAT		
	ORF Start: ATG at 4	ORF Stop: TAA at 1069	
	SEQ ID NO: 14	355 aa	MW at 40012.7kD
NOV5a, CG58473-01 Protein Sequence	MAQKENSYPWPYKQTAPAGLSTLLPRVLPRIPTAAARELPSCADPQPAAPGHEVVE NSCGKRSILTRPFLVDDLETGRPLGDKFVHVYLARKKTSHFIVALKAFKSQIEEGVE HQMRRQMEIQAPFQHPNLSLYNYFYDLRKIYWILEYAPATPTPEELYQELRKSRTFD KKPTATITGEVADALMYCHGKKVTPRDMKPDNLLSGLEGELKVADFGPCVHAPSLRRK TRQMCGLDYLSPETIEGRAHTEKVDLWYIGALGYEPLVGNPHTNEAYGRIVKVALKF PLLCPGEPQDLISKLLRHNPSERLPLAQVSAHPGILAHSSRVLPSPAHQSVPPWWSLTF TRGRLLCL		

Further analysis of the NOV5a protein yielded the following properties shown in Table 5B.

Table 5B. Protein Sequence Properties NOV5a	
Psort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1897 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV5a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 5C.

Table 5C. Geneseq Results for NOV5a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV5a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG67615	Amino acid sequence of a human	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129

	[WO200109316-A1, 08-FEB-2001]			
AAG67436	Amino acid sequence of a human polypeptide - Homo sapiens, 344 aa. [WO200109345-A1, 08-FEB-2001]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129
AAAY22475	Human AUR1 protein sequence - Homo sapiens, 344 aa. [WO9937788-A2, 29-JUL-1999]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129
AAW18083	Human Aurora-1 - Homo sapiens, 344 aa. [WO9722702-A1, 26-JUN-1997]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129
AAAY27052	Human protein kinase (HPKM)-1 (clone ID 2940) - Homo sapiens, 347 aa. [WO9938981-A2, 05-AUG-1999]	1..341 1..346	246/352 (69%) 274/352 (76%)	e-127

In a BLAST search of public sequence databases, the NOV5a protein was found to have homology to the proteins shown in the BLASTP data in Table 5D.

Table 5D. Public BLASTP Results for NOV5a				
Protein Accession Number	Protein/Organism/Length	NOV5a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O60446	AURORA-RELATED KINASE 2 (SERINE/THREONINE KINASE 12) - Homo sapiens (Human), 344 aa.	1..341 1..343	247/349 (70%) 274/349 (77%)	e-128
Q96GD4	UNKNOWN (PROTEIN FOR MGC:11031) - Homo sapiens (Human), 344 aa.	1..341 1..343	247/349 (70%) 274/349 (77%)	e-128
Q96DV5	UNKNOWN (PROTEIN FOR MGC:4243) - Homo sapiens (Human), 345 aa.	1..341 1..344	247/350 (70%) 274/350 (77%)	e-126
Q9UQ46	AIK2 - Homo sapiens (Human), 343 aa.	1..341 1..342	245/348 (70%) 272/348 (77%)	e-126
O14630	PROTEIN KINASE - Homo sapiens (Human), 347 aa.	1..341 1..346	245/352 (69%) 272/352 (76%)	e-125

PFam analysis predicts that the NOV5a protein contains the domains shown in the Table 5E.

Table 5E. Domain Analysis of NOV5a			
Pfam Domain	NOV5a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Pkinase: domain 1 of 1	76..325	81/293 (28%) 184/293 (63%)	6.5e-36

Example 6.

The NOV6 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 6A.

Table 6A. NOV6 Sequence Analysis			
	SEQ ID NO: 15	1524 bp	
NOV6a, CG58470-01 DNA Sequence	AGCATTATGAACACTAATGACCTTAAACTCAGGTTGTCCAAAGCTGAGCAAGAACACC CACTACGTTTTCTGGAATGAGCTTGAAGAAGCCCGACAGGTAGAAGCTTTATGACAGAGCT CCAGGCCATCGACTTTCAGGAACCTGAACCTTTTTCAAAAGGCCATTGAAGGATTT AACCAGTCCTCTCATCAAGAAAAGGTGGATGCGGGAATGGAACCTGTCCCTCGAGAAG TACTGGGCAGTGCTGCAGGGAAGCTAGATCAGCTCCAGGCTCGGGAAAGCAAAGTTT CCAGATTTCTGAGAACAAGTCACAGTTGTTCTAGCTGGTGGGCAAGGGACTAGACTC GTTGCATATCCAAAGGGGATGTATGATGTTGGTTTGCCATCCCATAAGACACTTTTTC AGATTCAAGCAGAGCATATCCTGAAGCTACAACAGTTAGCTGAAAAATATTATGGCAA CAAAATGCAATTATTCATATTACGTATGACCAAGCGAGTTCACTCTGGGGCCACGGCC GAGTTCTTCAGGGAGCACAACTTCTTCCACCTGGACCCCGCCAACGTGGTCATGTTTTG AGCAGCGCCTGCTGCCTGCTGTGACCTTTGATGGCAAGGTTATCCTGGAGCGGAAAGA CAAAGTTGCCATGGCCCCAGACGGCAACGGGGCCCTCTACTGCGCGCTGGAGGACCAC AAGATCCTGGAGGACATGGAGCGCCGGGGAGTGGAGTTTGTGCACGTGTACTGTGTGC ACAACATCCTGGTGGGCTGGCGGACCTGTCTTCATCGGCTTCTGTGTGTTGTCAGGG CGCAGACTGTGGCGCCAAGGTGGTGGAAAAGGCATACCCGAGGAGCCGTGGGCGTG GTGTGCCAGGTGGACGGTGTCCCCAGGTGGTGGAGTACAGCGAGATCAGTCTGAGT CCGCACAGCTACGTGTCTCCGACGGGAGCCTGTGTACAATGCAGGCAACATCTGCA CCACTTCTTCAACCGAGGCTTCTTTAAGGCGGTCAACAGGAGTTTGAAGCCTTGTGCT AAGCCACACGTGGCTGTGAAGAAGGTCCCGTATGTGGATGAGGAGGGGAATCTGGTA AGCCGCTAAACCGAACGGGATAAAGATGGAGAAGTTTGTGTTTGTATGTGTTCCGGTT TGCTAAGAACTTTGCTGCCTTGGAAAGTGCTGCGGGAGGAGGAATTTTCCCACTGAAG AACGCAGAGCCAGCCGACAGGGACAGTCCCGCACCGCTCGCCAGGCGCTGTCTACCC AGCACTACCGGTGGGCTCTGCGGGCCGGGGCCCGCTTCTGTGATGCCATGGGGCCCG GCTCCAGAGCTGCCAGCTTGCCCCAAATGGAGACCCTCCGGCCATCTGTGAGATA TCGCCCTTGGTGTCTTACTCTGGAGAGGGTTTAGAAGTGTACCTGCAAGGCCGGGAGT TCCAGTCCCGCTCATCTCTGGATGAAGACCGGCCAGGAGCTGGTGA AAAATGGTAT ATGAACCTGATACCAA		
	ORF Start: ATG at 7	ORF Stop: TGA at 1510	
	SEQ ID NO: 16	501 aa	MW at 56461.0kD
NOV6a, CG58470-01 Protein Sequence	MNTNDLKLRLSKAEQEHPLRFWNELEEARQVELYAEIQIDFQELNFFQKAIEGFNQ SSHQEKVDAGMEPVPREVLGSAAGKLDQLQAWESKVFQISENKVTVVLAGGQGRTLVA YPKMYDVGLP SHKTLFQIQAEHILKLQQLAEKYGNKCIIPYVMTSEFTLGP TAEF FREHNFFHLDPANVVMFEQRLLPAVTFDGKVI LERKDKVAMAPDNGGLYCALEDHKI LEDMERRGVFVHYVCDNILLRLADPVFI GFCVLQGADCGAKVVEKAYPEEPVGVVC QVDGVPQVVEYSEISPETAQLRVSDGSLLYNAGNICNHFFTRGFLKAVTREFEPLLPK HVAVKKVPYVDEEGNLVKPLKPNIGKMEKFVDFVFRFAKNFAALEVLREEEFSPLKNA EPADRDSPRTARQALLTQHYRWALRAGARFLDAHGARLP LPSLPNGDPPIAICEISP LVSYSGEGLEVYLQGREFQSPLILDEDQARELVKNGI		

Further analysis of the NOV6a protein yielded the following properties shown in Table 6B.

Table 6B. Protein Sequence Properties NOV6a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3490 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV6a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 6C.

Table 6C. Geneseq Results for NOV6a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV6a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB56960	Human prostate cancer antigen protein sequence SEQ ID NO:1538 - Homo sapiens, 524 aa. [WO200055174-A1, 21-SEP-2000]	1..501 3..524	353/522 (67%) 413/522 (78%)	0.0
AAG32392	Arabidopsis thaliana protein fragment SEQ ID NO: 39067 - Arabidopsis thaliana, 502 aa. [EP1033405-A2, 06-SEP-2000]	9..485 36..497	194/489 (39%) 275/489 (55%)	3e-84
AAG40236	Arabidopsis thaliana protein fragment SEQ ID NO: 49896 - Arabidopsis thaliana, 477 aa. [EP1033405-A2, 06-SEP-2000]	9..485 12..472	193/488 (39%) 272/488 (55%)	3e-82
AAG40235	Arabidopsis thaliana protein fragment SEQ ID NO: 49895 - Arabidopsis thaliana, 500 aa. [EP1033405-A2, 06-SEP-2000]	9..485 35..495	193/488 (39%) 272/488 (55%)	3e-82
AAG40234	Arabidopsis thaliana protein fragment SEQ ID NO: 49894 - Arabidopsis thaliana, 505 aa. [EP1033405-A2, 06-SEP-2000]	9..485 40..500	193/488 (39%) 272/488 (55%)	3e-82

- 5 In a BLAST search of public sequence databases, the NOV6a protein was found to have homology to the proteins shown in the BLASTP data in Table 6D.

Table 6D. Public BLASTP Results for NOV6a				
Protein Accession Number	Protein/Organism/Length	NOV6a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96GM2	UDP-N-ACTEYLGLUCOSAMINE PYROPHOSPHORYLASE 1 - Homo sapiens (Human), 505 aa.	1..501 1..505	351/505 (69%) 412/505 (81%)	0.0
Q16222	UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm- associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (AGX-2)] - Homo sapiens (Human), 522 aa.	1..501 1..522	352/522 (67%) 412/522 (78%)	0.0
Q91YN5	HYPOTHETICAL 58.6 KDA PROTEIN - Mus musculus (Mouse), 522 aa.	1..501 1..522	342/522 (65%) 407/522 (77%)	0.0
AAH17547	HYPOTHETICAL 58.5 KDA PROTEIN - Mus musculus (Mouse), 521 aa.	1..501 1..521	341/521 (65%) 407/521 (77%)	0.0
Q9Y0Z0	BCDNA:LD24639 PROTEIN - Drosophila melanogaster (Fruit fly), 520 aa.	6..492 44..513	236/491 (48%) 330/491 (67%)	e-124

PFam analysis predicts that the NOV6a protein contains the domains shown in the Table 6E.

Table 6E. Domain Analysis of NOV6a			
Pfam Domain	NOV6a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UDPGP: domain 1 of 1	40..434	108/428 (25%) 324/428 (76%)	8.4e-111

Example 7.

- 5 The NOV7 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 7A.

Table 7A. NOV7 Sequence Analysis			
	SEQ ID NO: 17	461 bp	
NOV7a, CG58593-01 DNA Sequence	ACGCAGAGATGCAGATCTTTGTGAAGACCCTCACGGGCAAGACCATCACCCCTTGAGGT CAAGCCCACCGACACCATTTGAGAATGTCAAACCAAAATTCAGGACAAGGAGGGTATC CCACCTGACCAGCAGCGTCTGATATTGCTGGGAAACGGCTGGAGGATGGCCACACTC TCTCAGGCTACAACATCCAGAAAGAGTCCACCCTAAACCTGGTGCTGCGCCTGCGAGG TGGCATTACTGAGCCTTCCCTCCGCCAGCTCGTCCAGAAATACAACCTGCGACGAGATG ATCTGCTGCAAGTGCTATGCTTGCCTGCACCCCGGTGCTATCAACTGCCACAAGAAGA AATGCGGCCACACCAACAACCTGTACCCAGGAAGAAGGTCAAATAAGGCTCTTCCTT CCTTGAAGGGCAGCAGCCTTCTGCCAGGCCCATGGCCCTGGGGCCTCAATAAA		
	ORF Start: ATG at 9	ORF Stop: TAA at 393	
	SEQ ID NO: 18	128 aa	MW at 14540.9kD
NOV7a, CG58593-01 Protein Sequence	MQIFVKTLTGKTTILEVKPTDTIENVKTKIQDKEGIPPDQORLIFAGKRLEDGHTLSG YNIQKESTLNLVLRRLRGGITPEPSLRQLVQKYNCEMICCKCYACLHPGAINCHKKKCG HTNNLYPRKKVK		

Further analysis of the NOV7a protein yielded the following properties shown in Table 7B.

Table 7B. Protein Sequence Properties NOV7a	
PSort analysis:	0.9800 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV7a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 7C.

Table 7C. Geneseq Results for NOV7a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV7a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB52080	Gene 16 human secreted protein homologous amino acid sequence #129 - Sus scrofa, 128 aa. [WO200061596-A1, 19-OCT-2000]	1..128 1..128	111/128 (86%) 118/128 (91%)	7e-61
AAG43861	Arabidopsis thaliana protein fragment SEQ ID NO: 54871 - Arabidopsis thaliana, 128 aa. [EP1033405-A2, 06-SEP-2000]	1..128 1..128	101/128 (78%) 113/128 (87%)	9e-55

AAG36188	Arabidopsis thaliana protein fragment SEQ ID NO: 44314 - Arabidopsis thaliana, 249 aa. [EP1033405-A2, 06- SEP-2000]	1..128 122..249	101/128 (78%) 113/128 (87%)	9e-55
AAG36187	Arabidopsis thaliana protein fragment SEQ ID NO: 44313 - Arabidopsis thaliana, 264 aa. [EP1033405-A2, 06- SEP-2000]	1..128 137..264	101/128 (78%) 113/128 (87%)	9e-55
AAG36186	Arabidopsis thaliana protein fragment SEQ ID NO: 44312 - Arabidopsis thaliana, 322 aa. [EP1033405-A2, 06- SEP-2000]	1..128 195..322	101/128 (78%) 113/128 (87%)	9e-55

In a BLAST search of public sequence databases, the NOV7a protein was found to have homology to the proteins shown in the BLASTP data in Table 7D.

Table 7D. Public BLASTP Results for NOV7a				
Protein Accession Number	Protein/Organism/Length	NOV7a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BX98	UBIQUITIN A-52 RESIDUE RIBOSOMAL PROTEIN FUSION PRODUCT 1 - Homo sapiens (Human), 141 aa (fragment).	1..128 14..141	111/128 (86%) 118/128 (91%)	3e-60
Q9UPK7	UBIQUITIN-52 AMINO ACID FUSION PROTEIN - Homo sapiens (Human), 128 aa.	1..128 1..128	111/128 (86%) 118/128 (91%)	3e-60
Q9PT09	UBIQUITIN - Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), 128 aa.	1..128 1..128	110/128 (85%) 118/128 (91%)	6e-60
O42388	UBIQUITIN-RIBOSOMAL PROTEIN FUSION PROTEIN - Gallus gallus (Chicken), 128 aa.	1..128 1..128	110/128 (85%) 117/128 (90%)	7e-60
Q9XSV1	UBIQUITIN-RIBOSOMAL PROTEIN L40 FUSION PROTEIN - Canis familiaris (Dog), 128 aa.	1..128 1..128	110/128 (85%) 117/128 (90%)	1e-59

PFam analysis predicts that the NOV7a protein contains the domains shown in the

Table 7E. Domain Analysis of NOV7a

Pfam Domain	NOV7a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	1..74	54/83 (65%) 72/83 (87%)	1.9e-38
Ribosomal_L40e: domain 1 of 1	77..128	30/52 (58%) 42/52 (81%)	7.3e-20

Example 8.

The NOV8 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 8A.

Table 8A. NOV8 Sequence Analysis

	SEQ ID NO: 19	2296 bp
NOV8a, CG57871-01 DNA Sequence	CGGCGGCGGCGGCAGTAGAAATGATGGAAGAATTGCATAGCCTGGACCCACGACGGCA GAAATTATTGGAGGCCAGGTTTACTGGAGTAGGTGTTAGTAAGGGACCACTTAATAGT GAGTCTTCCAACCAGAGCTTGTGCAGCGTCGGATCCTTGAGTGATAAAGAAGTAGAGA CTCCCAAGAAAAAGCAGAATGACCAGCGAAATCGGAAAAGAAAGCTGAACCATATGA AAGTAGCCAAAGGAAAGGCACTCCTAGGGGACATAAAATTAGTGATTACTTTGAGTTT GCTGGGGGAAGCGGGCCGGGAACAGCCCTGGCAGAAAGTGTCCACCAAGTTGCACGAT CCTCACTGCAACATTCTTTATCCAATCCCTTACCGCGACGAGTAGAACAGCCCCTCTA TGGTTTAGATGGCAGTGCTGCAAGGAGGCAACGGAGGAGCAGTCTGCTCTGCCAACC CTCATGTCAGTGATGTAGCAAAACCTCGGCTTGACACAGAGCAGCTGGCGCAAAGGG GAGCTGGCCTCTGCTTCACTTTTGTTCAGCTCAGCAAAACAGTCCCTCATCTACGGG ATCTGGCAACACAGAGCATTCTGCAGCTCCCAAAAACAGATCTCCATCCAGCAGAGA CAGACCAAGTCCGACCTCACAATAGAAAAAATATCTGCACCTAGAAAAACAGTAAGAATT CTGACTTAGAGAAGAAGGAGGGAAGAATAGATGATTTATTAAGAGCCATCTGTGATTT GAGACGGCAGATTGATGAACAGCAAAAGATGCTAGAGAAATACAAGGAACGATTAAAT AGATGTGTGCAATGAGCAAGAAACTCCTTATAGAAAAGTCAAAAACAGAGAAAGATGG CGTGTAGAGATAAGAGCATGCAAGACCGCTTGAGACTGGGCCACTTTACTACGTCTGA CCACGGAGCCAAATTTACTGAGCAGTGACAGATGGTTATGCTTTTCAGAATCTTATC AAGCAACAGGAAAGGATAAATTCACAGAGGGAAGAGATAGAAAGCAACGGAATGT TAGCAAAGCGAAACCTCCTGCCATGGGTGAGGCCCTCCTGCAACCAATGAGCAGAA ACAGTGGAAAAGCAAGACCAATGGAGCTGAAAATGAAACGTTAACGTTAAAGAAATAC CATGAACAAGAAGAAATCTTCAAACCTCAGATTAGGTCACTCTAGAAAAGAGGAGCAG AGATCCAGGCAGAGCTGGAGAGGCTAGAAAGGGTTAGAAAACATCATATCAGGGAAGT AAAAAGGATACATAATGAAGATAATTACAATTTAAATATCATCCAACGCTAAATGAC AGATATTTGTTGTTACATCTTTTGGGTAGAGGAGGTTTCAGTGAAGTTTACAAGGCAT TTGATCTAACAGAGCAAGATACGTAGCTGTGAAAATTACCAGTTAAATAAAACTG GAGAGATGAGAAAAGGAGAATTACCACAAGCATGCATGTAGGGAATACCGGATTCAT AAAGAGCTGGACCATCCAGAATAGTTAAGCTGTATGATTACTTTTCACTGGATACGT ACTCGTTTTGTACAGTATTAGAATACTGTGAGGGAAATGATCTGGACTTCTACCTGAA ACAGCACAATTAATGTGAGAGAAAGAGGCCCGGTCCATTATCATGCAGATTGTGAAT GCTTTAAAGTACTTAAATGAAATAAAACCTCCCATCATACACTATGACCTCAAACAG GTAATATTCTTTAGAAAATGGTACAGCGTGTGGAGAGATAAAAATTACAGATTTTGG TCTTTTGAAGATCATGGATGATGATAGCTACAATTCAGTGGATGGCATGGAGCTAACA TCACAAGGTGCTGGTACTTATTGGTATTACCACCAGAGTGTTTTGTGGTTGGGAAAG AACCACCAAGATCTCAAATAAAGTTGATGTGTGGTGGTGGTGTGATCTTCTATCA GTGTCTTTATGGAAGGAAGCCTTTTGCCATAACCAAGTCTCAGCAAGACATCTTACAA GAGAATACGATTCTTAAAGCTACTGAAGTGCAAGTCCCGCCAAAGCCGATGTAACAC CTGAAGCAAAGCGTTGATTCGACGATGCTTGGCCTACCGAAAGGAGGACCGCATTGA TGTCCAGCAGCTGGCCTGTGATCCCTACTTGTGCTCATCCGAAAGTCAGTCTCT ACGAGTAGCCCTGTGAGCTGTATTGCATCAACCTCTGGGGCGTCCAATAACAGTT CTTCTAATTGAGACTGACTCCAAGGCCACAACT	
	ORF Start: ATG at 24	ORF Stop: TGA at 2271
	SEQ ID NO: 20	749 aa MW at 85415.8kD
NOV8a, CG57871-01 Protein Sequence	MEELHSLDPRRQKLLLEARFTGVGVSKGPLNSESSNQSLCSVGSLSDEKVEETPKKKQND QRNRKRKAEPYESSQKGTFRGHKISDYFEFAGGSGPGTSPGRSVPVARSLLQHSLS NPLPRRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRLDTEQLAQRGAGLCFTF	

	VSAQQNSPSSSTGSGNTEHSCSSQKQISIQHRQTQSDLTIEKISALENSKNSDLEKKEG RIDDLLRAICDLRRQIDEQQKMLEKYKERLNRCVTMSKKLLIEKSKOEKMACRDKSMQ DRLRLGHFTTSDHGAKFTEQWTDGYAFQNLIKQQRINSQREEIERQRKMLAKRKP MGQAPPATNEQKQWKSKTNGAENETLTKEYHEQEEIFKLRLGHLKKEEAEIQAELE LERVRKLHIREVKRIHNEDNSQFYHPTLNDRYLLHLLGRGGFSEVYKAFDLTEQRY VAVKIHQLNKNWRDEKKNYHKKHACREYRIHKELDHPRIVKLYDYFSLDTSFCTVLE YCEGNDLDFYKQHKLMSEKEARSIIMQIVNALKYLNEIKPPIIHVDLKPGNILLENG TACGEIKITDFGLSKIMDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK VDVWSVGVIIFYQCLYGRKPFQHNQSQQDILQENTILKATEVQFPKPVVTPEAKALIR RCLAYRKEDRIDVQQLACDPYLLPHIRKSVSTSSPAGAAIASTSGASNNSSSN
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Further analysis of the NOV8a protein yielded the following properties shown in Table 8B.

Table 8B. Protein Sequence Properties NOV8a	
PSort analysis:	0.9600 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV8a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 8C.

Table 8C. Geneseq Results for NOV8a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM39278	Human polypeptide SEQ ID NO 2423 - Homo sapiens, 718 aa. [WO200153312-A1, 26-JUL-2001]	1..749 2..718	703/749 (93%) 707/749 (93%)	0.0
AAM41064	Human polypeptide SEQ ID NO 5995 - Homo sapiens, 809 aa. [WO200153312-A1, 26-JUL-2001]	1..749 92..809	695/750 (92%) 701/750 (92%)	0.0
AAR76062	Protein kinase PKU beta - Homo sapiens, 540 aa. [JP07132093-A, 23-MAY-1995]	210..749 1..540	525/540 (97%) 527/540 (97%)	0.0
AAR76061	Protein kinase PKU alpha - Homo sapiens, 787 aa. [JP07132093-A, 23-MAY-1995]	1..744 49..783	537/794 (67%) 592/794 (73%)	0.0
ABB20910	Protein #2909 encoded by probe	346..749 1..404	404/404 (100%) 404/404 (100%)	0.0

	expression - Homo sapiens, 404 aa. [WO200157274-A2, 09-AUG-2001]			
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In a BLAST search of public sequence databases, the NOV8a protein was found to have homology to the proteins shown in the BLASTP data in Table 8D.

Table 8D. Public BLASTP Results for NOV8a				
Protein Accession Number	Protein/Organism/Length	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UKI7	TOUSLED-LIKE KINASE 2 - Homo sapiens (Human), 749 aa.	1..749 1..749	731/749 (97%) 736/749 (97%)	0.0
O55047	TOUSLED-LIKE KINASE - Mus musculus (Mouse), 717 aa.	1..749 1..717	699/749 (93%) 705/749 (93%)	0.0
Q9Y4F7	PKU-ALPHA - Homo sapiens (Human), 719 aa (fragment).	1..749 3..719	700/749 (93%) 705/749 (93%)	0.0
Q9D5Y5	TOUSLED-LIKE KINASE 2 (ARABIDOPSIS) - Mus musculus (Mouse), 696 aa.	1..656 1..656	629/656 (95%) 640/656 (96%)	0.0
Q90ZY7	PKU-ALPHA PROTEIN KINASE - Brachydanio rerio (Zebrafish) (Zebra danio), 697 aa.	1..749 2..697	580/753 (77%) 626/753 (83%)	0.0

5 PFam analysis predicts that the NOV8a protein contains the domains shown in the Table 8E.

Table 8E. Domain Analysis of NOV8a			
Pfam Domain	NOV8a Match Region	Identities/ Similarities for the Matched Region	Expect Value
A2M: domain 1 of 1	501..523	10/23 (43%) 20/23 (87%)	4.6
Pkinase: domain 1 of 1	439..718	96/316 (30%) 213/316 (67%)	5.4e-70

Example 9.

The NOV9 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 9A.

Table 9A. NOV9 Sequence Analysis			
	SEQ ID NO: 21	2060 bp	
NOV9a, CG58590-01 DNA Sequence	GTTTTCATAGATAACCATGACAACATCCCATATGAATGGGCATGTTACAGAGGAATCA GACAGCGAAGTAAAAAATGTTGATCTTGCATCACCAGAGGAACATCAGAAGCACCAG AGATGGCTGTTGACTGCCCTGGAGATTGGGCACCAGGATGATGCCAATACGTCGAAG TGCACAGTTGGAGCGTATTTCGGCAACAACAGGAGGACATGAGGCGTAGGAGAGAGGAA GAAGGGAAAAAGCAAGAACTTGACCTTAATTCTTCCATGAGACTTAAGAAACTAGCCC AAATTCCTCCAAAGACCGGAATAGATAACCCATATGTTTGATACAGAGGAAGGAATTGT CTTAGAAAGTCCTCATTATGCTGTGAAAATATTAGAAATAGAAGACTTGTTTTCTTCA CTTTAAACATATCCAACATACTTTGGTAGATTCTCAGAGCCAGGAGGATATTTCACTGC TTTTTACAACCTTGTTCAAAATAAGGATTTCCAGAATGCATTTAAGATACACAATGCCAT CACAGTACACATGAACAAGGCCAGTCCTCCATTTCTCTTATCTCCAACGCACAAGAT CTTGCTCAAGAGGTACAAACTGTTTGAAGCCAGTTTCATCATAAGGAAGGACAAAGAAC TAACTGCTTTTGGTGAATACTCCACATATTCAAGCACTTTTACTGGGCCACGATAAGGT TGCTGAGCAGGAAATGCAGCTAGAGCCCATTACAGATGAGAGAGTTTATGAAAGTATT GGCCAGTATGGAGGAGAAAAGTGTAAAAATAGTTTCGTATAGAAAAGGCTCGTGATATTC CGTTGGGTGCTACAGTTTGTAAATGGAATGGACTCTGTCTATCATTAGCCGGATAGTAAA AGGGGGTGCTGCAGAGAAAAGTGGTCTGTTGCATGAAGGAGATGAAGTTCTAGAGATT AATGGCATTGAAATTCGGGGGAAAGATGTCAATGAGGTTTTTGACTTGTGTGTCTGATA TGCAATGGTACTTTGACTTTTGTCTGATTTCCAGTCAACAGATCAAGCCGCTCTCTGC CAAGGAAACAGTAATCCATGTAAAAGCTCATTTTGACTATGACCCCTCAGATGACCCCT TATGTTCCATGTGAGAGATTAGGTCTGTCTTTTCAAAAAGGTGATATACTTCATGTGA TCAGTCAAGAAGATCCAAACTGGTGGCAGGCCCTACAGGGAAGGGGACGATAAATCA ACCTCTAGCCGGGCTTGTTCAGGGGAAAAGCTTTTCAGCAGCAAGGGGAAGCCATGAAA CAAACCATAGAGAAGATAAGGAGGCCAGAAAAATCAGGTAACTGTGGTGTGCAAGA AGAATAAAAAGAAAGAGAAAAGGTTTTATATAATGCCAATAAAAAATGATGATTATGA CAACGAGGAGATCTTAACCTATGAGGAAATGTCACTTTATCATCAGCCAGCAAAATAGG AAGAGACCTATCATCTTGATTGGTCCACAGAACTGTGGCCAGAATGAATTGCGTCAGA GGCTCATGAACAAAGAAAAGGACCGCTTTGCATCTGCAGTTCCTCGTACAACCCGGAG TAGGCGAGACCAAGAAGTAGCCGGTAGAGATTACCACTTTGTTTTCGCGGCAAGCATTTC GAGGCAGACATAGCAGCTGGAAAAGTTTCATTGAGCATGGTGAATTTGAGAGAAGAAATTGT ATGGAACATAGCATAGATTCTGTACGGCAAGTGATCAACTCTGGCAAAATATGTCTTTT AAGTCTTCGTACACAGTCATTGAAGACTCTCCGAATTTCAGATTTGAAACCATATATT ATCTTCATTGCAACCCCTTCACAAGAAAAGACTTCGGGCATTATTGGCCAAAGAAAGGCA AGAATCCAAAGCCTGAAGAGTTGAGAGAAATCATTGAGAAGACAAGAGAGATGGAGCA GAACAATGGCCACTACTTTGATACGGCAATTGTGAATTCGATCTTGATAAAGCCCTAT CAGGAATTGCTTAGGTTAATTAACAAACTTGATACTGAACCTCAGTGGGTACCATCCA CTTGCTGAGGTGAAGAAACATCCATTCT		
	ORF Start: ATG at 17	ORF Stop: TGA at 2042	
	SEQ ID NO: 22	675 aa	MW at 77311.8kD
NOV9a, CG58590-01 Protein Sequence	MTTSHMNGHVTEESDSEVKNDLASPEEHQKHREMAVDCPGDLGTRMMPIRRSAQLER IRQQEDMRRRREEEGKKQELDNLNSMRLKKAQIPPKTGIDNPMFDTEEGIVLESFH YAVKILEIEDLFSSLKHIQHTLVDSQSQEDISLLQLLVQNKDFQNAFKIHNAITVHNM KASPPFPLISNAQDLAQEVQTVLKPVHHKEGQELTALLNTPHIQALLLAHDKVAEQEM QLEPITDERVYESIGQYGGETVKIVRIEKARDIPLGATVRNEMDSVVISRIVKGGAEE KSGLLHEGDEVLEINGIEIRGKDVNEVFDDLSDMHGTLTFVLI PSQIKPPPAKETVI HVKAHFDYDPSDDPYVPCRELGLSFQKGDILHVISQEDPNWQAYREGDEDNQPLAGL VPGKSFQQOREAMKQTI EEDKEPEKSGKLWCAKKNKKRKKVLYNANKNDYDNEEIL TYEEMSLYHQPANRKRPIILIGPQNCQONELRQLMNEKDRFASAVPRTRSRRDQE VAGRDRYHFVSRQAFEDIAAGKFIEHGEFEKNLYGTSIDSVRVQINSKICLLSLRTQ SLKTLRNSDLKPYIIFIAPPSQERLRALLAKEGNPKPEELREIIEKTREMEQNNGHY FDTAIVNSDLKAYQELLRLINKLDTEPQWVPSTWLR		
	SEQ ID NO: 23	2030 bp	
NOV9b, CG58590-02 DNA Sequence	CCATGACAACATCCCATATGAATGGGCATGTTACAGAGGAATCAGACAGCGAAGTAAA AAATGTTGATCTTGCATCACCAGAGGAACATCAGAAGCACCAGAGATGGCTGTTGAC TGCCCTTGAGATTGGGCACCAGGATGATGCCAATACGTCGAAGTGACAGTTGGAGC GTATTTCGGCAACAACAGGAGGACATGAGGCGTAGGAGAGAGGAAGGAAGGAAAAAGCA AGAACTTGACCTTAATCTTCCATGAGACTTAAGAAACTAGCCCAAAATCTCTCCAAAG ACCGGAATAGATAACCCATGTTTGATACAGAGGAAGGAATTGTCTTAGAAAGTCCTC ATTATGCTGTGAAAATATTAGAAATAGAAGACTTGTTTTCTCACTTAACATATCCA ACATACTTTGGTAGATTCTCAGAGCCAGGAGGATATTTCACTGCTTTTACAACCTTGT CAAAATAAGGATTTCCAGAATGCATTAAAGATACACAATGCCATGCATCACAGTACATATGA		

	ACAAGGCCAGTCCTCCATTTCTCTTATCTCCAACGCACAAGATCTTGCTCAAGAGGT ACAAACTGTTTTGAAGCCAGTTCATCATAAGGAAGGACAAGAACTAACTGCTTTGCTG AATACTCCACATATTACAGGCACCTTTACTGGCCCACGATAAGGTTGCTGAGCAGGAAA TGCAGCTAGAGCCCATACAGATGAGAGAGTTTATGAAAGTATTGGCCAGTATGGAGG AGAAACTGTAAAAATAGTTTCGTATAGAAAAGGCTCGTGATATTCGTTGGGTGCTACA GTTCGTAATGAAATGGACTCTGTCATCATTAGCCGATAGTAAAGGGGGTGTGTCAG AGAAAAGTGGTCTGTTGCATGAAGGAGATGAAGTTCTAGAGATTAATGGCATTGAAAT TCGGGGGAAGATGTCAATGAGGTTTTTGACCTGTTGTCTGATATGCATGGTACTTTG ACTTTTGCTCTGATTCCCAGTCAACAGATCAAGCCGCCTCTGCCAAGGAAACAGTAA TCCATGTAAAAGCTCATTTTGACTATGACCCCTCAGATGACCCCTATGTTCCATGTGCG AGAGTTAGGTCTGTCTTTCAAAAAGGTGATATACTTCATGTGATCAGTCAAGAAGAT CCAAAGTGGTGGCAGGCCTACAGGGAAGGGGACGAAGATAATCAACCTCTAGCCGGGC TTGTTCCAGGGAAAAGCTTTTCAGCAGCAAAGGGAAGCCATGAAACAAACCATAGAAGA AGATAAGGAGCCAGAAAATCAGGAAAAGTGGTGTGCAAGAAAGATAAAGAAAG AGGAAAAAGGTTTTATATAATGCCAATAAAAAATGATGATTATGACAACGAGGAGATCT TAACCTATGAGGAAAATGTCATTTATCATCAGCCAGCAAATAGGAAGAGACCTATCAT CTTGATTGGTCCACAGAACTGTGGCCAGAATGAATTGCGTCAGAGGCTCATGAACAAA GAAAAGGACCGCTTTGCATCTGCAGTTCCTCATACAACCCGGAGTAGGCGAGACCAAG AAGTAGCCGGTAGAGATTACCACTTTGTTTCGCGCAAGCATTGAGGCGAGACATAGC AGCTGGAAGTTCAATTGAGCATGGTGAATTTGAGAAGAATTTGATGGAAGTACGATA GATTCTGTACGGCAAGTATCAACTCTGGCAAAATATGTCTTTTAAGTCTTCGTACAC AGTCATTGAAGACTCTCCGGAATTCAGATTGAAACCATATATTATCTTCATGACCC CCCTTCACAAGAAAGACTTCGGGCATTATTGGCCAAAGAAGAGAAATCCAAGCCT GAAGAGTTGAGAGAAATCATTGAGAAGACAAGAGAGATGGAGCAGAACAATGGCCACT ACTTTGATACGGCAATTGTGAATTCCGATCTTGATAAAGCCTATCAGGAATTGCTTAG GTTAATTAACAACTTGATACTGAACCTCAGTGGGTACCATCTGCTGAGGTGA		
	ORF Start: ATG at 3	ORF Stop: TGA at 2028	
	SEQ ID NO: 24	675 aa	MW at 77292.8kD
NOV9b, CG58590-02 Protein Sequence	MTTSHMNHVTEESDSEVKNDLASPEEHQKHREMAVDCPGDLGTRMMPIRRSAQLER IRQQQEDMRRRREEEGKKQELDLNSSLRLKLAQIPPKTGIDNPMFDTEEGIVLESPH YAVKILEIEDLFSSSLKHIQHTLVDSQSEDISLLQLVQNKDFQNAFKIHNAITVHMN KASPPFPLISNAQDLAQEVQTVLKPVHKEGQELTALLNTPHIQALLLAHDKVAEQEM QLEPITDERVYESIGQYGGETVKIVRIEKARDIPLGATVRNEMDSVIIIRIVKGGAEE KSGLLHEGDEVLEINGIEIRGKDVNEVFDLLSDMHGTLTFVLIIPSQQIKPPAKETVI HVKAHFDYDPSDDPYVPCRELGLSFQKGDILHVISQEDPNWQAYREGDEDNQPLAGL VPGKSFOQREAMKQTIIEEDKEPEKSGKLWCAKKNKKKKVLYNANKNDYDNEEIL TYEEMSLYHOPANRKRPIILIGPQNCQONELRQRLMNKEKDRFASAVPHTRSRDQE VAGRDYHFVSRQAFEADIAAGKFIHGEFEKNLYGTSIDSVRQVINSKICLLSLRTO SLKTLRNSDLKPYIIFIAPPQERLRALLAKEGKNPKPEELREIIEKTREMEQNNGHY FDTAIVNSDLKAYQELRLINKLDTEPQWVPSTWLR		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 9B.

Table 9B. Comparison of NOV9a against NOV9b.		
Protein Sequence	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV9b	1..675 1..675	636/675 (94%) 636/675 (94%)

Further analysis of the NOV9a protein yielded the following properties shown in Table 9C.

Table 9C. Protein Sequence Properties NOV9a	
PSort analysis:	0.7000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV9a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 9D.

Table 9D. Geneseq Results for NOV9a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB94180	Human protein sequence SEQ ID NO:14494 - Homo sapiens, 503 aa. [EP1074617-A2, 07-FEB-2001]	173..675 1..503	501/503 (99%) 501/503 (99%)	0.0
AAB41921	Human ORFX ORF1685 polypeptide sequence SEQ ID NO:3370 - Homo sapiens, 269 aa. [WO200058473-A2, 05-OCT-2000]	406..675 1..269	261/270 (96%) 264/270 (97%)	e-147
AAU07123	Human novel human protein, NHP #23 - Homo sapiens, 576 aa. [WO200161016-A2, 23-AUG-2001]	143..674 31..574	224/564 (39%) 339/564 (59%)	e-109
AAU07119	Human novel human protein, NHP #19 - Homo sapiens, 560 aa. [WO200161016-A2, 23-AUG-2001]	143..654 31..554	213/544 (39%) 327/544 (59%)	e-102
AAU07115	Human novel human protein, NHP #15 - Homo sapiens, 520 aa. [WO200161016-A2, 23-AUG-2001]	143..606 31..495	196/481 (40%) 300/481 (61%)	5e-97

In a BLAST search of public sequence databases, the NOV9a protein was found to have homology to the proteins shown in the BLASTP data in Table 9E.

Table 9E. Public BLASTP Results for NOV9a				
Protein Accession Number	Protein/Organism/Length	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JLB2	PALS1 - Mus musculus (Mouse), 675 aa.	1..675 1..675	652/675 (96%) 665/675 (97%)	0.0

Q9H9Q0	CDNA FLJ12615 FIS, CLONE NT2RM4001629, WEAKLY SIMILAR TO MAGUK P55 SUBFAMILY MEMBER 3 - Homo sapiens (Human), 503 aa.	173..675 1..503	501/503 (99%) 501/503 (99%)	0.0
AAL40935	STARDUST PROTEIN MAGUK1 ISOFORM - Drosophila melanogaster (Fruit fly), 1289 aa.	252..674 829..1282	252/460 (54%) 327/460 (70%)	e-140
Q9W3H6	CG1617 PROTEIN - Drosophila melanogaster (Fruit fly), 794 aa.	252..674 294..787	252/500 (50%) 327/500 (65%)	e-132
Q9W7F1	P55-RELATED MAGUK PROTEIN DLG3 - Brachydanio rerio (Zebrafish) (Zebra danio), 576 aa.	142..673 30..573	209/556 (37%) 335/556 (59%)	e-105

PFam analysis predicts that the NOV9a protein contains the domains shown in the Table 9F.

Table 9F. Domain Analysis of NOV9a			
Pfam Domain	NOV9a Match Region	Identities/ Similarities for the Matched Region	Expect Value
L27: domain 1 of 1	186..238	19/56 (34%) 39/56 (70%)	0.049
PDZ: domain 1 of 1	256..335	21/83 (25%) 58/83 (70%)	9.7e-12
SH3: domain 1 of 1	348..415	19/68 (28%) 46/68 (68%)	0.026
Guanylate_kin: domain 1 of 1	515..624	54/113 (48%) 87/113 (77%)	6.2e-38
Peptidase_S15: domain 1 of 1	642..658	6/17 (35%) 13/17 (76%)	8.2
Caulimo_mov: domain 1 of 1	420..673	59/335 (18%) 156/335 (47%)	6.1

Example 10.

- 5 The NOV10 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 10A.

Table 10A. NOV10 Sequence Analysis			
	SEQ ID NO: 25	576 bp	
NOV10a, CG58572-01 DNA Sequence	ACCTTACTAGAAAAATGAAACCTGATGAAACTCCTATGTTTGACCCAAGTCTACTCAA AGAAGTGGACTGGAGTCAGAATACAGCTACATTTTCTCCAGCCATTTCCCCAACACAT CCTGGAGAAGGCTTGGTTTTGAGGCCCTTTGTACTGCTGACTTAAATAGAGGTTTTT TTAAGGTATTGGGTGAGCTAACAGAGACTGGAGTTGTGAGCCCTGAACAATTTATGGA ATCTTTTGAGCATATGAAGAAATCTGGGGATTATTATGTTACAGTTGTAGAAGATGTG ACTCTAGGACAGATTGTTGCTACGGCAACTCTGATTATAGAACATAAAATTCATCCATT CCTGTGCTAAGAGAGGAAGAGTAGAAGATGTTGTTGTTAGTGATGAATGCAGAGGAAA GCAGCTTGGCAAATGTTATTATCAACCCTTACTTTGCTAAGCAAGAACTGAACTGT TACAAGATTACCCTTGAATGTCTACCACAAAATGTTGGTTTCTATAAAAAGTTTGGAT ATACTGTATCTGAAGAAAACCTACATGTGTCTGGAGGTTTCTAAAGTAAAAATCTT		
	ORF Start: ATG at 15	ORF Stop: TAA at 567	
	SEQ ID NO: 26	184 aa	MW at 20749.9kD
NOV10a, CG58572-01 Protein Sequence	MKPDETPMFDPSLLKEVDWSQNTATFSPAISPTHPEGLVLRPLCTADLNRGFFKVLG QLTETGVVSPEQFMESFEHMKKSGDYVTVVEDVTLGQIVATATLI IEHKFIHSCAKR GRVEDVVVSDECRGKQLGKLLSLTLTLLSKLNCYKITLECLPQNVGFYKFGYTVSE ENYMCRRFLK		
	SEQ ID NO: 27	560 bp	
NOV10b, CG58572-02 DNA Sequence	ATGAAACCTGATGAAACTCCTATGTTTGACCCAAGTCTACTCAAAGAAGTGGACTGGA GTCAGAATACAGCTACATTTTCTCCAGCCATTTCCCCAACACATCCTGGAGAAGGCTT GGTTTTGGGGCCTCTTTGTAAGTCTGCTGACTTAAATAGAGGTTTTTTAAGGTATTGGGT CAGCTTAACAGAGACTGGAGTTGTGAGCCCTGAACAATTTATGAAATCTTTTGAGCATA TGAAGAAATCTGGGGATTATTATGTTACAGTTGTAGAAGATGTGACTCTAGGACAGAT TGTTGCTACGGCAACTCTGATTATAGAACATAAAATTCATCCATTCTGTGCTAAGAGA GGAAGAGTAGAAGATGTTGTTGTTAGTGATGAATGCAGAGGAAAGCAGCTTGGCAAAT TGTTATTATCAACCCTTACTTTGCTAAGCAAGAACTGAACCTGTTACAAGATTACCCT TGAATGTCTACCACAAAATGTTGGTTTCTATAAAAAGTTTGGATATACTGTATCTGAA GAAACTACATGTGTCTGGAGGTTTCTAAAGTAAAAATC		
	ORF Start: ATG at 1	ORF Stop: TAA at 553	
	SEQ ID NO: 28	184 aa	MW at 20649.8kD
NOV10b, CG58572-02 Protein Sequence	MKPDETPMFDPSLLKEVDWSQNTATFSPAISPTHPEGLVLGPLCTADLNRGFFKVLG QLTETGVVSPEQFMKSFEHMKKSGDYVTVVEDVTLGQIVATATLI IEHKFIHSCAKR GRVEDVVVSDECRGKQLGKLLSLTLTLLSKLNCYKITLECLPQNVGFYKFGYTVSE ENYMCRRFLK		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 10B.

Table 10B. Comparison of NOV10a against NOV10b.		
Protein Sequence	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV10b	1..184	163/184 (88%)
	1..184	164/184 (88%)

Further analysis of the NOV10a protein yielded the following properties shown in Table 10C.

Table 10C. Protein Sequence Properties NOV10a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.1206 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV10a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 10D.

Table 10D. Geneseq Results for NOV10a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG67123	Amino acid sequence of human 50287 transferase - Homo sapiens, 184 aa. [WO200164904-A2, 07-SEP-2001]	1..184 1..184	183/184 (99%) 184/184 (99%)	e-105
AAB73505	Human transferase HTFS-12, SEQ ID NO:12 - Homo sapiens, 184 aa. [WO200132888-A2, 10-MAY-2001]	1..184 1..184	183/184 (99%) 184/184 (99%)	e-105
AAB63700	Human gastric cancer associated antigen protein sequence SEQ ID NO:1062 - Homo sapiens, 200 aa. [WO200073801-A2, 07-DEC-2000]	1..184 17..200	183/184 (99%) 184/184 (99%)	e-105
AAU07779	Human novel transferase protein, NHP #22 - Homo sapiens, 184 aa. [WO200164903-A2, 07-SEP-2001]	1..184 1..184	182/184 (98%) 183/184 (98%)	e-104
AAM79992	Human protein SEQ ID NO 3638 - Homo sapiens, 206 aa. [WO200157190-A2, 09-AUG-2001]	1..184 23..206	181/184 (98%) 183/184 (99%)	e-104

- 5 In a BLAST search of public sequence databases, the NOV10a protein was found to have homology to the proteins shown in the BLASTP data in Table 10E.

Table 10E. Public BLASTP Results for NOV10a				
Protein Accession Number	Protein/Organism/Length	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96EK6	SIMILAR TO GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE - Homo sapiens (Human), 184 aa.	1..184 1..184	183/184 (99%) 184/184 (99%)	e-104
Q9JK38	EMEG32 PROTEIN (GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE) - Mus musculus (Mouse), 184 aa.	1..184 1..184	180/184 (97%) 182/184 (98%)	e-102
Q9VAI0	Probable glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine transacetylase) (Phosphoglucosamine acetylase) - Drosophila melanogaster (Fruit fly), 219 aa.	4..176 6..179	84/174 (48%) 123/174 (70%)	2e-43
Q17427	Probable glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine transacetylase) (Phosphoglucosamine acetylase) - Caenorhabditis elegans, 165 aa.	32..182 15..165	65/152 (42%) 98/152 (63%)	1e-28
O45811	T23G11.2 PROTEIN - Caenorhabditis elegans, 347 aa.	42..184 201..340	63/143 (44%) 88/143 (61%)	3e-26

Pfam analysis predicts that the NOV10a protein contains the domains shown in the Table 10F.

Table 10F. Domain Analysis of NOV10a			
Pfam Domain	NOV10a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Acetyltransf: domain 1 of 1	89..171	22/87 (25%) 62/87 (71%)	6.5e-13

Example 11.

- 5 The NOV11 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 11A.

Table 11A. NOV11 Sequence Analysis			
	SEQ ID NO: 29	709 bp	
NOV11a, CG58564-01 DNA Sequence	CCCCGCGGGCCAGCACCATGGAGGACGTGAAGCTGGAGTTCCTTCCCTTCCACAGTGC AAGGAAGACGCCGAGGAGTGGACCTACCTATGAGACGAGAGATGCAGGAAATTTTAC CTGGATTGTTCTTAGGCCCATATTCATCTGCTATGAAAAGCAAGCTACCTGTACTACA GAAACATGGAATAACCCATATAATATGCATACGACAAAATATTGAAGCAAATTTATT AAACCAAACCTTTCAGCAGTTATTTAGGTATTTAGTCTCTGGATATTGCAGATAATCCAG TTGAAAATATAATACGTTTTTCCCTATGACTAAGGAATTTATTGATGGGAGCTTACA AATGGGAGGTAAGTTCCTGTGCATGGAATGCAGGGATCTCCAGAAGTGCAGCCTTT GTTATTGCATACATTATGGAACATTGGAATGAAGTACAGGGATGCTTTTGCTTATG TTCAAGAAAGAAGATTTGTATTAATCCTAATGCTGGATTGTCCATCAACTTCAGGA ATATGAAGCCATCTACCTAGCAAAATTAACAATACAGATGATGTCAACCTCCAGATA GAAAGGTCAATTATCTGTTCAATCTGGTACCACAGGTAGTTTGAAGAGAACACATGAAG AAGAGGATGATTTTGAACCATGCAAGTGGCGACTGCACAGAATGGCTGACTTGAAGA GCAACATCATAGA		
	ORF Start: ATG at 17	ORF Stop: TGA at 686	
	SEQ ID NO: 30	223 aa	MW at 25492.2kD
NOV11a, CG58564-01 Protein Sequence	MEDVKLEFPSLPQCKEDAEEWTPMRREMQEILPGLFLGPYSSAMSKLPVLQKHGIT HIICIRQNIENFIKPNFQQLFRYLVDIADNPVENIIRFFPMTKEFIDGSLQMGKKV LVHGNAGISRSAAFIYIIMETFGMKYRDAFYVQERRFCINPNAGFVHQLQEYEAII LAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHEEEDDFGTMQVATAQNG		
	SEQ ID NO: 31	724 bp	
NOV11b, CG58564-02 DNA Sequence	ACTCTCCCACCCACCCACCAGAATGGCGGGCCAGCACCATGGAGGACGTGAAGCTGG AGTTCCCTTCCCTTCCACAGTGCAGGAAGACGCCGAGGAGTGGACCTACCTATGAG ACGAGAGATGCAGGAAATTTATCTGGATTGTTCTTAGGCCCATATTCATCTGCTATG AAAAGCAAGCTACCTGTACTACAGAAACATGGAATAACCCATATAATATGCATACGAC AAAATATTGAAGCAAACCTTTATTAACCAAACCTTCAGCAGTTATTTAGATATTTAGT CCTGGATATTGCAGATAATCCAGTTGAAAATATAATACGTTTTTCCCTATGACTAAG GAATTTATTGATGGGAGCTTACAAATGGGAGGAAAAGTTCTTGTGCATGGAATGCAG GGATCTCCAGAAGTGCAGCCTTTGTTATTGCATACATTATGGAACATTGGAATGAA GTACAGAGATGCTTTTGCTTATGTTCAAGAAAGAAGATTTGTATTAATCCTAATGCT GGATTTGTCCATCAACTTCAGGAATATGAAGCCATCTACCTAGCAAAATTAACAATAC AGATGATGTCAACCTCCAGATAGAAAGGTCAATTATCTGTTCAATCTGGTACCACAGG CAGTTTGAAGAGAACACATGAAGAAGAGGATGATTTTGAACCATGCAAGTGGCGACT GCACAGAATGGCTGACTTGAAGAGCAAC		
	ORF Start: ATG at 40	ORF Stop: TGA at 709	
	SEQ ID NO: 32	223 aa	MW at 25482.1kD
NOV11b, CG58564-02 Protein Sequence	MEDVKLEFPSLPQCKEDAEEWTPMRREMQEILSGLFLGPYSSAMSKLPVLQKHGIT HIICIRQNIENFIKPNFQQLFRYLVDIADNPVENIIRFFPMTKEFIDGSLQMGKKV LVHGNAGISRSAAFIYIIMETFGMKYRDAFYVQERRFCINPNAGFVHQLQEYEAII LAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHEEEDDFGTMQVATAQNG		
	SEQ ID NO: 33	545 bp	
NOV11c, CG58564-03 DNA Sequence	ACTCTCCCACCCACCCACCAGCCCGCGGGCCAGCACCATGGAGGACGTGAAGCTGGA GTTCCCTTCCCTTCCACAGTGCAGGAAGACGCCGAGGAGTGGACCTACCTATGAGA CGAGAGATGCAGGAAATTTTACCTGGATTGTTCTTAGGCCCATATTCATCTGCTATGA AAAGCAAGCTACCTGTACTACAGAAACATTGGAATGAAGTACAGAGATGCTTTTGCT TATGTTCAAGAAAGAAGATTTGTATTAATCCTAATGCTGGATTGTCCATCAACTTC AGGAATATGAAGCCATCTACCTAGCAAAATTAACAATACAGATGATGTCAACCTCCA GATAGAAAGGTCAATTATCTGTTTCAATCTGGTACCACAGGAGTTTGAAGAGAACACAT GAGGAAGAGGATGATTTTGAACCATGCAAGTGGCGACTGCACAGAATGGCTGACTTG AAGAGCAACATCATAGAGTGTGAATTTCTATTTGGGAAGGAGAAAAACAAGAGAAAA TTATAATGTAAATGGTAAAAAA		
	ORF Start: ATG at 39	ORF Stop: TGA at 210	
	SEQ ID NO: 34	57 aa	MW at 6695.7kD
NOV11c, CG58564-03 Protein Sequence	MEDVKLEFPSLPQCKEDAEEWTPMRREMQEILPGLFLGPYSSAMSKLPVLQKHLE		
	SEQ ID NO: 35	663 bp	
NOV11d, CG58564-04 DNA Sequence	ACTCTCCCACCCACCCACCAGCCCGCGGGCCAGCACCATGGAGGACGTGAAGCTGGA GTTCCCTTCCCTTCCACAGTGCAGGAAGACGCCGAGGAGTGGACCTACCTATGAGA CGAGAGATGCAGGAAATTTTACCTGGATTGTTCTTAGGCCCATATTCATCTGCTATGA AAAGCAAGCTACCTGTACTACAGAAACATGGAATAACCCATATAATATGCATACGACA AAATATTGAAGCAAACCTTTATTAACCAAACCTTCAGCAGTTATTTAGACTAAGGAAT		

	<u>TTATTGATGGGAGCTTACAAATGGGAGGAAAAGTTCTTGTGCATGGAAATGCAGGGAT</u> <u>CTCCAGAAGTGCAGCCTTTGTTATTGCATACATTATGGAACATTTGGAATGAAGTAC</u> <u>AGAGATGCTTTTGCTTATGTTCAAGAAAGAAGATTTGTATTAAATCCTAATGCTGGAT</u> <u>TTGTCCATCAACTTCAGGAATATGAAGCCATCTACCTAGCAAAATTAACAATACAGAT</u> <u>GATGTCACCACTCCAGATAGAAAGGTCATTATCTGTTCAATCTGGTACCACAGGCAGT</u> <u>TTGAAGAGAACACATGAAGAAGAGGATGATTTTGAACCATGCAAGTGGCGACTGCAC</u> <u>AGAATGGCTGACTTGAAGAGCAACT</u>		
	ORF Start: ATG at 39	ORF Stop: TGA at 399	
	SEQ ID NO: 36	120 aa	MW at 14245.6kD
NOV11d, CG58564-04 Protein Sequence	MEDVKLEFPSPQCKEDAEWTPMRREMQEILPGLFLGPYSSAMKSLPVLQKHGITH HIICIRQNIENAFIKPNFQQLFRLRNLLMGAYKWEKFLCMEMQGSPEVQPLLHTLW KHLE		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 11B.

Table 11B. Comparison of NOV11a against NOV11b through NOV11d.		
Protein Sequence	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV11b	1..223	222/223 (99%)
	1..223	222/223 (99%)
NOV11c	1..55	55/55 (100%)
	1..55	55/55 (100%)
NOV11d	1..81	81/81 (100%)
	1..81	81/81 (100%)

Further analysis of the NOV11a protein yielded the following properties shown in Table 11C.

5

Table 11C. Protein Sequence Properties NOV11a	
PSort analysis:	0.4698 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1958 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV11a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 11D.

Table 11D. Geneseq Results for NOV11a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU09017	Human dual specificity phosphatase 38692 - Homo sapiens, 223 aa. [WO200173059-A2, 04-OCT-2001]	1..223 1..223	223/223 (100%) 223/223 (100%)	e-128
AAE08552	Human phosphatase protein - Homo sapiens, 223 aa. [WO200160992-A2, 23-AUG-2001]	1..223 1..223	223/223 (100%) 223/223 (100%)	e-128
AAM41520	Human polypeptide SEQ ID NO 6451 - Homo sapiens, 236 aa. [WO200153312-A1, 26-JUL-2001]	1..223 14..236	223/223 (100%) 223/223 (100%)	e-128
AAM39734	Human polypeptide SEQ ID NO 2879 - Homo sapiens, 223 aa. [WO200153312-A1, 26-JUL-2001]	1..223 1..223	223/223 (100%) 223/223 (100%)	e-128
AAU23521	Novel human enzyme polypeptide #607 - Homo sapiens, 190 aa. [WO200155301-A2, 02-AUG-2001]	25..171 7..145	55/147 (37%) 80/147 (54%)	1e-18

In a BLAST search of public sequence databases, the NOV11a protein was found to have homology to the proteins shown in the BLASTP data in Table 11E.

Table 11E. Public BLASTP Results for NOV11a				
Protein Accession Number	Protein/Organism/Length	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAD10219	SEQUENCE 4 FROM PATENT WO0173059 - Homo sapiens (Human), 223 aa.	1..223 1..223	223/223 (100%) 223/223 (100%)	e-127
Q9DCF8	0610039A20RIK PROTEIN - Mus musculus (Mouse), 223 aa.	1..223 1..223	215/223 (96%) 221/223 (98%)	e-124
Q60970	PROTEIN TYROSINE PHOSPHATASE-LIKE - Mus musculus (Mouse), 223 aa.	1..223 1..223	214/223 (95%) 221/223 (98%)	e-124

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Q60969	PROTEIN TYROSINE PHOSPHATASE-LIKE - Mus musculus (Mouse), 205 aa.	1..168 1..168	163/168 (97%) 167/168 (99%)	2e-93
Q99850	TYROSINE PHOSPHATASE-LIKE PROTEIN HOMOLOG HSTYXB - Homo sapiens (Human), 66 aa (fragment).	116..181 1..66	66/66 (100%) 66/66 (100%)	3e-31

PFam analysis predicts that the NOV11a protein contains the domains shown in the Table 11F.

Table 11F. Domain Analysis of NOV11a			
Pfam Domain	NOV11a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DSPc: domain 1 of 1	28..173	64/172 (37%) 127/172 (74%)	2.2e-63
Y_phosphatase: domain 1 of 1	35..179	35/279 (13%) 93/279 (33%)	1.7

Example 12.

The NOV12 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 12A.

Table 12A. NOV12 Sequence Analysis		
	SEQ ID NO: 37	3696 bp
NOV12a, CG57819-01 DNA Sequence	GTGTA AAAA TACTGTCCATTTAATGTTTTCTGGGACTTTAGGTAAGAATATGAAACT CAACCAACCTTGAGCAGGATGAACCGGGAGGAATTGGAGGACAGTTTCTTTTCGACTTC GCGAAGATCACATGTTGGTGAAGGAGCTTTCTTGGAAAGCAACAGGATGAGATCAAAAG GCTGAGGACCACCTTGCTGCGGTTGACCGCTGCTGGCCGGGACCTGCGGGTCGCGGAG GAGGCGGCGCCGCTCTCGGAGACCGCAAGGCGGGGAGAGGCGGGATGGCGGCAGC GCCTCTCCATGCACCAAGCGCCCCAGATGCACCGACTGCAAGGGCATTTCCACTGCGT CGGCCCTGCCAGCCCCCGCGCGCCAGCCTCGCGTCCAAGTGGGACACAGACAGCTC CACACAGCCGGTGACCCGGTGCCCGGAGAAACCAAGAGGGGTAGGGACAGGCTGAGCT ACACAGCCCCCTCCATCGTTTAAGGAGCATGCGACAAATGAAAACAGAGGTGAAGTAGC CAGTAAACCCAGTGAAGTGGCCACATCATGGCCAGCAATACCATGCAAGTGAAGAG CCACCCAAGTCTCCTGAGAAAATGTGGCCTAAAGATGAAAATTTGAAACAGAGAAGCT CATTGGAGTGTGCTCAGAAGGCTGCAGAGCTTCGGGCTTCCATTAAAGAGAAGGTAGA GCTGATTTCGACTTAAGAAGCTCTTACATGAAAGAAATGCTTCATTGGTTATGACAAAA GCACAATTAACAGAAGTTCAAGAGGTGAGTTGCCATCTTTTGACCCAGAATCAGGGAA TCCTGAGTGCAGCCCATGAGGCCCTCCTCAAGCAAGTGAATGAGCTCAGGGCAGAGCT GAAGGAAGAAAGCAAGAAGGCTGTGAGCTTGAAGAGCCAACCTGGAAGATGTGCTATC TTGCAGATGACTCTGAAGGAGTTTCAGGAGAGAGTTGAAGATTTGGAAAAAGAACGAA AATTGCTGAATGACAATTATGACAACTCTTAGAAAGCAGTGACAGCTCCAGTCAGCC CCACTGGAGCAACGAGCTCATAGCGGAACAGCTACAGCAGCAAGTCTCTCAGCTGCAG GATCAGCTGGATGCTGAGCTGGAGGACAAGAGAAAAGTTTTTACTTGAGCTGTCCAGGG AGAAAGCCCAAAATGAGGATCTGAAGCTTGAAGTCACCAACATACTTCAGAAGCATAA ACAGGAAGTAGAGCTCCTCCAAAATGCAGCCACAATTTCCCAACCTCCTGACAGGCCAA TCTGAACCAAGCCACTCACCCAGCTGTATTGCAAGAGAACACTCAGATCCAGCCAAAGTG AACCCAAAAACCAAGAAGAAAAGAACTGTCCAGGTGCTAAATGAGTTGCAAGTATC ACACGCAGAGACCACATTGGAACCTAGAAAAGACCAGGGACATGCTTATTCTGCAGCGC AAAATCAACGTGTGTTATCAGGAGGAAGTGGAGGCAATGATGACAAAAGCTGACAATG	

	ATAATAGAGATCACAAAGAAAAGCTGGAGAGGTTGACTCGACTACTAGACCTCAAGAA TAACCGTATCAAGCAGCTGGAAGAACAGCTCAAAGATGTTGCTTATGGCACCCGACCG TTGTCGTTATGTTTGGAAACACTGCCAGCCCATGGAGATGAGGATAAAGTGGATATTT CTCTGCTGCATCAGGGTGAGAATCTTTTGAAGTGCACATCCACAGGCCTTCTCTGAC ATCTGCCGCCCTAGCTCAGGCTGGAGATACCAACCTACCCTTTCTGCACCTATTCC TTCTATGACTTTGAAACCCACTGTACCCCATTTATCTGTGGGGCCACAGCCCTCTATG ACTTCACCTCCAGTATGTGATGGAGACAGATTGCTTTTCTTACACTACCTTCAAGA GGCTTCAGCCCGGCTTGACATACACCAGGCCATGGCCAGTGAACACAGCACTCTTGCT GCAGGATGGATTTGCTTTGACAGGGTGCTAGAGACTGTGGAGAAAGTCCATGGCTTGG CCACACTGATTGGTGCTGGTGGAAGAAGTTCCGGGGTTCTAGAGTACTGGATGAGGCT GCGTTTCCCATAAAACCCAGCCTACAGGCGTGCAATAAACGAAAGAAAGCCAGGTC TACCTGTCAACCGATGTGCTTGGAGGCCGGAAGGCCAGGAAGAGGAGGTGAGATCGG AGTCTTGGGAACCTCAGAACGAGCTGTGGATTGAAATCACCAGTGTGCTGGCCCTCCG GAGTCGATGGCTGGGAACCAACCCAGTCCATATGCTGTGTACCGCTTCTTACCTTT TCTGACCATGACACTGCCATCATTTCCAGCCAGTAACAACCCCTACTTTAGAGACCGG CTCGATTCCCAGTGCTTGTGACCTCTGACCTGGACCATTATCTGAGACGGGAGGCCTT GTCTATACATGTTTTTGTATGATGAAGACTTAGAGCCTGGCTCGTATCTTGGCCGAGCC CGAGTGCCTTTACTGCCTCTTGCAAAAAATGAATCTATCAAAGGTGATTTTAACTCA CTGACCCCTGCAGAGAAACCCACGGATCTATTCAAGTGCAACTGGATTGGAAGTTTCC CTACATACCCCTGAGAGCTTCTGAAACCGAAGCTCAGACTAAGGGGAAGGATACC AAGGACAGTTCAAAGATCTCATCTGAAGAGGAAAAGGCTTCATTTCTTCCAGGATC AGATGGCATCTCCTGAGGTTCCCATTTGAAGCTGGCCAGTATCGATCTAAGAGAAAACC TCTCTATGGGGGAGAAAGAAAGGAGAAGGAGCACCAGGTTGTGAGCTACTCAAGAAGA AAACATGGCAAAAGAAATAGGTGTTCAAGGAAAAGAAATAGAATGGAGTATCTTAGCCTTA ACATCTTAAATGGAATACACTGAAGCAGGTGAATTACACTGAGTGAAGTTCTCAGA GACTAACAGCTTTCATAGGTGATGGCTTTAAAAATCAGCAGGAGGAAGGAAATGACA TTATCCCATTCAGCACTGAAACAGAAGGAACCTCTACATCCTGTAATGACAAAGAAAT CCTCTGAACAAGGTTCTGAAGTCAGTGAAGCACAACCTACCGACAGTGATGATGTCTAT AGTGCCACCCATGTCTCAGAAATATCCTAAGGCAGATTGAGAGAAGATGTGATTTGAA ATTGTTCTCCCTGGCCTTCTACCCAGAGGCAGAAGTGATGTCTGATGAGAACATAAAAC AGGTGTATGTGGAGTACAAATCTACGACCTACCTTGTGCGGAGACAGAGACTCCAGT GTCCCTAAGGAAGCTTAGGGCAGGAGAAGAAATCCACTTTCACCTTAGCAAGGTAATA GACCTGGACCCACAGGAGCAGCAAGGCCGAAGGCGGTTTCTGTTGACATGCTGAATG GACAAGATCCTGATCAAGGACAGTTAAAGTTTACAGTGGTAAGTGTCTCTGGATGA AGAAAAGAAAGAAATGTGAAGAAGTGGGATATGCATATCTTCAACTGTGGCAGATCTG GAGTCAGGAAGAGATATTCTAGAGCAAGAGCTAGACGTTGTTAGCCCTGAAGATCTGG CTACCCCAATAGGAAGGCTGAAGGTTTCCCTTCAAGCAGCTGCTGTCTCCATGCTAT TTACAAGGAGATGACTGAAGATTGTTTTTCAAGGAACA		
	ORF Start: ATG at 23	ORF Stop: TGA at 3686	
	SEQ ID NO: 38	1221 aa	MW at 139825.2kD
NOV12a, CG57819-01 Protein Sequence	MFSGTLGKNMKTQPLSRMNREELEDSFFRLREDHMLVKELSWKQQDEIKRLRTLLR LTAAGRDLRVAAEAAFLSETARRGQKAGWRQRLSMHQRPMHRLQGHFHCVGPAAPRR AQPRVQVGHRLHTAGAPVPEKPKRGRDRLSYTAPPSFKEHATNENRGEVASKPSELA HIMASNTMQVEEPPKSPKMWPKDENFEQRSSLECAQKAELRASIKKVELIRLKKL LHERNASLVMTKAQLTEVQEVSVCHLLTQNGILSAAHEALLQVNLRAELKEESKKA VSLKSQLEDVSILOMTLKEFQERVEDLEKERKLLNDNYDKLLESSDSSSPHWSNELI AEQLQQQVSQLQDQDAELEDKRVLLELSREKAQNEIDLKLEVTNIIQKHKQEVLLQ NAATISQPPDRQSEPATHPAVLQENTQIQPSEPKNQEEKLSQVLNQLQVSHAETTL LEKTRDMLILQRKINVCYQEELEAMMTKADNDNRDHKEKLERLRLDLKNNRIKQLE EQLKDVAYGTRPLSLCLETLPAHGEDKVDISLLHQGENLFELHIIHQAFITSAALAAQ GDTQPTTFCTYSFYDFETHCTPLSVGPQPLYDFTSQYVMTDSLFHLQLQASARLDI HQAMASEHSTLAAGWICFDRVLETVEKVHGLATLIGAGGEEFGVLEYWMRLRFPKPS LQACNKRKKAQVYVLTDLVGGKKAQEEVRSSESWEPQNELWIEITKCCGLRSRWLGTQ PSPYAVYRFFTFSDHDTAII PASNNPYFRDQARFPVLVTSDDLHLYLRREALSIHVFD EDLEPGSYLGRARVPLPLAKNESIKGDFNLTPAEKPNNGSIQVQLDWKFPYIPPEF LKPEAQTKGDKTDSKISSEEEKASFPSQDQMASPEVPIEAGQYRSKRKPPHGGERR EKEHQVVSYSRRKHGKRIGVQGNRMEYLSLNIILNGNTLKQVNYTEWKFSETNSFIGD GFKNQHEEEMTLSSALKQKEPLHPVNDKESSEQGEVSEAQTDSDDVIVPPMSQK YPKADSEKMCIEIVSLAFYPEAEVMSDENIKQVYVEYKFYDLPLSETETPVSLRKPR GEEIHFFHFSKVIDLDPQEQGRRRFLFDMLNGQDPDQGLKFTVSDPLDEEKECEE VGYAYLQLWQILESGRDILEQELDVVSPEDLATPIGRKLVSLQAAAVLHAIYKEMTED LFS		

Further analysis of the NOV12a protein yielded the following properties shown in Table 12B.

Table 12B. Protein Sequence Properties NOV12a	
PSort analysis:	0.9600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV12a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 12C.

Table 12C. Geneseq Results for NOV12a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV12a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM78558	Human protein SEQ ID NO 1220 - Homo sapiens, 1179 aa. [WO200157190-A2, 09-AUG-2001]	63..1219 47..1177	400/1193 (33%) 640/1193 (53%)	e-172
AAM79542	Human protein SEQ ID NO 3188 - Homo sapiens, 1160 aa. [WO200157190-A2, 09-AUG-2001]	63..1219 28..1158	400/1193 (33%) 640/1193 (53%)	e-172
AAM41414	Human polypeptide SEQ ID NO 6345 - Homo sapiens, 1160 aa. [WO200153312-A1, 26-JUL-2001]	63..1219 28..1158	400/1193 (33%) 640/1193 (53%)	e-172
AAM39628	Human polypeptide SEQ ID NO 2773 - Homo sapiens, 1128 aa. [WO200153312-A1, 26-JUL-2001]	118..1219 47..1126	390/1138 (34%) 623/1138 (54%)	e-171
AAG75661	Human colon cancer antigen protein SEQ ID NO:6425 - Homo sapiens, 118 aa. [WO200122920-A2, 05-APR-2001]	445..523 33..111	40/79 (50%) 56/79 (70%)	1e-13

- 5 In a BLAST search of public sequence databases, the NOV12a protein was found to have homology to the proteins shown in the BLASTP data in Table 12D.

Table 12D. Public BLASTP Results for NOV12a				
Protein Accession Number	Protein/Organism/Length	NOV12a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96KN7	RPGR-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1286 aa.	7..1221 29..1286	1203/1258 (95%) 1207/1258 (95%)	0.0
Q96QA8	RPGR-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1286 aa.	7..1221 29..1286	1203/1258 (95%) 1207/1258 (95%)	0.0
Q9GLM3	RPGR-INTERACTING PROTEIN-1 - Bos taurus (Bovine), 1221 aa.	1..1221 1..1221	922/1234 (74%) 1031/1234 (82%)	0.0
Q9NR40	RPGR-INTERACTING PROTEIN - Homo sapiens (Human), 902 aa.	331..1221 1..902	883/902 (97%) 888/902 (97%)	0.0
Q9HBK6	RPGR-INTERACTING PROTEIN-1 - Homo sapiens (Human), 762 aa.	471..1221 1..762	742/763 (97%) 746/763 (97%)	0.0

PFam analysis predicts that the NOV12a protein contains the domains shown in the Table 12E.

Table 12E. Domain Analysis of NOV12a			
Pfam Domain	NOV12a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PFEMP: domain 1 of 1	293..413	23/176 (13%) 82/176 (47%)	7.9
C2: domain 1 of 1	736..825	14/101 (14%) 54/101 (53%)	1.4

Example 13.

- 5 The NOV13 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 13A.

Table 13A. NOV13 Sequence Analysis			
	SEQ ID NO: 39	678 bp	
NOV13a, CG57789-01 DNA Sequence	TGGGGCGGGAGGCATGGTCTCCACCTACCGGGTGGCCGTGCTGGGGCGCGAGGTGTG GGCAAGAGTGCCATCGTGCGCCAGTTCTTGTAACAGAGTTACAGCGAGGTCTGCGTCC CCACCACCGCCCGCCGCTTTACCTGCCTGCTGTGTCGTATGAACGGCCACGTGCACGA CCTCCAGATCCTCGACTTTCACCCATCAGCGCCTTCCCTGTCAATACGCTCCAGGAG TGGGCAGACACCTGCTGCAGGGGACTCCGGAGTGTCCACGCCTACATCCTGGTCTACG ACATCTGCTGCTTTGACAGCTTTGAGTACGTCAAGACCATCCGCCAGCAGATCCTGGA GACGAGGTGATCGGAACCTCAGAGACGCCCATCATCATCGTGGGCAACAAGCGGGAC CTGCAGCGCGGACGCGTGATCCCGCGCTGGAACGTGTGCGACCTGGTACGCAAGACCT GGAAGTGCGGCTACGTGGAATGCTCGGCCAAGTACAACCTGGCACATCCTGCTGCTCTT CAGCGAGCTGCTCAAGAGCGTCCGCTCGCCCGTTCGAAGCACGTGCACGCTGCCCTG CGCTTCCAGGGCGCGTGCGCCGCAACCGCTGCGCCATCATGTGACGCCCTGCGCGCCC CTCGGCTGCACCGGCACTGGCCGAGCGGAGGGCGGGGC		
	ORF Start: ATG at 14	ORF Stop: TGA at 623	
	SEQ ID NO: 40	203 aa	MW at 23229.0kD
NOV13a, CG57789-01 Protein Sequence	MVSTYRVAVLGARGVGKSAIVRQFLYNEFSEVCPVTARRLYLPAVVMNGHVHDLQIL DFPPISAFPVNTLQEWADTCCRGLRSVHAYILVYDICCDFSFEYVKTIHQIILETRVIG GTSETPIIIVGNKRDLQRGRVPRWNVSHLVKRTWKCGYVECSAKYNWHILLFSELL KSVGCARCKHVHAALRFQALRRNRCAIM		
	SEQ ID NO: 41	682 bp	
NOV13b, CG57789-02 DNA Sequence	TGGGAGGCATGGTCTCCACCTACCGGGTGGCCGTGCTGGGGCGCGAGGTGTGGGCAA GAGTGCCATCGTGCGCCAGTTCTTGTAACAGAGTTACAGCGAGGTCTGCGTCCCCACC ACCGCCCGCGCCTTTACCTGCCTGCTGTGTCGTATGAACGGCCACGTGCACGACCTCC AGATCCTCGACTTTCACCCATCAGCGCCTTCCCTGTCAATACGCTCCAGGAGTGGGG AGACACCTGCTGCAGGGGACTCCGGAGTGTCCACGCCTACATCCTGGTCTACGACATC TGCTGCTTTGACAGCTTTGAGTACGTCAAGACCATCCGCCAGCAGATCCTGGAGACGA GGGTGATCGGAACCTCAGAGACGCCCATCATCATCGTGGGCAACAAGCGGGACCTGCA GCGCGGACGCGTGATCCCGCGCTGGAACGTGTGCGACCTGGTACGCAAGACCTGGAAG TGGCGGTACGTGGAATGCTCGGCCAAGTACAACCTGGCACATCCTGCTGCTCTTACGG AGCTGCTCAAGAGCGTCCGCTGCGCCCGTTGCAAGCACGTGCACGCTGCCCTGCGCTT CCAGGGCGCGTGCGCCGCAACCGCTGCGCCATCATGTGACGCCCTGCGCGCCCCTCGG GCTGCACCGGCACTGGCCGAGCGGAGGGCACTGGCCGAGCGGAG		
	ORF Start: ATG at 9	ORF Stop: TGA at 618	
	SEQ ID NO: 42	203 aa	MW at 23229.0kD
NOV13b, CG57789-02 Protein Sequence	MVSTYRVAVLGARGVGKSAIVRQFLYNEFSEVCPVTARRLYLPAVVMNGHVHDLQIL DFPPISAFPVNTLQEWADTCCRGLRSVHAYILVYDICCDFSFEYVKTIHQIILETRVIG GTSETPIIIVGNKRDLQRGRVPRWNVSHLVKRTWKCGYVECSAKYNWHILLFSELL KSVGCARCKHVHAALRFQALRRNRCAIM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 13B.

Table 13B. Comparison of NOV13a against NOV13b.		
Protein Sequence	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV13b	1..203	203/203 (100%)
	1..203	203/203 (100%)

Further analysis of the NOV13a protein yielded the following properties shown in Table 13C.

Table 13C. Protein Sequence Properties NOV13a	
PSort analysis:	0.6500 probability located in plasma membrane; 0.5064 probability located in mitochondrial matrix space; 0.3844 probability located in microbody (peroxisome); 0.2556 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV13a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 13D.

Table 13D. Geneseq Results for NOV13a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB42840	Human ORFX ORF2604 polypeptide sequence SEQ ID NO:5208 - Homo sapiens, 136 aa. [WO200058473-A2, 05-OCT-2000]	1..136 1..136	136/136 (100%) 136/136 (100%)	2e-75
AAM41682	Human polypeptide SEQ ID NO 6613 - Homo sapiens, 206 aa. [WO200153312-A1, 26-JUL-2001]	5..174 15..173	66/171 (38%) 89/171 (51%)	4e-18
AAM39896	Human polypeptide SEQ ID NO 3041 - Homo sapiens, 199 aa. [WO200153312-A1, 26-JUL-2001]	5..174 8..166	66/171 (38%) 89/171 (51%)	4e-18
AAY99656	Human GTPase associated protein-7 - Homo sapiens, 281 aa. [WO200031263-A2, 02-JUN-2000]	5..173 25..191	59/179 (32%) 87/179 (47%)	3e-14
AAR05075	RAP1A Gene product incorporating at least one peptide associated with ras oncogene - Synthetic, 184 aa. [WO9000179-A, 11-JAN-1990]	5..177 4..165	57/175 (32%) 90/175 (50%)	5e-14

In a BLAST search of public sequence databases, the NOV13a protein was found to have homology to the proteins shown in the BLASTP data in Table 13E.

Table 13E. Public BLASTP Results for NOV13a				
Protein Accession Number	Protein/Organism/Length	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96S79	RAS-LIKE PROTEIN/VTS58635 - Homo sapiens (Human), 203 aa.	1..203 1..203	203/203 (100%) 203/203 (100%)	e-118
Q92737	Ras-like protein RRP22 (RAS-related protein on chromosome 22) - Homo sapiens (Human), 203 aa.	1..203 1..203	105/204 (51%) 134/204 (65%)	3e-50
Q95KD9	HYPOTHETICAL 22.5 KDA PROTEIN - Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), 199 aa.	5..174 8..166	66/171 (38%) 89/171 (51%)	1e-17
Q96HU8	SIMILAR TO CG8500 GENE PRODUCT - Homo sapiens (Human), 199 aa.	5..174 8..166	66/171 (38%) 89/171 (51%)	1e-17
Q9NF75	EG:BACR37P7.8 PROTEIN - Drosophila melanogaster (Fruit fly), 306 aa.	5..174 48..210	61/174 (35%) 88/174 (50%)	4e-16

Pfam analysis predicts that the NOV13a protein contains the domains shown in the Table 13F.

Table 13F. Domain Analysis of NOV13a			
Pfam Domain	NOV13a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Semialdehyde_dh: domain 1 of 1	4..14	4/11 (36%) 11/11 (100%)	0.75
ras: domain 1 of 1	6..203	56/224 (25%) 125/224 (56%)	1.2e-12

Example 14.

- 5 The NOV14 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 14A.

Table 14A. NOV14 Sequence Analysis			
	SEQ ID NO: 43	1790 bp	
NOV14a, CG57758-01 DNA Sequence	TCTCCCTCCCGCGCATGGCCTCGGCGCTGAGCTATGTCTCCAAGTTCAAGTCCTTCG TGATCTTGTTCGTACCCCGCTCCTGCTGCTGCCACTCGTCATTCTGATGCCCGCAA GGTCAGTTGTGCTACGTCATCATCTCATGGCCATTTACTGGTGACACAGAAGTCATC CCTCTGGCTGTACCTCTCTCATGCCTGTCTTGCTTTTCCCACTCTTCCAGATTCTGG ACTCCAGGCAGGTGTGTGTCCAGTACATGAAGGACACCAACATGCTGTTCTGGGCGG CCTCATCGTGGCCGTGGCTGTGGAGCGCTGGAACCTGCACAAGAGGATCGCCCTGCGC ACGCTCCTCTGGGTGGGGGCCAAGCCTGCACGGCTGATGCTGGGCTTCATGGGCGTCA CAGCCCTCCTGTCCATGTGGATCAGTAACACGGCAACCACGGCCATGATGGTGCCCAT CGTGGAGGCCATATTGCAGCAGATGGAAGCCACAAGCGCAGCCACCGAGGCCGCTG GAGCTGGTGGACAAGGGCAAGGCCAAGGAGCTGCCAGGGAGTCAAGTGATTTTGAAG GCCCCACTCTGGGGCAGCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGAC CCTGTGCATCTGCTACGCGGCCAGCATCGGGGGCACCGCCACCTGACCGGGACGGGA CCCCACGTGGTGCTCCTGGGCCAGATGAACGAGTTGTTTCTGACAGCAAGGACCTCG TGAACCTTGTCTCCTGGTTTGCAATTTGCCCTTTCCCAACATGCTGGTGATGCTGCTGTT CGCTTGGCTGTGGCTCCAGTTTGTGTTTACATGTTTCTCCAGTTTAAAAAGTCTCTGGGG TGCGGGCTAGAGAGCAAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGT ACCGGAAGCTGGGGCCCTTGTCTTTCGCGGAGATCAACGTGCTGATCTGCTTCTTCTCT GCTGGTCACTCTGTGGTTCTCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTT GCCTGGGTGGAGGGTGAGACAAAGTATGTCTCCGATGCCACTGTGGCCATCTTTGTGG CCACCCTGCTATTTCATTGTGCCTTTCACAGAAGCCCAAGTTTAACTTCCGACGCCAGAC TGAGGAAGGTAAGTCTCCTGTTCTGATCGCCCCCTCCCTGCTGGATTGGAAGGTA ACCCAGGAGAAAGTGCCTTGGGGCATCGTGCTGCTACTAGGGGGCGGATTGCTCTGG CTAAAGGATCCGAGGCCCTCGGGGCTGTCGCTGTGGATGGGGAAGCAGATGGAGCCCTT GCACGCAGTGCACCCCGCAGCCATCACCTTGATCTTGCTTCTGCTGCTGGTCCGTGTT ACTGAGTGACAAGCAACGTGGCCACCACCACCTTGTTCTGCCCATCTTTGCCTCCA TGCTCTCGCTCCATCGGCCCTCAATCCGCTGTACATCATGCTGCCCTGTACCCTGAGTGC CTCCTTTGCTTTCATGTTGCTGTGGCCACCCTCCAAATGCCATCGCTTTCACCTAT GGGCACCTCAAGGTTGCTGACATGGTGAAACAGGAGTCATAATGAACATAATTGGAG TCTTCTGTGTGTTTTTGGCTGTCAACACCTGGGGACGGGCCATATTGACTTGGATCA TTTCCCTGACTGGGCTAATGTGACACATATTGAGACTTAGGAAGAGCCACAAGACCAC ACACACAGCCCTTACCCTCCTCAGGACTACCGAACCTTCTGGCACACCTT		
	ORF Start: ATG at 16	ORF Stop: TAG at 1720	
	SEQ ID NO: 44	568 aa	MW at 62592.9kD
NOV14a, CG57758-01 Protein Sequence	MASALSYVSKFKSFVILFVTPLLLLPLVILMPAKVSCAYVILMAIYWCTEVIPLAVT SLMPVLLFLPLFQILDNRQVCVQYMKDTNMLFLGGLIVAVAVERNLHKRIALRLTLWV GAKPARLMLGFMGVNTALLSMWISNTATTAMVPIVEAILQMEATSAATEAGLELVDK GKAKELPGSQVIFEGPTLGGQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVVL LGQMNELFPDSKDLVNFASWFAFAFPNMLVMLLFAWLWLQFVYMFSSFKKSWGCGLES KKNEKAALKVLQEEYRKLGPLSFAEINVLICFFLLVILWFSRDPGFMPGWLTVAWVEG ETKYVSDATVAIFVATLLFIVPSQKPKFNFRSQTEEGKSPVLIAPPLLDWKVTQEKV PWGIVLLGGGFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLVAVTTECTS NVATTTFLFPIFASMSRSIGLNPLYIMLPCTLSASFAMLPVATPPNAIVFTYGHCLKV ADMVKTGVIMNIIGVPCVFLAVNTWGRAIFDLDFPDWANVTHIET		
	SEQ ID NO: 45	1899 bp	
NOV14b, CG57758-02 DNA Sequence	CGTCTCGCCCGCCAGTCTCCCTCCGCGCGATGGCCTCGGCGCTGAGCTATGTCTCCA AGTTCAAGTCCTTCGTGATCTTGTTCGTACCCCGCTCCTGCTGCTGCCACTCGTCAT TCTGATGCCCGCAAGGTCAAGTGTGCTGTGCCTACGTCATCATCCTCATGGCCATTTAC TGGTGACAGAAGTCATCCTCTGGCTGTGCACTCTCTCATGCTGTCTTGCTTTTCC CACTCTTCCAGATTCTGGAATCCAGGCAGGTGTGTGTCCAGTACATGAAGGACACCAA CATGCTGTTCTTGGGCGGCCTCATCGTGGCCGTGGCTGTGGAGCGCTGGAACCTGCAC AAGAGGATCGCCCTGCGCACGCTCCTCTGGGTGGGGCCAAGCCTGCACGGCTGATGC TGGGCTTCATGGGCGTACAGCCCTCCTGTCCATGTGGATCAGTAACACGGCAACCAC GGCCATGATGGTGCCCATCGTGGAGGCCATATTGCAGCAGATGGAAGCCACAAGCGCA GCCACCGAGGCCGCGCTGGAGGGACAAGGTACCACAATAAACAACTGAATGCATCGG AGGATGATACAGTGAAGCAGTACTAGGAGGAAAGTGTGTAGCTATAATAAGCACTTA CGTCAAAAAGTAGAAAACTTCAAATAACAATCTAATGACACCTCTTAAAAAATA GAAAAGCAAGAGCAACAGGACCTAGGGCCTGGCATCAGGCCTCAGGACTCTGCCCACT GCCAGGAAGACCAAGAGCGGAAGAGTTGTGTAAGGCCATGACCTGTGCATCTGTGTA CGCGGCCAGCATCGGGGGCACCGCCACCCTGACCGGGACGGGACCAACGTTGGTGCTC CTGGGCCAGATGAACGAGTTGTTTCTGACAGCAAGGACCTCGTGAACCTTGTCTTCT GGTTTGCACTTGCTTTTCCCAACATGCTGGTGATGCTGCTGTTGCTGCTGGCTGTGGCT CCAGTTTGTGTTTACATGTTCTCCAGTTTAAAAAGTCTTGGGGCTGCGGGCTAGAGAGC AAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGTACCGGAAGCTGGGGC CCTTGCTCTTCGCGGAGATCAACGTGCTGATCTGCTTCTTCTGCTGGTCACTCTGTG GTTCTCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTTGCTCGGTGGTGGAGGT GAGACAAAGTCAGTCTCCGATGCCACTGTGGCCATCTTTTGTGGCCACCTGCTATTCA TTGTGCCTTCACAGAAGCCCAAGTTTAACTTCCGAGCCAGACTGAGGAAGGTAAGTC TCCTGTTCTGATCGCCCCCTCCCTGCTGGATTGGAAGGTAACCCAGGAGAAAGTG CCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGCTGCTAAAGGATCCGAGG		

	CCTCGGGGCTGTCCGTGTGGATGGGAAGCAGATGGAGCCCTTGACGCGAGTGCCCCC GGCAGCCATCACCTTGATCTTGTCTCTGCTCGTTGCCGTGTTCACTGAGTGCAACAAGC AACGTGGCCACCACCACCTTGTTCCTGCCCATCTTGCCTCCATGTCTCGCTCCATCG GCCTCAATCCGCTGTACATCATGCTGCCCTGTACCCTGAGTGCCCTCCTTTGCCCTCAT GTTGCTGTGGCCACCCCTCCAATGCCATCGTGTTCACCTATGGGCACCTCAAGGTT GCTGACATGGTAAAAACAGGAGTCATAATGAACATAATTGGAGTCTTCTGTGTGTTTT TGGCTGTCAACACCTGGGGACGGGCCATATTGACTTGGATCATTTCCCTGACTGGGC TAATGTGACACATATTGAGACTTAGGAAGAGCCACAAGACCAC		
	ORF Start: ATG at 31	ORF Stop: TAG at 1879	
	SEQ ID NO: 46	616 aa	MW at 67816.9kD
NOV14b, CG57758-02 Protein Sequence	MASALSYSVKFSFVILFVTPLLLLPLVILMPAKVSCCAYVILMAIYWCTEVIPLAV TSLMPVLLFPLFQILDSRQVCVQYMKDTNMLFLGGLIVAVAVERNLHKRIALRTLLW VGAKPARMLMGFMGTALLSMWISNTATTAMVPIVEAILQMEATSAAEAGLEGQG TTINNLNALEDDTVKAVLGGKCVAIISTYVKKVEKLQINNLMTPKKLEKQEQDGLG GIRPQDSAQCQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVLLGQMNELFPD SKDLVNFASFAPFAPNMLVMLLFAWLWLQFVYMFSSFKKSWCGLESKKNEKAALKV LQEEYRKLGPLSFAEINVLI CFLLVILWFSRDPGFMPGWLTVAVVEGETKSVSDATV AIFVATLLFIVPSQPKPFNFRSQTEEGKSPVLIAPPPLLDWKVTOEKVPWGI VLLLGG GFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLLVAVFTECTSNVATTTFLFP IFASMSRSIGLNPLYIMLPCTLSASFAMLPVATPPNAIVFTYGHKLKVDMMVKTGVM NIIGVFCVFLAVNTWGRAIFDLDFPDWANVTHIET		
	SEQ ID NO: 47	1899 bp	
NOV14c, CG57758-03 DNA Sequence	CGTCTCGCCCGCCAGTCTCCCTCCCGCGCGATGGCCTCGGCGCTGAGCTATGTCTCCA AGTTCAAGTCCTTCGTGATCTTGTTCGTACCCCGCTCCTGCTGCTGCCACTCGTCAT TCTGATGCCCGCCCAAGTCAAGTTCGTGTGCTACGTCATCATCTCATGGCCATTAC TGGTGACACAGAAGTCATCCCTCTGGCTGTACCTCTCTCATGCCCTGTCTTGCTTTTCC CACTCTTCCAGATTCTGGACTCCAGGCAGGTGTGTGTCCAGTACATGAAGGACACCAA CATGCTGTTCTCGGGCGGCCTCATCGTGGCCGTGGCTGTGGAGCGCTGGAACCTGCAC AAGAGGATCGCCCTGCGCACGCTCCTCTGGGTGGGGGCCAAGCCTGCACGGCTGATGC TGGGCTTCATGGGCGTCACAGCCCTCCTGTCCATGTGGATCAGTAACACGGCAACCAC GGCCATGATGGTGCCCATCGTGGAGGCCATATTGCAGCAGATGGAAGCCACAAGCGCA GCCACCGAGCGCGCCTGGAGGGACAAGGTACCACAATAAACAACTGAATGCACTGG AGGATGATACAGTGAAAGCAGTACTAGGAGGAAAGTGTGTAGCTATAATAAGCACTTA CGTCAAAAAGTAGAAAACTTCAAATAAACAATCTAATGACACCTCTTAAAAAACTA GAAAAGCAAGAGCAACAGGACCTAGGGCCTGGCATCAGGCCTCAGGACTCTGCCCACT GCCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGACCCTGTGCATCTGCTA CGCGGCCAGCATCGGGGCGACCGCCACCCTGACCGGGACGGGACCAACCGTGGTGCTC CTGGGCCAGATGAACAGAGTTGTTTCTTGACAGCAAGGACCTCGTGAACCTTGTCTTCT GGTTTGCAATTGTCCTTTCCCAACATGCTGGTGATGCTGCTGTTTCGCTGGCTGTGGCT CCAGTTTGTTTACATGTTCTCCAGTTTAAAAAGTCTCGGGGCTCGGGGCTAGAGAGC AAGAAAAAGCAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGTACCGGAAGCTGGGGC CCTTGTCCTTCGCGGAGATCAACGTGCTGATCTGCTTCTTCTGCTGGTCACTCCTGTG GTTCTCCCGAGACCCCGGCTTCATGCCCGCTGGCTGACTGTTGCTTGGTGGGAGGGT GAGACAAAGTCAGTCTCCGATGCCACTGTGGCCATCTTGTGGCCACCCTGCTATTCA TTGTGCTTTCACAGAAGCCCAAGTTTAACTTCCGACGCCAGACTGAGGAAGGTAAGTC TCCTGTTCTGATCGCCCCCTCCTGCTGCGATTGGAAGGTAACCCAGGAGAAAGTG CCCTGGGGCATCGTGCTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGGATCCGAGG CCTCGGGGCTGTCCGTGTGGATGGGGAAGCAGATGGAGCCCTTGACGCGAGTGCCCCC GGCAGCCATCACCTTGATCTTGTCTTGTCTCGTTGCCGTGTTCACTGATGACACAAGC AACGTGGCCACCACCACCTTGTTCCTGCCCATCTTTGCCTCCATGTCTCGCTCCATCG GCCTCAATCCGCTGTACATCATGCTGCCCTGTACCCTGAGTGCCCTCCTTGCCTTCAT GTTGCTGTGGCCACCCCTCCAATGCCATCGTGTTCACCTATGGGCACCTCAAGGTT GCTGACATGGTAAAAACAGGAGTCATAATGAACATAATTGGAGTCTTCTGTGTGTTTT TGGCTGTCAACACCTGGGGACGGGCCATATTGACTTGGATCATTTCCCTGACTGGGC TAATGTGACACATATTGAGACTTAGGAAGAGCCACAAGACCAC		
	ORF Start: ATG at 31	ORF Stop: TAG at 1879	
	SEQ ID NO: 48	616 aa	MW at 67816.9kD
NOV14c, CG57758-03 Protein Sequence	MASALSYSVKFSFVILFVTPLLLLPLVILMPAKVSCCAYVILMAIYWCTEVIPLAV TSLMPVLLFPLFQILDSRQVCVQYMKDTNMLFLGGLIVAVAVERNLHKRIALRTLLW VGAKPARMLMGFMGTALLSMWISNTATTAMVPIVEAILQMEATSAAEAGLEGQG TTINNLNALEDDTVKAVLGGKCVAIISTYVKKVEKLQINNLMTPKKLEKQEQDGLG GIRPQDSAQCQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVLLGQMNELFPD SKDLVNFASFAPFAPNMLVMLLFAWLWLQFVYMFSSFKKSWCGLESKKNEKAALKV LQEEYRKLGPLSFAEINVLI CFLLVILWFSRDPGFMPGWLTVAVVEGETKSVSDATV AIFVATLLFIVPSQPKPFNFRSQTEEGKSPVLIAPPPLLDWKVTOEKVPWGI VLLLGG GFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLLVAVFTECTSNVATTTFLFP IFASMSRSIGLNPLYIMLPCTLSASFAMLPVATPPNAIVFTYGHKLKVDMMVKTGVM NIIGVFCVFLAVNTWGRAIFDLDFPDWANVTHIET		
	SEQ ID NO: 49	1606 bp	

NOV14d, CG57758-04 DNA Sequence	GATGGCCTCGGCGCTGAGCTATGTCTCCAAGTTCAAGTCTTCGTGATCTTGTTGCTG ACCCCGCTCCTGCTGCTGCCACTCGTCATTCTGATGCCCGCCAAGTTTGTGAGGTGTG CCTACGTCATCATCTCATGGCCATTACTGGTGACACAGAAGTCATCCCTCTGGCTGT CACCTCTCTCATGCTGTCTTGCTTTTCCCACTCTTCCAGATTCTGGACTCCAGGCAG GTGTGTGTCCAGTACATGAAGGACACCAACATGCTGTTCTCTGGGCGGCTCATCGTGG CCGTGGCTGTGGAGCGCTGGAACCTGCACAAGAGGATCGCCCTGCGCACGCTCCTCTG GGTGGGGGCCAAGCCTGCACGGCTGATGCTGGGCTTCATGGGCGTCACAGCCCTCCTG TCCATGTGGATCAGTAACACGGCAACACGGCCATGATGGTGCCCATCGTGGAGGCCA TATTGCAGCAGATGGAAGCCACAAGCGCAGCCACCGAGGCGGCGCTGGAGCTGGTGGGA CAAGGGCAAGGCCAAGGAGCTGCCAGGGAGTCAAGTGATTTTGAAGGCCCACTCTG GGGCAGCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGACCCTGTGTCATCT GCTACGCGGCCAGCATCGGGGGCACGCCACCCTGACCGGGACGGGACCCAACTGGT GCTCTTGGGCCAGATGAACGAGTTGTTTCTGACAGCAAGGACCTCGTGAACCTTTGCT TCCTGGTTTGCATTTGCCTTTTCCCAACATGCTGGTGATGCTGCTGTTGCTGCTGGCTGT GGCTCCAGTTTGTTTACATGAGATTCAATTTTAAAAAGTCTGGGGCTGCGGGCTAGA GAGCAAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGATACCGGAAGTTG GGGCCCTTGTCTTCGCGGAGATCAACGTGCTGATCTGCTTCTTCTGCTGGTCTATCC TGTGTTTCTCCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTTGCTGGGTGGGA GGGTGAGACAAAGTATGTCTCCGATGCCACTGTGGCCATCTTTGTGGCCACCCCTGCTA TTCATTGTGCCCTTCACAGAAGCCCAAGTTTAACTTCCGCAGCCAGACTGAGGAAGAAA GGAAAACTCCATTTTATCCCCCTCCCTGCTGGATTGGAAGGTAACCCAGGAGAAAAGT GCCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGGATCCGAG GCCTCGGGGCTGTCCGTGTGGATGGGAAGCAGATGGAGCCCTTGCACGCAGTGCCCC CGGCAGCCATCACCTTGATCTTGCTCTTGCTCGTTGCCGTGTTCACTGAGTGCACAAAG CAACGTGGCCACCACCTTGTTCCTGCCCATCTTTGCCATGATGAGTGAACACAGGA GTCTAATGAACATAATTGGAGTCTTCTGTGTGTTTTTGGCTGTCAACACCTGGGGAC GGGCCATATTTGACTTGGATCATTTCCCTGACTGGGCTAATGTGACACATATTGAGAC TTAGGAAGAGCCACAAGACCACACATAGCCCTTACCCT		
	ORF Start: ATG at 2	ORF Stop: TAG at 1568	
	SEQ ID NO: 50	522 aa	MW at 58109.6kD
NOV14d, CG57758-04 Protein Sequence	MASALSYVSKFKSFVILFVTPLLPLVILMPAKFVRCAYVILMAIYWCTEVIPLAV TSLMPVLLPFLFQILDSRQVCVQYMKDTNMLFLGGLIVAVAVERNLHKRIALRLLW VGAKPARLMLGFMGVTALLSMWISNTATTAMVPIVEAILQOMEATSATEAGLELVD KGKAKELPGSQVIFEGPTLQQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVV LLGQMNELFPDSKDLVNFASWFAFAPNMLVMLLFAWLWLQFVYMRPNFKKSWGCGLE SKKNEKAALKVLEQYRKLGLPLSFAEINVLICFFLLVILWFSRDPGFMGPWLTVAWVE GETKYVSDATVAIFVATLLFIVPSQKPKFNFRSQTEERKTPFPYPPPLLDWKVTQEKV PWGIVLLGGGFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLLVAVFTECTS NVATTTFLFPIFASMVKTGVINNIIGVFCVFLAVNTWGRAIFDLDFPDWANVTHIET		
	SEQ ID NO: 51	1781 bp	
NOV14e, CG57758-05 DNA Sequence	GATGGCCTCGGCGCTGAGCTATGTCTCCAAGTTCAAGTCTTCGTGATCTTGTTGCTG ACCCCGCTCCTGCTGCTGCCACTCGTCATTCTGATGCCCGCCAAGTTTGTGAGGTGTG CCTACGTCATCATCTCATGGCCATTACTGGTGACACAGAAGTCATCCCTCTGGCTGT CACCTCTCTCATGCTGTCTTGCTTTTCCCACTCTTCCAGATTCTGGACTCCAGGCAG GTGTGTGTCCAGTACATGAAGGACACCAACATGCTGTTCTCTGGGCGGCTCATCGTGG CCGTGGCTGTGGAGCGCTGGAACCTGCACAAGAGGATCGCCCTGCGCACGCTCCTCTG GGTGGGGGCCAAGCCTGCACGGCTGATGCTGGGCTTCATGGGCGTCACAGCCCTCCTG TCCATGTGGATCAGTAACACGGCAACACGGCCATGATGGTGCCCATCGTGGAGGCCA TATTGCAGCAGATGGAAGCCACAAGCGCAGCCACCGAGGCGGCGCTGGAGCTGGTGGGA CAAGGGCAAGGCCAAGGAGCTGCCAGGGAGTCAAGTGATTTTGAAGGCCCACTCTG GGGCAGCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGACCTGTGTCATCT GCTACGCGGCCAGCATCGGGGACCGCCACCCTGACCGGGACGGGACCCAACTGGT GCTCCTGGGCCAGATGAACGAGTTGTTTCTGACAGCAAGGACCTCGTGAACCTTTGCT TCCTGGTTTGCATTTGCCTTTTCCCAACATGCTGGTGATGCTGCTTTCGCTGGCTGT GGCTCCAGTTTGTTTACATGAGATTCAATTTTAAAAAGTCTGGGGCTGCGGGCTAGA GAGCAAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGTACCGGAAGTTG GGGCCCTTGTCTTCGCGGAGATCAACGTGCTGATCTGCTTCTCTGCTGGTCTATCC TGTGGTTCTCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTTGCTCGGTGGTGA GGGTGAGACAAAGTATGTCTCCGATGCCACTGTGGCCATCTTTGTGGCCACCCCTGCTA TTCATTGTGCCCTTCACAGAAGCCCAAGTTTAACTTCCGCAGCCAGACTGAGGAAGAAA GGAAAACTCCATTTTATCCCCCTCCCTGCTGGATTGGAAGGTAACCCAGGAGAAAAGT GCCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGGATCCGAG GCCTCGGGGCTGTCCGTGTGGATGGGAAGCAGATGGAGCCCTTGCACGCAGTGCCCC CGGCAGCCATCACCTTGATCTTGCTCTTGCTCGTTGCCGTGTTCACTGAGTGCACAAAG CAACGTGGCCACCACCACTTGTTCCTGCCCATCTTTGCCCTCATGAATCAGTCCCC AAGAGCTTCTGTGTTCTGTACGGTGATGTTGCAGTGCTGTCTTTCGCGAGTCTCGCTG CATCGGCTCAATCCGCTGTACATCATGCTGCCCTGTACCTGAGTGAGTGCCTTTTGCC TTCATGTTGCCCTGTGGCCACCCCTCCAAATGCCATCGTGTTCACCTATGGGCACTTCA AGGTGTGTCATGGTGAAGAACAGGAGTCATAATGAACATAATTGGAGTCTTCTGTGT GTTTTTGGCTGTCAACACCTGGGGACGGGCCATATTTGACTTGGATCATTTCCTGTGAC TGGGCTAATGTGACACATATTGAGACTTAGGAAGAGCCACA		
	ORF Start: ATG at 2	ORF Stop: TGA at 1550	

Table 14D. Geneseq Results for NOV14a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB23625	Human secreted protein SEQ ID NO: 50 - Homo sapiens, 627 aa. [WO200049134-A1, 24-AUG-2000]	10..566 9..623	256/623 (41%) 386/623 (61%)	e-137
AAB36158	Novel human transporter protein SEQ ID NO: 2 - Homo sapiens, 627 aa. [WO200065055-A2, 02-NOV-2000]	10..566 9..623	256/623 (41%) 386/623 (61%)	e-137
AAB42213	Human ORFX ORF1977 polypeptide sequence SEQ ID NO:3954 - Homo sapiens, 627 aa. [WO200058473-A2, 05-OCT-2000]	10..566 9..623	256/623 (41%) 386/623 (61%)	e-136
AAB36164	Novel human transporter protein SEQ ID NO: 14 - Homo sapiens, 626 aa. [WO200065055-A2, 02-NOV-2000]	10..566 9..622	252/623 (40%) 382/623 (60%)	e-136
AAB36159	Novel human transporter protein SEQ ID NO: 4 - Homo sapiens, 627 aa. [WO200065055-A2, 02-NOV-2000]	10..566 9..623	256/623 (41%) 385/623 (61%)	e-136

In a BLAST search of public sequence databases, the NOV14a protein was found to have homology to the proteins shown in the BLASTP data in Table 14E.

Table 14E. Public BLASTP Results for NOV14a				
Protein Accession Number	Protein/Organism/Length	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O57661	INTESTINAL SODIUM/LITHIUM-DEPENDENT DICARBOXYLATE TRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) - Xenopus laevis (African clawed frog), 622 aa.	1..564 1..619	336/619 (54%) 444/619 (71%)	0.0
Q9ES88	NA/DICARBOXYLATE COTRANSPORTER (SOLUTE CARRIER FAMILY 13 (SODIUM-	1..561 1..567	311/572 (54%) 421/572 (73%)	e-179

	TRANSPORTER), MEMBER 2) - Mus musculus (Mouse), 586 aa.			
O35055	SODIUM/DICARBOXYLATE COTRANSPORTER 1 (NA(+)/DICARBOXYLATE COTRANSPORTER 1) (KIDNEY DICARBOXYLATE TRANSPORTER) (SDCT1) (ORGANIC ANION TRANSPORTER 1) (OAT1) - Rattus norvegicus (Rat), 587 aa.	1..562 1..568	311/572 (54%) 419/572 (72%)	e-179
Q13183	Renal sodium/dicarboxylate cotransporter (Na(+)/dicarboxylate cotransporter) - Homo sapiens (Human), 592 aa.	1..561 1..572	318/581 (54%) 428/581 (72%)	e-179
Q28615	Renal sodium/dicarboxylate cotransporter (Na(+)/dicarboxylate cotransporter) - Oryctolagus cuniculus (Rabbit), 593 aa.	1..562 1..576	300/586 (51%) 418/586 (71%)	e-172

PFam analysis predicts that the NOV14a protein contains the domains shown in the Table 14F.

Table 14F. Domain Analysis of NOV14a			
Pfam Domain	NOV14a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Na_sulph_symp: domain 1 of 1	6..554	163/604 (27%) 424/604 (70%)	8.3e-140

Example 15.

- 5 The NOV15 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 15A.

Table 15A. NOV15 Sequence Analysis		
	SEQ ID NO: 53	1547 bp
NOV15a, CG57732-01 DNA Sequence	AACCCCTTGACTGAAGCAATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGG GCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATG GTGGCCAGAGCCTACTAGAAACGGTGTGGACCCCCACCACGGGCCAGAGCTGCCTC TGTGATCCCTGGCAGTACTTCAAGACTGCTCCCAGCCCCGGCCTAGCCTCTCAGCCAGG AAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGCTATCTGGAGGCGCAGGCTGGGCCTT ATGCCACGGGGCTGCCAGCCACATCTCCCCCGGGCCTGGCGGAGGCCACCATCGA GTCCACACAGTGGCCATCTCAGATGCAGAGGACTGCGTGACGTGAACAGTACAAG CTGCAGAGTGAGATTGGCAAGGGTGCCTACGGTGTGGTGAAGGCTGGCTACAACGAA GTGAAGACAGACACTATGCAATGAAAGTCCTTTCCAAAAGAAGTTACTGAAGCAGTA	

	TGGCTTTCCACGTCGCCCTCCCCGAGAGGGTCCCAGGCTGCCAGGGAGGACCAGCG AAGCAGCTGCTGCCCTTGGAGCGGGTGTAACCAGGAGATTGCCATCCTGAAGAAGCTGG ACCACGTGAATGTGGTCAAACCTGATCGAGGTACTGGATGACCCAGCTGAGGACAACCT CTATTTCGCCCGCATCCTTCTCCATAGGCCCGTCATGGAAGTGCCCTGTGACAAGGCC TTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTATCTTGGGCCTCGAGTACG TGCATCTGCCAAGATCGTCCACAGGGACATCAAGCCATCCAACCTGCTCTCTGGGGGA TGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTTGAGGGGAACGAC GCTCAGCTGTCCAGCACGGCGGGAACCCAGCATTATGGCCCCGAGGCCATTTCTG ATTCCGGCCAGAGCTTCAGTGGGAAGTTGGATGTATGGGCCACTGGCGTCACGTTGTA CTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTTCATCTTGGCCCTCCACAGG AAGATCAAGAATGAGCCCGTGGTGTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCA AGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTTGGGTGCCAGA CATCAAGTTGCACCTTGGGTGACCAAGAACGGGGAGGAGCCCTCTCTTCGGAGGAG GAGCACTGCAGCGTGGTGGAGGTGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCA TCCCCAGCTGGACCAAGGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTTCTTTGG GAACCGCTTGAGCCCCAAGCACGGAGGGGAAGAGCGATCCATGTCTGTCTCCAGGAAC CTACTGGTGAAAGAAGGGTTTGGTGAAGGGGGCAAGAGCCAGAGCTCCCCGGCGTCC AGGAAGACGAGGCTGCATCTCGAGCCCTGCATGCACCC		
	ORF Start: ATG at 20		ORF Stop: TGA at 1529
	SEQ ID NO: 54	503 aa	MW at 55606.7kD
NOV15a, CG57732-01 Protein Sequence	MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVPIGST SRLLPARPSLSARKLSLQERPAAGSYLEAQAGPYATGPASHISPAWRRTPIESHVVAI SDAEDCVQLNQYKLQSEIGKAYGVVRLAYNESEDRHYAMKVLKSKLLKQYGFPRRP PPRGSQAAGGPAKQLPLERVYQETAILKKLDHVNVLKLEVLDDPAEDNLYLPRIL LHRPVMVEVPCDKPFSEEQARLYLRDVLGLEVYHCQKIVHRDIKPSNLLGGDDGHVKI ADFGVSNQFEGNDAQLSSTAGTAPAFMAPEAISDSGQSFSGKLDVWATGVTLYCFVYK CPFIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPW VTKNGEELPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQ ARREERSMSAPGNLLVKEGFGEGGKSPELPGVQDEAAS		
	SEQ ID NO: 55	1611 bp	
NOV15b, CG57732-02 DNA Sequence	GCGCCAGGTTCCCAACAAGGCTACGCAGAAGAACCCCTTGACTGAAGCAATGGAGG GGGGTCCAGCTGTCTGTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTGGCAGC CATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCAGAGCCTACTAGAACCGGT GTGGACCCCCACACGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGAC TGCTCCAGCCCGGCCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGC AGGAAGCTATCTGGAGGCGCAGGCTGGGCCTTATGCCACGGGGCTGCCAGCCACATC TCCCCCGGGCCTGGCGGAGGGCCACCATCGAGTCCCACCACGCTGGCCATCTCAGATG CAGAGGACTGCGTGCAGCTGAACAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGC CTACGGTGTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAA GTCCTTTCCAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGGA GAGGTTCCAGGCTGCCAGGAGGAGACCAGCCAAGCAGCTGCTGCCCTGGAGCGGGT GTACCGAGGAGATTGCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACCTGATC GAGGTCTGGATGACCCAGCTGAGGACAACCTCTATTGGTGTGTTGACCTCCTGAGAA AGGGCCCGCTCATGGAAGTGCCCTGTGACAAGTCTTCTCGGAGGAGCAAGCTCGCCT CTACTGCGGGACGTCATCCTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCAC AGGGACATCAAGCCATCCAACCTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCG ACTTTGGCGTCAGCAACAGTTTGAGGGGAACGACGCTCAGTGTCTCAGCAGCGGGGG AACCAGCATTATAGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGG AAGGCCTTGGATGTATGGGCCACTGGCGTCACGCTGTACTGCTTTGTCTATGGGAAGT GCCGCTTCATCGACGATTTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCCGT GGTGTTCCTGAGGGGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATG TTAGACAAGAATCCCGAGACGAGAATTGGGGTGCAGACATCAAGTTGCACCCCTGGG TGACCAAGAACGGGAGGAGCCCCCTTCCTTCGGAGGAGGAGCACTGCAGCGTGGTGGA GGTGACAGAGGAGGAGGTTAAGAATCAGTCAGGCTCATCCCCAGCTGGACCAAGGTC ATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTTTGAGCCCCAAG CACGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGGGTT TGGTGAAGGGGGCAAGAGCCAGAGCTCCCCGGCGTCCAGGAAGACGAGGCTGCATCC TGAGCCCTGCATGCACCCAGGGCCACCCGGCAGCACACTCATCC		
	ORF Start: ATG at 52		ORF Stop: TGA at 1567
	SEQ ID NO: 56	505 aa	MW at 55652.7kD
NOV15b, CG57732-02 Protein Sequence	MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVPIGST SRLLPARPSLSARKLSLQERPAAGSYLEAQAGPYATGPASHISPAWRRTPIESHVVAI SDAEDCVQLNQYKLQSEIGKAYGVVRLAYNESEDRHYAMKVLKSKLLKQYGFPRRP PPRGSQAAGGPAKQLPLERVYQETAILKKLDHVNVLKLEVLDDPAEDNLYLVFDL LRKGPVMEVPCDKSFSEEQARLYLRDVLGLEYLHCQKIVHRDIKPSNLLGGDDGHVK IADFGVSNQFEGNDAQLSSTAGTAPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVY KCPFIIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLH PWVTKNGEELPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEP PQARREERSMSAPGNLLVKEGFGEGGKSPELPGVQDEAAS		

	SEQ ID NO: 57	1725 bp
NOV15c, CG57732-03 DNA Sequence	<p> GCGCCCAGGTTCCCAACAAGGCTACGCAGAAGAACCCCTTGACTGAAGTAATGGAGG GGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTGGCAGC CATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCAGAGCCTACTAGAAACGGT GTGGACCCCCACCACGGGCCAGAGTGCCTCTGTGATCCCTGGCAGTACTTCAAGAC TGCTCCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGC AGGAAGCTATCTGGAGGCGCAGGCTGGGCCTTATGCCACGGGGCTGCCAGCCATC TCCCCCGGGCCTGGCGGAGGCCACCATCGAGTCCCACCACGTGGCCATCTCAGATG CAGAGGACTGCGTGACGTGAACAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGC CTACGGTGTGGTGAAGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAA GTCCTTTCCAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGA GAGGGTCCCAGGCTGCCCAGGAGGACCAGCCAAGCAGCTGCTGCCCTGGAGCGGGT GTACCAGGAGATTGCCATCTGAAGAAGCTGGACCAGTGAATGTGGTCAAAGTGATC GAGGTCTGGATGACCGGCTGAGGACAACCTCTATTGGCCCTGCAGAACAGGCCCC AGAATATCCAGTTAGATTCAACAAATATCGCAAGTCCCACTCCCTGCTTCCCTCTGA GCAGCAAGACAGTGGATCCACGTGGGCTGCGCGCTCAGTGTGACCTCTGAGAAAG GGGCCCCGTATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGACCAAGCTCGCCTCT ACCTGCGGGACGTCTATCTGGGCCTCGAGTACTTGCAGTCCAGAAAGATCGTCCACAG GGACATCAAGCCATCCAACCTGCTCTGGGGATGATGGGCAGTGAAGATGCCCGAC TTTGGCGTCAGCAACCAGTTTGAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGAA CCCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAA GGCCTTGGATGTATGGGCCACTGGCGTCACGTTGTACTGCTTTGTCTATGGGAAGTGC CCGTTTCATCGACGATTTCATCTGGCCCTCCACAGGAAGACCAAGAATGAGCCCGTGG TGTTTCCTGAGGGGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTT AGACAAGAATCCCGAGACGAGAATTGGGGTGCCAGACATCAAGTTGCACCTTTGGGTG ACCAAGAACGGGAGGAGCCCTTCCCTCGGAGGAGGAGCAGCTGACGCTGGTGGAGG TGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCACCGTGAT CCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCAAGCA CGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGGTTTG GTGAAGGGGGCAAGAGCCAGAGCTCCCCGGCGTCCAGGAAGACGAGGTGCATCCTG AGCCCTGCATGCACCAGGGCCACCGGCAGCACACTCATCC </p>	
	ORF Start: ATG at 52	ORF Stop: TGA at 1681
	SEQ ID NO: 58	543 aa MW at 59729.0kD
NOV15c, CG57732-03 Protein Sequence	<p> MEGPAVCQDPRAE LVERVA AIDVTHLEADGGPEPTRNGVDP PPRARAASV I PGST SRLLPARPSLSARKLSLQERPA GSYLEAQAGPYATGPASHI SPRAWRRPTIESHHVAI SDAEDCVQLNQYKLQSEIGKAYGVVRLAYNESEDRHYAMKVL SKKLLKQYGFPRRP PPRGSQAAGGPAKQLPLERVYQEIA I LKKLDHVN VVKLIEVLDDPADNLYLALQN QAQNIQLDSTNIAKSHLLPSEQD SGSTWAARSVFDLLRKGPMVEVPCDKPFSEEQ RLYL RDVILGLEYLHCQKIVHRDIKPSNLLGLDDGHVKIADFGVSNQFEGNDAQLSST AGTPAFMAPEAISDSGQSFS GKALDVWATGVTLYCFVYKCPFI DDFILALHRKTNE PVVFPPEGPEISEELKDLILKMLDKNPETRI GVPDIKLHPVWTKNGEELPSEEEHCSV VEVTEEEVKNSVRLIPSWTTVILVKSMLRKR SFGNPFEPQARREERSMSAPGNLLVKE GFGEGGKSPELPGVQEDEAAS </p>	

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 15B.

Table 15B. Comparison of NOV15a against NOV15b through NOV15c.		
Protein Sequence	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV15b	1..503 1..505	495/505 (98%) 497/505 (98%)
NOV15c	1..503 1..543	492/543 (90%) 495/543 (90%)

Further analysis of the NOV15a protein yielded the following properties shown in Table 15C.

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A search of the NOV15a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 15D.

In a BLAST search of public sequence databases, the NOV15a protein was found to have homology to the proteins shown in the BLASTP data in Table 15E.

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Table 15E. Public BLASTP Results for NOV15a				
Protein Accession Number	Protein/Organism/Length	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BQH3	HYPOTHETICAL 55.7 KDA PROTEIN - Homo sapiens (Human), 505 aa.	1..503 1..505	497/505 (98%) 499/505 (98%)	0.0
P97756	CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - Rattus norvegicus (Rat), 505 aa.	1..503 1..505	465/505 (92%) 478/505 (94%)	0.0
AAH17529	SIMILAR TO CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE 1, ALPHA - Mus musculus (Mouse), 505 aa.	1..503 1..505	464/505 (91%) 478/505 (93%)	0.0
Q64572	CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) - Rattus norvegicus (Rat), 505 aa.	1..503 1..505	463/505 (91%) 476/505 (93%)	0.0
Q9R054	CALCIUM/CALMODULIN DEPENDENT PROTEIN KINASE KINASE ALPHA - Mus musculus (Mouse), 505 aa.	1..503 1..505	454/505 (89%) 471/505 (92%)	0.0

PFam analysis predicts that the NOV15a protein contains the domains shown in the Table 15F.

Table 15F. Domain Analysis of NOV15a			
Pfam Domain	NOV15a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Pkinase: domain 1 of 2	128..228	28/101 (28%) 81/101 (80%)	8.4e-16
Pkinase: domain 2 of 2	245..407	70/201 (35%) 129/201 (64%)	1.7e-52

Example 16.

The NOV16 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 16A.

Table 16A. NOV16 Sequence Analysis			
	SEQ ID NO: 59	688 bp	
NOV16a, CG57709-01 DNA Sequence	<u>GACGCGGACCCGCCATGGCGCGGAAGAAGGTGCGTCCGCGGCTGATCGCGGAGCTGGC</u> <u>CCGCCGCGTGCGCGCCCTGCGGGAGCAACTGAACAGGCGCGCGACTCCCAGCTCTAC</u> <u>GCGGTGGACTACGAGACCTTGACGCGGCCGTTCTCTGGACGCGCGCTGCCGCTCCGGG</u> <u>CCTGGGCCGACGTGCGCCGCGAGAGCCGCTCTTGTCAGCTGCTCGGCCGCTCCCGCT</u> <u>CTTCGGCCTGGGCCGCTGGTCACGCGCAAGTCTTGGCTGTGGCAGCACGACGAGCCG</u> <u>TGCTACTGGCGCCTCACGCGGGTGCGGCCCGACTACACGCGCAGAACTTGGACCACG</u> <u>GGAAGGCCTGGGCGATCCTGACCTTCAAAGGTAAGGCTCGGAGAGAGCGCGGGAGAT</u> <u>CGAACACGTCATGTACCATGACTGGCGGCTGGTGCCCCAAGCACGAGGAGGAGGCCCTC</u> <u>ACCGCGTTCAGCCGCGCGCCGGAAGACAGCCTGGCCTCCGTGCCGTACCCGCTCTCC</u> <u>TCCGGGCCATGATTATCGCAGAAACGACAGAAAAATGGAGACACAAGCACCGAGGAGCC</u> <u>CATGCTGAATGTGCAGAGGATACGCATGGAACCTGGGATTACCCTGCAAAACAGGAA</u> <u>GACAAAGGAAGGCCAAGGGCACCCCGCTCTAGAATGCCAGAACCAGCGG</u>		
	ORF Start: ATG at 15	ORF Stop: TAG at 669	
	SEQ ID NO: 60	218 aa	MW at 25647.2kD
NOV16a, CG57709-01 Protein Sequence	MARKKVRPLRIAE LARRVRALREQLNRPRDSQLYAVDYETLTRPFSGRRLPVRAWADV RRESRLQLLGRLLPLFGLGRLVTRKSWLWQHDEPCYWRLTRVRPDYTAQNLDHGKAWG ILTFKGKARESAREIEHVMYHDWRLVPKHEEEAFTFTAPEDSLASVPYPPLLRAMI IAERQKNGDSTEEPMLNVQIRMEPWDYPAKQEDKGRAKPTV		

Further analysis of the NOV16a protein yielded the following properties shown in Table 16B.

Table 16B. Protein Sequence Properties NOV16a	
PSort analysis:	0.9081 probability located in mitochondrial matrix space; 0.6000 probability located in mitochondrial inner membrane; 0.6000 probability located in mitochondrial intermembrane space; 0.6000 probability located in mitochondrial outer membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV16a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 16C.

Table 16C. Geneseq Results for NOV16a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81356	Human AFP protein sequence SEQ ID NO:230 - Homo sapiens, 218 aa. [WO200129221-A2, 26- APR-2001]	1..218 1..218	212/218 (97%) 212/218 (97%)	e-125
AAU30525	Novel human secreted protein	135..218 1..84	84/84 (100%) 84/84 (100%)	3e-45

	[WO200179449-A2, 25-OCT-2001]			
AAU30526	Novel human secreted protein #1017 - Homo sapiens, 62 aa. [WO200179449-A2, 25-OCT-2001]	187..217 12..42	31/31 (100%) 31/31 (100%)	4e-12

In a BLAST search of public sequence databases, the NOV16a protein was found to have homology to the proteins shown in the BLASTP data in Table 16D.

Table 16D. Public BLASTP Results for NOV16a				
Protein Accession Number	Protein/Organism/Length	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BVI7	HYPOTHETICAL 25.7 KDA PROTEIN - Homo sapiens (Human), 218 aa.	1..218 1..218	214/218 (98%) 214/218 (98%)	e-125
P82930	MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) – Homo sapiens (Human), 218 aa.	1..218 1..218	213/218 (97%) 213/218 (97%)	e-124
CAC38606	SEQUENCE 229 FROM PATENT WO0129221 - Homo sapiens (Human), 218 aa.	1..218 1..218	212/218 (97%) 212/218 (97%)	e-124
Q9JIK9	TCE2 (0610007F04RIK PROTEIN) - Mus musculus (Mouse), 218 aa.	1..218 1..218	194/218 (88%) 205/218 (93%)	e-114
Q9D957	0610007F04RIK PROTEIN - Mus musculus (Mouse), 218 aa.	1..218 1..218	193/218 (88%) 205/218 (93%)	e-114

PFam analysis predicts that the NOV16a protein contains the domains shown in the Table 16E.

Table 16E. Domain Analysis of NOV16a			
Pfam Domain	NOV16a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 17.

The NOV17 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 17A.

Table 17A. NOV17 Sequence Analysis			
	SEQ ID NO: 61	894 bp	
NOV17a, CG57700-01 DNA Sequence	<u>CTCCGTGACCATGAAGGTCAAGGTCATCCCCGTGCTCGAGGACAACATACGTACCTG</u> <u>GTCATCGAGGAGCTCACGCGCGAGGCGGTGGCCGTGGACGTGGCTGTGCCAAGAGGC</u> <u>TGCTGGAGATCGTGGGCGGGAGGGGGTGTCTCTGACCGCTGTGCTGACCACCCACCA</u> <u>TCACTGGGACCACGCGCGGGGAAACCCGGAGCTGGCGCGGCTTCGTCCCGGGCTGGCG</u> <u>GTGCTGGGCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCACGGCGGAG</u> <u>AGCTGCAGTTCGGGGCCATCCACGTGCGTTGCCTCCTGACGCCCCGGCCACACGCCCGG</u> <u>CCACATGAGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCCGCCCTGTTCTCG</u> <u>GGTGGCGACGCGCTGTGCGTGGCCGGCTGCGGCTCGTGCTGGAGGGCAGCGCCAGC</u> <u>AGATGTACCAAGAGCTGGCCGAGCTGGGTACCTGCCCCCGAGACGAAGGTGTTCTG</u> <u>CGGCCACGAGCACACGCTTAGCAACCTGGAGTTTGCCCAAGAAAGTGGAGCCCTGCAAC</u> <u>GACCACGTGAGAGCCAAGCTGTCTTGGGCTCAGAAGAGGGATGAGGATGACGTGCCCA</u> <u>CTGTGCCGTCGACTCTGGGCGAGGAGCGCTCTACAACCCCTTCTGCGGGTGGCGGA</u> <u>GGAGCCGGTGCAGTTCACGGGCAAGGCGGTCCCCGCCGACGTCCTGGAGGCGCTA</u> <u>TGCAAGGAGCGGGCGCGCTTCGAACAGGCGGGCGAGCCGCGGCAGCCACAGGCGCGG</u> <u>CCCTCCTTGCCTGCAGTGGGGGCTCCTGAGTGCAGCCCCACAGACTGAGCCACCCA</u> <u>GACCCTCACAGGGCTGGGGCTGCG</u>		
	ORF Start: ATG at 11	ORF Stop: TGA at 860	
	SEQ ID NO: 62	283 aa	MW at 31262.3kD
NOV17a, CG57700-01 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLEIVGREGVSLTAVLTTHHHWD HARGNPELARLRPLAVLGADERIFSLRRLAHGEELQFGAIHVRCLLTPGHTAGHMS YFLWEDDCPDPPALFSGGDALSVAGCGSCLGSAQMYQSLAELGTLPPETKVFCEGHE HTLSNLEFAQKVEPCNDHVRKLSWAQKRDEDDVPTVPSTLGEERLYNPFRLVAEPEV RKFTGKAVPADVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD		
	SEQ ID NO: 63	888 bp	
NOV17b, CG57700-02 DNA Sequence	<u>CTCCGTGACCATGAAGGTCAAGGTCATCCCCGTGCTCGAGGACAACATACGTACCTG</u> <u>GTCATCGAGGAGCTCACGCGCGAGGCGGTGGCCGTGGACGTGGCTGTGCCAAGAGGC</u> <u>TGCTGGAGATCGTGGGCGGGAGGGGGTGTCTCTGACCGCTGTGCTGACCACCCACCA</u> <u>TCACTGGGACCACGCGCGGGGAAACCCGGAGCTGGCGCGGCTTCGTCCCGGGCTGGCG</u> <u>GTGCTGGGCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGACGGCGAGG</u> <u>AGCTGCAGTTCGGGGCCATCCACGTGCGTTGCCTCCTGACGCCCCGGCCACACGCCCGG</u> <u>CCACATGAGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCCGCCCTGTTCTCG</u> <u>GGCGACGCGCTGTGCGTGGCCGGCTGCGGCTCGTGCTGGAGGGCAGCGCCAGCAGA</u> <u>TGTACCAGAGCCTGGCCGAGCTGGGTACCTGCCCCCGAGACGAAGGTGTTCTGCGG</u> <u>CCACGAGCACACACTAGCAACCTGGAGTTTGCCCAAGAAAGTGGAGCCCTGCAACGAC</u> <u>CACGTGAGAGCCAAGCTGTCTGGGCTAAGAAGAGGGATGAGGATGACGTGCCCACTG</u> <u>TGCCGTCGACTCTGGGCGAGGAGCGCTCTACAACCCCTTCTGCGGGTGGCAGAGGA</u> <u>GCCGGTGCAGTTCACGGGCAAGGCGGTCCCCGCCGACGTCCTGGAGGCGCTATGC</u> <u>AAGGAGCGGGCGGCTTCGAACAGGCGGGCGAGCCGCGGCAGCCACAGCGCGGGCCC</u> <u>TCCTTGCCTGCAGTGGGGGCTCCTGAGTGCAGCCCCACAGACTGAGCCACCCAGAC</u> <u>CCTCACAGGGCTGGGGCT</u>		
	ORF Start: ATG at 11	ORF Stop: TGA at 857	
	SEQ ID NO: 64	282 aa	MW at 31205.3kD
NOV17b, CG57700-02 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLEIVGREGVSLTAVLTTHHHWD HARGNPELARLRPLAVLGADERIFSLRRLAHGEELQFGAIHVRCLLTPGHTAGHMS YFLWEDDCPDPPALFSGGDALSVAGCGSCLGSAQMYQSLAELGTLPPETKVFCEGHEH TLSNLEFAQKVEPCNDHVRKLSWAKRDEDDVPTVPSTLGEERLYNPFRLVAEPEVR KFTGKAVPADVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD		
	SEQ ID NO: 65	882 bp	
NOV17c, CG57700-03 DNA Sequence	<u>ACCATGAAGGTCAAGGTCATCCCCGTGCTCGAGGACAACATACGTACCTGGTCATCG</u> <u>AGGAGCTCACGCGCGAGGCGGTGGCCGTGGACGTGGCTGTGCCAAGAGGCTGCTGGA</u> <u>GATCGTGGGCGGGAGGGGGTGTCTCTGACCGCTGTGCTGACCACCCACCATCACTGG</u> <u>GACCACGCGCGGGGAAACCCGGAGCTGGCGCGGCTTCGTCCCGGGCTGGCGGTGCTGG</u> <u>GCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCAGGCGAGGAGCTGCG</u> <u>GTTGCGGGCCATCCACGTGCGTTGCCTCCTGACGCCCCGGCCACACCGCGGCCACATG</u> <u>AGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCCGCCCTGTTCTCGGGCGACG</u> <u>CGCTGTCGGTGGCCGCTGCGGCTCGTGCTGGAGGGCAGCGCCAGCAGATGTACCA</u>		

	GAGCCTGGCCGAGCTGGGTACCCTGCCCCCGAGACGAAGGTGTTCTGCGGCCACGAG CACACGCTTAGCAACCTGGAGTTTGCCAGAAAGTGGAGCCCTGCAACGACCACGTGA GAGCCAAGCTGTCTGGGCTAAGAAGAGGGATGAGGATGACGTGCCCACTGTGCCGTC GACTCTGGGCGAGGAGCGCCTCTACAACCCCTTCTGCGGGTGGCAGAGGAGCCGGTG CGCAAGTTCACGGGCAAGGCGGTCCCCGCCGACGTCTGGAGGCGCTATGCAAGGAGC GGGCGCGCTCCGAACAGGCGGGCGAGCCGCGGCAGCCACAGGCGCGGGCCCTCTTGC GCTGCAGTGGGGGTCTCTGAGTGCAGCCCCACGACTGAGCCACCCAGACCTCACA GGGCTGGGGCCT		
	ORF Start: ATG at 4	ORF Stop: TGA at 850	
	SEQ ID NO: 66	282 aa	MW at 31173.2kD
NOV17c, CG57700-03 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLIEIVGREGVSLTAVLTTHHHWD HARGNPELARLRPLAVLGADERIFSLTRRLAHGEELRFGAIHVRCLLTPGHTAGHMS YFLWEDDCPDPPALFSGDALSVAGCGSCLEGSQQMYQSLAELGTLPPETKVFPGHEH TLNLEFAQKVEPCNDHVRAKLSWAKKRDEDDVPTVPSTLGEERLYNPFLRVAEPPVR KFTGKAVPADVLEALCKERARSEQAGEPRQPQARALLALQWGLLSAAPHD		
	SEQ ID NO: 67	855 bp	
NOV17d, CG57700-04 DNA Sequence	ACCATGAAGGTCAAGGTCATCCCCGTGCTCGAGGACAACATACGTACCTGGTCATCG AGGAGCTCACGCGCAGGCGGTGGCCGTGGACGTGGCTGTGCCAAGAGGCTGCTGGA GATCGTGGGCGGGAGGGGGTGTCTCTGACCGCTGTGCTGACCACCCACTATCACTGG GACCACGCGCGGGGAAACCCGGAGCTGGCGCGGCTTCGTCCCGGGCTGGCGGTGCTGG GCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCAGGCGAGGAGCTGCG GTTGCGGGCCATCCACGTGCGTTGCCTCCTGACGCCCCGCCACACCGCGGCCACATG AGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCGCCCTGTTCTCGGGCGACG CGCTGTGCGTGGCGGCTGCGGCTCGTGCTGGAGGGCAGCGCCAGCAGATGTACCA GAGCCTGGCCGAGCTGGGTACCCTGCCCCCGAGACGAAGGTGTTCTGCGGCCACGAG CACACGCTTAGCAACCTGGAGTTTGCCAGAAAGTGGAGCCCTGCAACGACCACAAGA GGGATGAGGATGACGTGCCACTGTGCCGTGCACTCTGGGCGAGGAGCGCCTTACAA CCCCTTCTGCGGGTGGCAGAGGAGCGGTGCGCAAGTTCACGGGCAAGGCGGTCCCC GCCGACGTCTGGAGGCGCTATGCAAGGAGCGGGCGCGCTTGGAACAGGCGGGCGAGC CGCGGCAGCCACAGGCGCGGGCCCTCTTGCCTGCACTGGAGGGCTCCTGAGTGCAGC CCCACAGACTGAGCCACCCAGACCTCACAGGGCTGGGGCCT		
	ORF Start: ATG at 4	ORF Stop: TGA at 823	
	SEQ ID NO: 68	273 aa	MW at 30219.1kD
NOV17d, CG57700-04 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLIEIVGREGVSLTAVLTTHYHWD HARGNPELARLRPLAVLGADERIFSLTRRLAHGEELRFGAIHVRCLLTPGHTAGHMS YFLWEDDCPDPPALFSGDALSVAGCGSCLEGSQQMYQSLAELGTLPPETKVFPGHEH TLNLEFAQKVEPCNDHKRDEDDVPTVPSTLGEERLYNPFLRVAEPPVRKFTGKAVPA DVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 17B.

Table 17B. Comparison of NOV17a against NOV17b through NOV17d.		
Protein Sequence	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV17b	1..283	281/283 (99%)
	1..282	282/283 (99%)
NOV17c	1..283	279/283 (98%)
	1..282	281/283 (98%)
NOV17d	1..283	271/283 (95%)
	1..273	273/283 (95%)

Further analysis of the NOV17a protein yielded the following properties shown in Table 17C.

Table 17C. Protein Sequence Properties NOV17a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1682 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV17a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 17D.

Table 17D. Geneseq Results for NOV17a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW80783	Human bisphosphonate binding protein, DP1 (hDP1) - Homo sapiens, 260 aa. [WO9836064-A1, 20-AUG-1998]	1..256 1..256	128/257 (49%) 184/257 (70%)	6e-72
AAG10987	Arabidopsis thaliana protein fragment SEQ ID NO: 9531 - Arabidopsis thaliana, 258 aa. [EP1033405-A2, 06-SEP-2000]	1..245 1..246	107/248 (43%) 160/248 (64%)	5e-53
AAG10986	Arabidopsis thaliana protein fragment SEQ ID NO: 9530 - Arabidopsis thaliana, 268 aa. [EP1033405-A2, 06-SEP-2000]	1..245 11..256	107/248 (43%) 160/248 (64%)	5e-53
AAM78721	Human protein SEQ ID NO 1383 - Homo sapiens, 385 aa. [WO200157190-A2, 09-AUG-2001]	1..226 119..344	100/227 (44%) 135/227 (59%)	6e-45
AAY71110	Human Hydrolase protein-8 (HYDRL-8) - Homo sapiens, 361 aa. [WO200028045-A2, 18-MAY-2000]	1..226 95..320	100/227 (44%) 135/227 (59%)	6e-45

- 5 In a BLAST search of public sequence databases, the NOV17a protein was found to have homology to the proteins shown in the BLASTP data in Table 17E.

Table 17E. Public BLASTP Results for NOV17a

Protein Accession Number	Protein/Organism/Length	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BT45	SIMILAR TO RIKEN CDNA 1500017E18 GENE - Homo sapiens (Human), 282 aa.	1..283 1..282	280/283 (98%) 282/283 (98%)	e-163
Q9DB32	1500017E18RIK PROTEIN - Mus musculus (Mouse), 283 aa.	1..278 1..278	231/279 (82%) 251/279 (89%)	e-133
Q96S11	SIMILAR TO HAGH - Homo sapiens (Human), 218 aa.	1..228 1..218	217/228 (95%) 218/228 (95%)	e-123
Q96NR5	CDNA FLJ30279 FIS, CLONE BRACE2002772, MODERATELY SIMILAR TO HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6) - Homo sapiens (Human), 202 aa.	1..133 1..133	132/133 (99%) 133/133 (99%)	3e-73
O35952	Hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase II) (Glx II) (Round spermatid protein RSP29) - Rattus norvegicus (Rat), 260 aa.	1..256 1..256	128/257 (49%) 184/257 (70%)	1e-71

PFam analysis predicts that the NOV17a protein contains the domains shown in the Table 17F.

Table 17F. Domain Analysis of NOV17a

Pfam Domain	NOV17a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lactamase_B: domain 1 of 1	7..173	55/221 (25%) 129/221 (58%)	5.8e-32

Example 18.

- 5 The NOV18 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 18A.

Table 18A. NOV18 Sequence Analysis			
	SEQ ID NO: 69	2109 bp	
NOV18a, CG58553-01 DNA Sequence	GGGTCGGCGGGCATCGGCAAGACCATGGCGGCCAAAAATATCCTGTACGACTGGGCG GCGGGCAAGCTGTACCAGGGGCCAGGTGGACTTCGCCTTCTTCATGCCCTGCGGCGAGC TGCTGGAGAGGCCGGGACGCGCAGCCTGGCTGACCTGATCCTGGACCAAGTGCCTCCGA CCGCGGCGCGCCGGTGCAGATGCTGGCCCAGCCGAGCGGCTGCTCTTCATCCTG GACGGCGCGGACGAGCTGCCGCGCGCTGGGGGGCCCGAGGCCGCGCCCTGCACAGACC CCTTCGAGGCGCGGAGCGGCGCGCGGGTGTAGGCGGGCTGCTGAGTAAGGCGCTGCT GCCCACGGCCCTCCTGCTGGTGACCACGCGCGCCGCGCCCGGGAGGCTGCAGGGC CGCCTGTGTTCCCGCAGTGCGCCGAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGA AGTATTTCTACAAGTTCTTCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGT GAAGGAGAACGAGACGCTGTTGCGCGTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTG TGCACCGTGCTGCGCCAGCAGCTGGAGCTCGGTGCGGACCTGTGCGCGCAGCTCCAAGA CCACCACGTCAGTGTACCTGCTTTTCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGC CGACGGGCCCCGGTTGAGGGCGACCTGCGCAATCTGTGCCGCTGGCCCGCGAGGGC GTCCTCGGACGCAGGGCGCAGTTTGCCGAGAAGGAACTGGAGCAACTGGAGCTTCGTG GCTCCAAAGTGACAGCGCTGTTTCTCAGCAAAAAGGAGCTGCCGGCGCTGTGGAGAC AGAGGTCACCTACCAGTTCATCGACCAGAGCTTCCAGGAGTCCCTGCGGCACTGTCC TACCTGCTGGAGGACGCGGGGTGCCAGGACCGCGGCTGGCGGCGTTCGGGACACTCC TGCGTGGGGACGCCAGCCGACAGCCACTTGGTGCTCACCACGCGCTTCCTTCTCGG ACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCCACTTCGGCTGCATGGTTTCA GAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGACAGGGACAGGGCTGCCCG GAGTGGCACCAGAGGTGACCAGAGGGGGCCAAAGGGCTCGAGGACACCGAAGAGCCAGA GGAGGAGGAGGAGGAGGAGGAGGCCAACTACCACTGGAGTTGCTGTACTGCCTGTAC GAGACGCGAGGAGGACGCGTTTGTGCGCCAAGCCCTGGGCGGTTCCCGGAGCTGGCGC TGACGCGAGTGCCTTCTGCCGATGGACGTGGCTGTTCTGAGCTACTGCGTGAGGTG CTGCCCTGCTGCACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTGCGCAGGAG AAGAAGAAGAAGAGCCTGGGGAAGCGGCTCCAGGCCAGCCTGGGCAACCAAAACAAC TGCCAGCCTCCCTTCTTCATCACTCTTTAGGCAATGACTGAGCCACTGTGCCATCT GAGCAGCCTCAGCTGTCCCACTGCAAACTCCCTGACGCGGCTGCGCGAGACCTTTCT GAGGCCCTGAGGGCAGCCCCGCACTGACGGAGCTGGGCTCCTCTCCACAACAGGCTCA GTAGGCGAGGACTGCGTATGCTGAGTGAGGGCCTAGCCTGGCCGCACTGCAGGGTGCA GACGGTCAGGGTACAGTGCCTGACCCCCAGCGAGGGCTCCAGTACCTGGTGGGTATG CTTCGGCAGAGCCCTGCCCTGACCACTGGATCTCAGCGGCTGCCAAGTCCCGCCC CCATGGTGACCTACCTGTGTGAGTCTGACGACACAGGGATGCGGCTGCAGACCTC CAGTCTGGCCTCTGTGGAGCTGAGCGAGCAGTCACTACAGGAGCTTCAGGCTGTGAAG AGAGCAAAGCCGAGTCTGGTCATCACACACCCAGCGCTGGACGGCCAGCCACAACCTC CCAAGGAATCATCTCGACCTTCTGAGGCTCTGGTGGCCAGAGCAGGGTGAAGACCC TAGTCAAAGTCCCTGTGGAGA		
	ORF Start: ATG at 26	ORF Stop: TGA at 2054	
	SEQ ID NO: 70	676 aa	MW at 74650.3kD
NOV18a, CG58553-01 Protein Sequence	MAAKNI LYDWAAGKLYQGQVDFAFFMPCGELLERPGTRSLADLILDQCPDRGAPVPQM LAQPORLLFILDGADELPA LGGPEAAPCTDPFEAASGARVLGGLLSKALLPTALLLV TRAAAPGRLOGLRCS PQCAEVRGFS DKDKKKYFYKFFRDERRAERAYRFVKENETLFA LCFVPFVCWIVCTVLRQQLELGRDLSRTSKTTTSVYLLFITSVLSSAPVADGPRLOQD LRNLRLAREGVLRRAQFAEKELEQLELRGSKVQTLFLSKKELPGVLETEVTYQFID QSFFQESFAALS YLLEDGGVPRTAAGGVGTLRLGDAQPHSHLVLTTRFLFGLLSAERM DIERHFGCMVSERVKQEARWVQGGQCGCPGVAPEVTEGAKGLEDTEPEEEEEEGEEP NYPLELLYCLYETQEDAFVRQALGRFPALALQVRVFCRMDVAVLSYCVRCPPAAQALR LISCRLVAAQEKKKSLGKRLQASLGTTKQLPASLLHPLFQAMTDPLCHLSSLTLSHC KLPAVCRDLSEALRAAPALTELGLLHNRLSEAGLRMLSEGLAWPQCRVQTVRVQLPD PQRGLQYLVGMLRQSPALTTLDLSGQLPAPMVITYLCAVLQHQCGLQTLASVELS EQSLQELQAVKRAKPDLVITHPALDGHPPPKELISTF		

Further analysis of the NOV18a protein yielded the following properties shown in Table 18B.

Table 18D. Public BLASTP Results for NOV18a				
Protein Accession Number	Protein/Organism/Length	NOV18a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC34689	SEQUENCE 3 FROM PATENT WO0114564 - Homo sapiens (Human), 1851 aa.	1..633 210..904	605/695 (87%) 610/695 (87%)	0.0
Q91WS2	HYPOTHETICAL 62.5 KDA PROTEIN - Mus musculus (Mouse), 556 aa (fragment).	107..659 1..554	390/557 (70%) 450/557 (80%)	0.0
Q63035	VASOPRESSIN RECEPTOR - Rattus norvegicus (Rat), 483 aa.	193..670 1..482	324/483 (67%) 372/483 (76%)	e-173
AAL12498	CRYOPYRIN - Homo sapiens (Human), 920 aa.	3..657 234..914	232/709 (32%) 355/709 (49%)	5e-94
AAL12497	CRYOPYRIN - Homo sapiens (Human), 1034 aa.	3..648 234..848	223/658 (33%) 344/658 (51%)	6e-93

PFam analysis predicts that the NOV18a protein contains the domains shown in the Table 18E.

Table 18E. Domain Analysis of NOV18a			
Pfam Domain	NOV18a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 19.

The NOV19 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 19A.

Table 19A. NOV19 Sequence Analysis		
	SEQ ID NO: 71	2686 bp
NOV19a, CG58626-01 DNA Sequence	CCGGCGGCGTCTCCACAGCATGAATTACCCGGGCGCGGGTCCCCACGGAGCCCCGAG CATAACGGCCGAGGCGGCGGCGGCGGCGCTGGGAGCTGGGCTCAGACGCGAGGCCAG CGTTCGGCGGGCGGCGTCTGCTGCTTCGAGCACCTGCCCGCGGGGACCCGGACGACGG CGACGTGCCCCCTGGCCCTGCTGCGCGGGGAACCCGGGCTGCATTGGCGCCGGGCACC GACGACCACAACCACCACTCGCGCTGGACCCCTGCCTCAGTGACGAGAATATGACT TCAGCTCCGCGAGTCGGGCTCCTCGCTGCGCTACTACAGCGAGGTGAGAGCGGCGG CGGCGGCGAGTCTTGTGCTGCACCCGCGCAGCAGCCTCCGCTGGTCCCGACGAAC TCGGGGGGCGGCGGCGGACAGGAGGGTCCCCGGGGAAGGAAACGTACCCGGCTTG GCGGCCCGGCGGCGGCGGCGGCGGCTATGAGGTAGTGACGAGCTGGGCGCGGAGGAGT ACGCTGTTCTACAAGGAGGACAAGAAGACCTGGAAGCCTTCATCGGCTACGACTCG CTCCGCATCGAGCTCGCCTTCCGGACCTGCTGCAGACCACGGGTGCCCGGCCCCAGG GCGGGGACCGGGACGGCGACCATGTGTGCTCCCCACGGGCCAGCCTCCAGTTCCGG AGAAGATGACGATGAGGACCGCGCTGCGGCTTCTGCCAGAGTACGACGGGGCACGAG CCGGAGATGGTGGAGCTTGTGAACATCGAGCCTGTGTGCGTGGCGGGCGGCTCTACG	

	<p>AGGTGGATGTGACCAAGGAGAGTGTACCCGGTGTACTGGAACCGTGTGATAAAAT ACCAGTAATGCGTGGACAGTGGTTTATTGACGGCACTTGGCAGCCTCTAGAAGAGGAA GAAAGTAATTTAATTGAGCAAGAACATCTCAATTGTTTTAGGGGCCAGCAGATGCAGG AAAATTTTCGATATTGAAGTGTCAAAATCCATAGATGGAAAAGATGCTGTTTCATAGTTT CAAGTTGAGTCGAAACCATGTGGACTGGCACAGTGTGGATGAAGTATATCTTTATAGT GATGCAACAACATCTAAAATTGCAAGAACAGTTACCCAAAACTGGGATTTTCTAAAG CATCAAGTAGTGGTACCAGACTTCATAGAGGTTATGTAGAAGAAGCCACATTAGAAGA CAAGCCATCACAGACTACCCATATTGTATTGTTGTGCATGGCATTGGGCAGAAAATG GACCAAGGAAGAAATTATCAAAAATACAGCTATGATGAGAGAAGCTGCAAGAAAAATAG AAGAAAGGCATTTTTCCAACCATGCAACACATGTTGAATTTCTGCCTGTTGAGTGGCG GTCAAAACCTTACTCTTGATGGAGACACTGTTGATTCCATTACTCTGACAAAGTACGA GGTTTAAGGGATATGCTGAACAGCAGTGCATGGACATAATGTATTATACTAGTCCAC TTTATAGAGATGAAGTAAAGGCTTTCAGCAAGAGCTGAATCGATTGTATTCCTC TTTCTGTTCTCGGAATCCAGACTTTGAAGAAAAGGGGTAAAGTCTCAATAGTATCA CATTCTTGGGATGTGAATTACTTATGACATAATGACTGGTGAATCCAGTTTCGGC TGTATGAACAGTTGCTGCAAAAGGAAGAAGAGTTGCCTGATGAACGATGGATGAGCTA TGAAGAACGACATCTTCTGATGAACCTATATACTAAACGACGGCTGAAGGAAATA GAAGAACGGCTTCACGGATTGAAAGCATCATCTATGACACAAACACCTGCCTTAAAT TTAAGGTAGAGAATTTCTTCTGATGGGATCCCCATTAGCAGTTTCTTGGCGTTGCG TGGCATCCGCCAGGAAATACTGGAAGTCAAGACCATATTTGCTAGAGAGATTTGT AACCGGTTACTAAATATTTTTCATCCTACAGATCCAGTGGCTTATAGATTAGAACCAT TAATACTGAAACACTACAGCAACATTTACCTGTCCAGATCCACTGGTACAATACCTC AAATCCTTTACCTTATGAACATATGAAGCCAAGCTTTCTCAACCAGCTAAAGAACCT ACCTCAGTTTCAGAGAATGAAGGCATTTCAACCATACCAAGCCCTGTGACCTCACCAG TTTTGTCCCGCCGACACTATGGAGAATCTATAACAAATATAGGCAAAGCAAGCATATT AGGTGCTGCTAGCATTGGAAGGGACTTGGAGGAATGTTGTTCTCAAGATTGGACGT TCATCTACAACACAGTCATCTGAAACATCAAAAGACTCAATGGGAAGATGAGAAGAAGC CAGTTGCCTCACCTTCTGCTACCACCGTAGGGACACAGACCCCTCCACATAGCAGTTC TGGCTTCTCGATTCTGCAGTGGAGTTGGATCACAGGATTGATTTGAACCTAGAGAA GGCCTTGTGGAGAGCCGCTATTGGTCAGCTGTACGTCGCATATGCTTATGGTCTAT CCTTGGATGTTGCCCTTTTCTTTAACCTTCATGTATAAACATGAGCACGATGATGA TGCAAAACCAATTTAGATCCAATCTGAACCTCTCTTGAAGGACATGAATGGCCATAAA CTGATTTTTTTTTTTTCC</p>
	<div>ORF Start: ATG at 20</div> <div>ORF Stop: TGA at 2636</div>
	<div>SEQ ID NO: 72</div> <div>872 aa</div> <div>MW at 97063.4kD</div>
<p>NOV19a, CG58626-01 Protein Sequence</p>	<p>MNYPGRGSPRSPENHNGRGGGAWELGSDARPAFGGGVCCFEHLPGGDPDDGDVPLAL LRGEPLHLAPGTDHNNHLLDPLCLSDENYDFSSAESGSSLRYYSEGESSGGGSSLS LHPPQPPPLVPTNSGGGATGGSPGERKRLGGAARHRYEVVTELGPPEVRWFYKE DKKTWKPFIFYDSLRIELAFRTLLQTGARPGGGDRDGDHVCSPTPGPASSSGEDDDDED RACGFCQSTTGHEPEMVELVNIIEPVCVRGGLYEVDVTQGECPVYWNRADKIPVMRGQ WFIGDTWQPLEEEESNLIEQHLNCFRGQQMQENFDIEVSKSIDGKDAVHSFKLSRNH VDWHSVDEVYLYSDATTSKIARTVTQKLGFSSKASSSGTRLHRGYVEEATLEDKPSQTT HIVFVVHIGIQKMDQGR I I KNTAMMREAARKIEERHFSNHATHVEFLPVEWRSKLTLD GDTVDSITPDKVRGLRDLNLSAMDIMYYTSPLYRDELVKGLQELNLRLYSLFCSRNP DFEEKGGKVSIVSHSLGCVITYDIMGWNPVRLYEQLLQKEEELPDERWMSYEERHLL DELYITKRRLKEIEERLHGLKASSMTQTPALKFKVENFFCMGSPFLAVFLALRGIRPGN TGSQDHILPREICNRLNIFHPTDPVAYRLEPLILKHYSNISPVQIHWYNTSNPLPYE HMKPSFLNPAKEPTSVSENEGISTIPSPVTSFVLSRRHYGESITNIGKASILGAASIG KGLGGMFLSRFGRSSTTQSSETSKDSMEDEKKPVASPSATTVTGQTLPHSSSGFLDSA VELDHRIDFELREGLVESRYSAVTSHTAYWSSLDVALFLTLTFMYKHEHDDDAKPNDL PI</p>

Further analysis of the NOV19a protein yielded the following properties shown in Table 19B.

Table 19B. Protein Sequence Properties NOV19a	
PSort analysis:	0.4555 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV19a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 19C.

Table 19C. Geneseq Results for NOV19a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV19a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG64151	Arabidopsis thaliana gravitropism protein - Arabidopsis thaliana, 933 aa. [JP2001120279-A, 08-MAY-2001]	257..547 156..454	104/316 (32%) 156/316 (48%)	1e-38
AAM41595	Human polypeptide SEQ ID NO 6526 - Homo sapiens, 677 aa. [WO200153312-A1, 26-JUL-2001]	261..548 52..328	94/301 (31%) 138/301 (45%)	6e-25
AAB92643	Human protein sequence SEQ ID NO:10972 - Homo sapiens, 1000 aa. [EP1074617-A2, 07-FEB-2001]	119..608 226..664	132/524 (25%) 204/524 (38%)	2e-24
AAM39809	Human polypeptide SEQ ID NO 2954 - Homo sapiens, 615 aa. [WO200153312-A1, 26-JUL-2001]	274..548 3..266	90/288 (31%) 131/288 (45%)	4e-23
AAB93825	Human protein sequence SEQ ID NO:13636 - Homo sapiens, 694 aa. [EP1074617-A2, 07-FEB-2001]	404..608 227..449	76/229 (33%) 113/229 (49%)	6e-23

- 5 In a BLAST search of public sequence databases, the NOV19a protein was found to have homology to the proteins shown in the BLASTP data in Table 19D.

Table 19D. Public BLASTP Results for NOV19a				
Protein Accession Number	Protein/Organism/Length	NOV19a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O46606	PHOSPHATIDIC ACID-PREFERRING PHOSPHOLIPASE A1 - Bos taurus (Bovine), 875 aa.	1..872 1..875	802/876 (91%) 829/876 (94%)	0.0
Q9C0F8	KIAA1705 PROTEIN - Homo sapiens (Human), 498 aa (fragment).	378..872 4..498	493/495 (99%) 494/495 (99%)	0.0
Q96LL2	CDNA FLJ25408 FIS, CLONE TST02965, HIGHLY SIMILAR TO BOS TAURUS PHOSPHATIDIC ACID-PREFERRING PHOSPHOLIPASE A1 MRNA - Homo sapiens (Human), 454 aa.	419..872 1..454	453/454 (99%) 454/454 (99%)	0.0
AAH18552	HYPOTHETICAL 27.3 KDA PROTEIN - Mus musculus (Mouse), 249 aa (fragment).	624..869 1..246	224/246 (91%) 236/246 (95%)	e-130
AAL32232	HYPOTHETICAL 85.1 KDA PROTEIN - Caenorhabditis elegans, 753 aa.	122..867 11..750	255/794 (32%) 374/794 (46%)	6e-91

PFam analysis predicts that the NOV19a protein contains the domains shown in the Table 19E.

Table 19E. Domain Analysis of NOV19a			
Pfam Domain	NOV19a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF203: domain 1 of 1	252..458	42/219 (19%) 105/219 (48%)	7.5
DDHD: domain 1 of 1	611..858	96/266 (36%) 236/266 (89%)	3.3e-116

Example 20.

The NOV20 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 20A.

Table 20A. NOV20 Sequence Analysis			
	SEQ ID NO: 73	773 bp	
NOV20a, CG57597-01 DNA Sequence	GGTAAGGACACAAGATGCCAAATAGGGTAAGGAATGGTCCAGAAACCTGTGAACCTCTG CATTGCAGGCATGCACCACCACTCCTGGCTAATTTTTTGTATTTTGTAGTCCATCGAA TCCGGCTCAAACCTTTTATTCTCTTATGTAAAAGCTGTGTACTTCAGAAAAACATGT ACAGTTATCCCTGGCAGTGCCGGGTGGGGTCTGCGCGGCCCTGGAGGCCTGGCCGGC CTTGACAGATCGCTGTGGAGAATGGCTTCGGGGGTGTGCACAGCCAGGAGAAGGCCAAG TGGCTGGGGGGTGCAGTGGAGGATTACTTCATGCGCAATGCTGACTTGGAGCTAGATG AGGTGGAAGACTTCCTTGGAGAGCTGTTGACCAACGAGTTTGATACAGTTGTGGAAGA CGGGAGTCTGCCCCAGGTGAGCCAGCAACTGCAGACCATGTTCCACCCTTCCAGAGG GGTGATGGGGCTGCTCTGAGGGAGATGGCCTCCTGCATCACTCAGAGAAAATGCAAGG TCACAGCCACTGCACCTAAGACAGCTAGAGAGACTGATGAGGATGAAGATGATGTGGA CAGTGTGGAAGAGATGGAGGTCACAGCTACGAATGATGGGGCTGTACAGATGGGGTC TGCCCCAGCCTGAACCTCTGATCCAGACGCTCAGACTATTAAGGAAGAGGATATAG TGGAAGATGGCTGGACCATTGTCCGGAGAAAAAATGAGTGGGGATGATTGGAATGG CTTTGGGCCCTTATTGCT		
	ORF Start: ATG at 15	ORF Stop: TGA at 732	
	SEQ ID NO: 74	239 aa	MW at 26579.5kD
NOV20a, CG57597-01 Protein Sequence	MPNVRNRNGPETCELCIAGMHHSWLIFCIFSALIESGSNLLFLCKSCVLQKNMYSYPW QCRGGVCAALEAWPALQIAVENFGGVHSQEKAKWLGGAVEDYFMRNADLEDEVEDF LGELLTNEFDTVVEDGSLPQVSQQLQTMFHHFQRGDGAALREMA SCITQRKCKVTATA LKTARETDEDEDVDVSVEEMEV TATNDGAATDGVCPQPEPSDPDAQTIKEEDIVEDGW TIVRRKK		

Further analysis of the NOV20a protein yielded the following properties shown in Table 20B.

Table 20B. Protein Sequence Properties NOV20a	
PSort analysis:	0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV20a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 20C.

Table 20C. Geneseq Results for NOV20a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81374	Human AFP protein sequence SEQ ID NO:266 - Homo sapiens, 191 aa. [WO200129221-A2, 26-APR-2001]	61..239 13..191	178/179 (99%) 178/179 (99%)	e-101
AAG57770	Arabidopsis thaliana protein	63..239 18..178	56/182 (30%) 94/182 (50%)	1e-13

	Arabidopsis thaliana, 184 aa. [EP1033405-A2, 06-SEP-2000]			
AAG57771	Arabidopsis thaliana protein fragment SEQ ID NO: 74487 - Arabidopsis thaliana, 156 aa. [EP1033405-A2, 06-SEP-2000]	74..239 1..150	52/171 (30%) 89/171 (51%)	2e-11

In a BLAST search of public sequence databases, the NOV20a protein was found to have homology to the proteins shown in the BLASTP data in Table 20D.

Table 20D. Public BLASTP Results for NOV20a				
Protein Accession Number	Protein/Organism/Length	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q969E8	UNKNOWN (PROTEIN FOR MGC:20451) (PROTEIN FOR IMAGE:3953868) - Homo sapiens (Human), 191 aa.	61..239 13..191	178/179 (99%) 178/179 (99%)	e-101
Q9NAD8	Y51H4A.15 PROTEIN - Caenorhabditis elegans, 225 aa.	1..239 1..225	66/239 (27%) 122/239 (50%)	5e-23
Q06672	HIGHLY ACIDIC C-TERMINUS - Saccharomyces cerevisiae (Baker's yeast), 249 aa.	63..238 79..244	46/177 (25%) 82/177 (45%)	5e-11
Q9VBI0	CG14543 PROTEIN - Drosophila melanogaster (Fruit fly), 195 aa.	71..238 24..195	49/174 (28%) 81/174 (46%)	2e-10
Q9UUA9	HYPOTHETICAL HIGHLY ACIDIC C-TERMINUS PROTEIN - Schizosaccharomyces pombe (Fission yeast), 179 aa.	70..239 22..178	42/172 (24%) 83/172 (47%)	2e-06

5 PFam analysis predicts that the NOV20a protein contains the domains shown in the Table 20E.

Table 20E. Domain Analysis of NOV20a			
Pfam Domain	NOV20a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 21.

The NOV21 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 21A.

Table 21A. NOV21 Sequence Analysis		
	SEQ ID NO: 75	7741 bp
NOV21a, CG57804-01 DNA Sequence	<p>TTGTCTCTTTGTGTTTTCCAGACATTCTAAGTGAGACTGTCCACATCATCTAGGAAAA TGGTGGCCCTGTCTTAAAGATTTGTGTGCGCCACTGCAACGTGGTGAAGACCATGCA GTTTGAACCATCTACAGCTGTGTACGATGCGTGTGAGTCAATCGGGAACGGGTGCCT GAGGCACAACTGGGCAAGCTTCTGACTATGGACTCTTTCTTTCCGGATGAAGACCCGA GGAAAGGGATTGGCTGGAAAGCGGGCAGAACACTGGATTACTACATGTTGCGGAATGG GGATATTTTGAATATAAAAAGAAACAGAGACCTCAGAAAATCGGATGCTGGATGGA TCTGTGAAGACAGTGATGGTGGATGATTCCAAGACTGTGGGGGAGCTCCTGGTCACTA TTGTAGCAGAATAGGAATAACAATTATGAAGAATACTCCTTAATCCAAGAACTAT TGAAGAAAAGAAAGAGGAAGGAACGGGCACACTCAAAAAGACAGGACACTGTTACGA GATGAGAGGAAAATGGAGAAGTTGAAGGCCAAGCTGCACACAGATGATGACCTAAATT GGCTGGATCAGAGCCGAACATTGAGAGAACAGGAGTAGATGAAAACGAAACGTTGCT GCTTAGACGGAAGTTCTTTACTCTGATCAGAAATGTAGATTGAGAGACCCCGTGCAG CTGAACCTTGCTTTATGTTTCAAGGCACGGGATGACATCCTGAATGGCTCTCACCTGTCT CCTTCGAGAAAGCTTGTGATTTTGGTGGATTTCAAGCCAGATACAAATTTGGACCTCA TGTGGAACATAAAACACAACTGGATTTTAGATCTGAAGGAATCTGCGCCAAAGAA TATATCAAGCAGAGAGGAGCTGAAAAGAGGATCTTTCAGGAGCATAAGAACTGCGGAG AGATGAGTGAGATAGAAGCCAAGGTCAAGTACGTCAAACCTCGCAGCGTCCCTCCGCAC ATATGGCGTGTCTTCTTCTGTGTAAGGAGAAGATGAAAGGCAAGAACAGCTGGTG CCTCGCTGTGTTGGGATCACCAAGACTCGGTGATGCGCGTGGATGAGAAGACCAAGG AAGTGCTGCAGAGAGTGGCCCTCACACCGTCAAGCGTGGGACGCTCACCAAGAG CTTCACACTGGATTTTGGGGAGTATCAGGAAAGCTACTATTGATACAAACCCAGGAG GGAGAGCAGATATCCAGCTGATTGCAGGCTACATTGACATCATCTGAAAAGGGAA CATACGTGACATCTGTGGGGTCTCCTCATTGCACTCCACATGGCTGGTGTCTCTCAG TGACCAAAACCTTTTCCCGCAGGTCCACCATCTTGACAGCAGCTTCAACCGGACC GGGAAGGCAGAGCAGGCTCAGTGGCGCTGCCGGCCGTGATGCGCTCGGGCTCCAGCG GGCCTGAGACCTTCAACGTTGGCAGCATGCCCTCGCCACAGCAGTGGGGATTTGG GCAGATGCACCGAGGCCACATGCCGCCACTGACCTCAGCCAGCAGGCCCTGATGGGG ACCATCAACACAAGCATGCACGCCGTCCAGCAGGCCAGGATGATCTCAGTGAGCTCG ACTCGCTGCCACCTCTCGGCCAGGATATGGCATCTAGGGTATGGGTTTCAAGAACAAAGT CGACGAATCCAAACACGAAATCCATTCTCAAGTTGATGCTATCAGGCCCGGAACGGCT TCAGTTGTTAACCTCACAGCTGGTGACCTGCAGACACTGACTACACAGCTGTGGGAT GTGCGATCACCACTATTTCTTCAACCTGACGGAGATGTCCAAGGGTGTGAAGCTATT GGCCGCCCTCATGGATGATGAGGTGGGCAGCGGGGAGGACTTGCTCAGAGCTGCCAGG ACCCTCGCTGGGGCGGTGTGAGCTTGTGAAAGCTGTGCAGCCTACTTCTGGAGAGC CTCGACAGACAGTTTGTACTGCTGCTGGCAGCATCGGACAAGCCAGTGGGGATTTCT GAGACAGATTGGAGAGAATGAGACTGATGAGCGATTCCAGGATGTTTAAATGAGTTTG GCCAAAGCTGTTGCCAATGCAGCTGCCATGTTGGTACTAAAGGCCAAGAATGTTGCC AAGTGGCCGAAGACACTGTCTACAGAACAGGGTAATTGCTGCCACCCAGTGTGC CCTCTCCACCTCCAGCTTGTGGCATGTGCCAAGGTTGTGAGCCCCACTATTAGCTCC CCTGTGTGCCAGGAGCAGCTGATTGAAGCAGGGAAGCTGGTGGACCGCTCGGTGGAGA ACTGTGTCCGTGCCCTGCCAGGCCGCACTACCGATAGTGAGCTTCTGAAGCAGGTGAG CGCAGCGGCCAGCGTGGTCAAGCCAGGCCCTCATGATCTCTGCAGCATGTGCGGCAG TTTGCCAGCCGAGGCGAGCCATCGGCCGCTACGACCCAGGCTACTGACACCATCATGT GTGTCACCGAGAGCATCTTCAGCTCCATGGGTGACGCTGGTGAATGGTGGCGCAGGC GCGGGTCTTGCCCAAGCCACATCAGACCTCGTCAATGCCATGAGGTGAGATGCAGAA GCCGAAATCGACATGGAGAATTCAAAGAAGCTCCTGGCAGCAGCAAACTCTTAGCTG ACTCCACTGCTCGCATGGTGGAAAGCTGCAAAGGGGGCTGCAGCCAACCCAGAGAATGA GGACCAGCAGCAAAGGCTGAGAGAAGCTGCAGAAGGCCTCCGGGTAGCAACCAACGCA GCTGCCCAAGATGCTATTAAGAAAAAATTTCAACCGACTGGAGGTTGCAGCCAAAGC AGGCCGAGCGGCAGCCACACAGACCATCGCCGCTCCAGGCTGGAAGCAAGCACTACAC CAAGAACCTGCGGCCAGCAGCAGCTGGTCCAGAGTTGCAAGGCAGTGGCTGATCAC ATCCCTCAGCTGGTCCAGGGAGTGAAGGGGAGCCAAGCTCAAGCTGAAGACCTGAGTG CCCAGCTGGCTCTCATCTCTCAGCCAGAACTTCTCCAGCTGGAAGCAAGTGTGTTGCT GTCTCTGCCAAGCGCAGTGGCCACCGTGAAGTACAGGCGCCAGCCATGCAGCTG AGCCAGTGTGCCAAGAACCTGGCCACAGCTTGGCGGAGCTGCGTACCGCTCGCAGA AGGCCATGAAGCTTGTGGTCCGATGGAATCGATTGAGCTCTGAATACGGTGCAGAG GCTTAAGAATGAATGCAGGATGCCAAGATGGCAGCCGTGGAGAGCCAGCTGAAGCCA CTTCCAGGGGAAACGCTGGAAAAATGTGCTCAGGACCTGGGAAGCACATCCAAGGCGG TGGGCTCTCCATGGCACAGCTGCTGACCTGTGCTGCTCAAGGCAACCACTACAC AGGGGTGGCTGCTAGAGAGACGGCCCAAGCTCTGAAAACACTGGCCCGAGGCCCGCT GGAGTGGCTGCATCGACAACCGACCCCGCGGCCCGCCATGCCATGTTAGATTCTGCTC GAGACGTGATGGAGGGCTCCGCCATGCTCATTCAAGAGGCCAAGCAGGCGCTGATTGC ACCTGGAGATGCAGAGCGTCAACAAGACTGGCTCAGGTGGCTAAAGCCGTCTCACAC TCCTTGAATAACTGCGTAAATTGCTCCTCGGCCAGAGGATGTGGACGTGGCCTTGA</p>	

2020E0 0062600T

AGAGCATCGGGGAGTCCAGCAAGAAGCTGCTTGTGGATTGCTACCTCCAAGCACGAA GCCTTTCCAGGAAGCCAGAGTGAAGTGAACAGGCAGCAGCTGATCTGAACCAAGTCT GCTGGGGAAGTGGTCCATGCCACCCGGGGCCAGAGTGGAGAGTTGGTGCAGCCTCTG GAAAGTTCAGTGATGATTTTGGTGAATTCCTCGATGCTGGCATTGAGATGGCTGGCCA AGCTCAGACAAAAGAAGACCAGATCCAAGTGATAGGGAACCTCAAGAATATCTCGATG GCATCCAGCAAGCTGCTGTAGCTGCCAAGTCTCTCTGTAGATCCAGGAGCTCCCA ATGCGAAAAATCTCCTGGCTGCAGCTGCAAGAGCTGTGACAGAGAGCATCAATCAACT CATCACTCTGTGTACCAACAAGCTCCGGGCCAGAAAGAGTGGCAATATGCCCTGCGG GAGCTCGAGACTGTGAAGGGGATGTTGGACAATCCTAATGAACCTGTTAGTGACCTCT CTTACTTTGACTGCATTGAGAGTGTGATGGAAAACTCCAAGGTTCTGGGTGAATCGAT GGCAGGGATTTACAGAATGCCAAGACCGGAGACCTCCCTGCCCTTTGGGGAATGTGTG GGGATTGCATCCAAGGCTCTCTGTGGGCTGACAGAGGCTGCAGCCCAGGCTGCATACT TGGTTGGCATCTCTGATCCAAACAGCCAGGCAGGCCACCAGGGCCTGGTGGACCCAT CCAGTTTGGCCAGGCTAACCAAGGCCATCCAGATGGCATGGCAGAACCTGTGGACCCCT GGCAGCAGCCCATCAGAGTCTCTGTCAGCCGCCACAATTGTTGCCAAGCACACGTCAG CCTTGTGCAATGCCTGCCGTCATCGCTCATCAAGACGGCCAAACCAAGTAGCCAAGAG GCACTTCTGTCAGTCAGCCAAGGAAGTCCCAACAGCACTCGGCAAGCTGTGCTGAGACC ATCAAGGCCCTGGATGGGGATTTCTCTGAAGACAACCGCAATAAGTGTGCGATCGCCA CCGCACCTTGATTGAAGCTGTGGAGAACCTGACAGCGTTCCGCTCAAAACCTGAGTT TGTGAGCATTCCTGCCAGATCAGCTCCGAGGTTCCAGGCACAGGAACCACTGCTG GTCTCAGCCAAGACCATGCTGGAGAGTTCATCGTACCTCATTGCACTGCAGCTCTC TGGCCATCAACCCCAAAGACCCACCCACCTGGTCTGTACTGGCTGGACATTCCTCAT AGTGTCCGACTTCATCAAGAGTCTCATCACTTCTATCAGGGAACAGGCCCTGTCGAG AGGGAGTGTGATTACTCCATCGATGGCATCAACCGGTGCATCCGGGACATCGAGCAGG CCTCGCTGGCCGCGCTCAGCCAGAGCCTGGCCACGAGGGACGACATCTCTGTGGAGGC CCTGCAAGAGCAGTGAAGTTCGGTCCAGGAAATCGGACCACTTATCGATCCCATC GCCACAGCGCTCGGGGAGAAGCAGCTCAGCTGGGACATAAGGTGACACAACCTGGCAA GCTATTTTGAAGCTTGATCTTAGCCGAGTGTGGTGTGGCCTCAAGATTCTTGATCA TCAGCAGCAGATGACGGTGTGGACAGACCAAGACTCTGCAAGAGTCTGCTGAGCAG ATGTTGTATGCAGCCAAAGAAGTGGCGGAAACCCAAAGGCACAACACCCATGACG CCATCAGAGAGGCCGCGCCAGTTGATGAAGGAAGCCGTGGATGACATCATGTTGACGCT GAACGAAGCTGCCAGTGAAGTGGGGCTGGTTGGGGCATGTTGGACGCCATTGCGAGAA GCCATGAGCAAGCTGGATGAAGGCACTCTCCAGAACCAAAGGGAACATTTGTGCACT ATCAGACGACTGTGGTTAAATACTCCAAAGCCATTGCGGTGACAGCTCAGGAAATGAT GACTAAGTTCGGTTACTAACCCGGAGGAGTGGGAGGACTGGCTTCAAAATGACCACT GACTATGGGCACCTGGCTTTCCAGGGCCAGATGGCAGCAGCCACGGCGGAACAGAGG AGATCGGATTCCAGATTGCACTCGTGTGAGGACCTGGGCCACGGCTGTATCTTCTCT GGTGCAAGAGGCGGGCCCTCCAGGTCTGCCCAACAGACAGCTGCAAGTGTGGTGGAG CTGATCGAATGCGCCCGTGGCGTCACGGAAAAGTCTCCTTGGTGCTCTCGGCTCTCC AGGCCGGGAACAAAGGAACCCAGGCATGCATTACAGCCGCCACCGCTGTGTCTGGGAT CATTGCCGAGCTGGAACCAACCATATATGTTTGCAACAGCGGGGACGCTGAATGCAAG AACAGTGAGACCTTCGAGACCACAGGGAGAATCTCTCAAGACGGCCAAGGCCCTTGG TAGAAGACACGAACTACTTGTGTGAGGAGTGCCTCCACTCTGACAAGCTGGGCCA GGCGGCCAGTCTCAGCAGCCACCATCACCCAGCTCGCAGAGTGGTCAAGCTGGGG GCAGCCAGCCTGGGCTCCGACGACCCCGAGACCCAGGTGGATTGATCAATGCCATCA AAGATGTGGCCAAGGCCCTTCTGATCTCATAGTGTACCAAGGGAGCTGCCAGCAA GCCAGTGGACGACCTTCCATGTACAGCTCAAGGGGGCTGCCAAGGTGATGGTGACC AATGTACCTCGCTCCTCAAGACTGTAAAGGCAGTGGAGGATGAGGCCACCCGGGGCA CCAGGGCGCTTGAGGCCACAATGAATGCATAAAGCAGGAGCTTACGGTGTTCAGCT AAAAGACGTACCTGAAAAGACATCATCACTGAAGAATCCATAAGGATGACGAAAGGC ATCACCATGGCAACAGCCAAAGCCGTGGCAGCTGGGAATCATGTAGACAGGAGGACG TGATTGTACTGCCAAGCTGAGCCGGAAGCCGTGTGAGATATGTTGACGGCTTGCAA GCAAGCATCCTTCCACCCGATGTCAAGTACGAGGTGAGAACAGAGCCTTGCCTTTC GGGACGGAGTGACCCCTTGGCTACTTGGACCTCTGGAGCACGCTTGGTGATTCTTC AGAAACCAACCCAGAATTCAAGCAGCAGCTGGCCGCTTCTCCAAGCGAGTCGCCGG CGCTGTGACAGAGCTCATCCAGGCGGCGGAAGCCATGAAGGAACAGAGTGGGTGGAT CCAGAAGACCAACTGTCTATGCAAGAACAGAGTTACTGGGGGCTGCAGCATCCATCG AAGCTGCTGCTAAGAAGTTAGAGCAACTGAAGCCAAGAGCAAAACCAAAACAAGCGGA TGAGACCTTGACTTTGAGGAACAGATCTTGAAGCTGTCTAAATCCATTGCTGTGCC ACAAGCGCCCTGGTCAAATCGGCCTCAGCAGCCAGAGGGAGCTGGTGGCCCAAGGAA AGGTGGGCTCCATCCCTGCCAATGCTGCAGACGACGGACAGTGGTACAGGGGCTGAT TTCTGCTGCCCGGATGGTGGCGGCTGCGACCAAGCAGTCTCTGTGAGGCGGCCAATGCC TCCGTTTCAAGGACACGCCAGCGAGGAGAAGCTCATCTCATCTGCCAAGCAGGTGCGCG CTTCCAGCGCTCAGCTGCTGGTGGCCTGCAAGGTGAAGGCCGACAGGATTGAGAGGC CATGAGCGGCTCAGCGCGGAGGAAATGCTGTGAAAAGAGCTGCAAGCAATCTTGTG CGTGCAGCCCAAGAGGCAGCTTTTGGCAAAGCTGATGACGACGATGTTGTAGTGGAAA CCAAGTTTGTGGGGGGCATTGCTCAGATCATCGCCGCCAGGAAGAAATGCTAAAGAA AGAGCGAAGAACTGGAAGAAGCAAGGAAAAAAGTGGCCCAATCCGCGCAGCAGTAT AAGTTTTTACCCACCGAGCTGAGGGAAGATGAGGGCTAAAGGTGCGAGCCAGATGGC GAGCCCCAGGGGATGGCCCTGGCTGAA			
ORF Start: ATG at 58		ORF Stop: TAA at 7693	
SEQ ID NO: 76		2545 aa	MW at 271692.8kD

NOV21a,
CG57804-01 Protein
Sequence

MVALSLKICVRHNCNVVTKMQFEPSTAVDYACRVIRERVPEAQGTQASDYLFLSDSDP
RKGIWLEAGRTLDTYMLRNGDILEYKKKQRPQKIRMLDGSVKTVMVDDSKTVGELLVT
ICSRIGITINYEESLIQETIEEKKEEGTGLKKDRTLRLDRERKMEKLKAKLHTDDDLN
WLDHSRTTFREGVDENETLLLRKFFYSQDNVDSRDPVQNLNLLYVQARDDILNGSHPV
SFEKACEFGGFGQAQIQFGPHVEHKHPGFLDLKEFLPKEYIKQGAEKRIQEHKNCG
EMSEIEAKVKYVKLARSRLTYGVSFVLVKEKMKGNKLVPRLLGITKDSVMVRDEKTK
EVLQEWPLTVKRWASPKSFTLDFGEYQESYYSVQTTEGEQISQLIAGYIDILKKG
TYVTSVGSPhCTPHGWCSLSDQTTFFPGRSTILQQQFNRTGKAHGSVALPAVMRSGSS
GPETFNVGSMSPSPQQQVMVGMHRGHMPLTSAQQALMGTTINTSMHAVQAQQDDLSEL
DSLPLPGQDMASRVVWQNKVDSEKHEIHSQVDAITAGTASVUNLTAGDPADTDYTAGV
CAITTISSNLTEMSKGVKLLAALMDDEVSGSGEDLLRAARTLAGAVSDDLKAVQPTS
PRQTVTLTAAGSIGQASGDLRLQIGENETDERFQDVLMSLAKAVANAAMLVKAKNVA
QVAEDTVLQNRVIAAATQCALSTSQLVACAKVVSPTISSPVCQEQLIEAGKLVDRSVE
NCVRACQAATTDSELLKQVSAAASVVSQALHDLHLQHVRFQASRGEPIGRYDQATDTIM
CVTESIFSSMGDAGEMVRQARVLAQATSDLVNAMRSDAEAEIMDENSEKLLAAAKLLA
DSTARMEAAKGAAANPENEDQQORLREAAEGLRVATNAAQNAIKKKIUNRLEVAAK
QAAAAATQTIAASQNAAVSNKNPAAQQQLVQSCKAVADHIPLQVQGVGRGSAQAEDLS
AQLALIISSQNFLPGSKMVSSAKAAVPTVSDQAAAMQLSQCAKNLATSALERTASQ
KAHEACGPMEIDSALNTVQTLKNEQLDAKMAAVESQLKPLGETELEKCAQLDGLSTSKA
VGSSMAQLLITCAAQGNHEHYTGVAARETAQALKTLQAARGVAASTTDPAAAHAMLD
RDVMEGSAMLIQEAQALIIAPGDAERQORLAQVAKAVSHSLNNCNVCLPGQKQDVVVAL
KSGIESSKKLLVDSLPPSTKPFQEAQSELNQAADLNQASAGEVNHATRQSGSELAAS
KIFSDDFGEFLDAGIEMAGQAQTKEDQIQVIGNLKNI SMASKLLAAKSLVDPGPAP
NAKNLLAAARAVTESINQLITLCTQAPGQKECDNALRELETVKGMLDNPNPEVSD
SYFDCIESVMENKVLGESMAGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAY
LVGISDPNSQAGHGVLDPVIFARANAQIIMACQNLVDPGSSPSQVLSAATIVAKHTS
ALCNACRIASSKTANPVAKRHFVQSAKEVANSTANLVKTIKALDGDSEDNRNKCR
IATPLIEAVENLTAFASNPFEVSI PAQISSEGSQAQEPILVSAKTMLESSYLIARTS
LAINPKDPPTWSVLGASHSTVSDSIKSLITSRDKAPGQRECDYSIDGINRCIRIDIEQ
ASLAAVSQLATRDDISVEALQEQLTSVVQEI GHLIDPIATAARGEAAQGLGHKVTQLA
SYFEPLIQLAVGVASKILDHQQQMTVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHD
AITEAQAALMKEAVDDIMVTLNEAASEVGLVGGMVDAIEAMSKLDEGTTPPEKGT
YQTTVVVYKSKAIAVTAQEMMTKSVTNPEELGLGLASQMTSDYGHFLAFQGGMAAATAE
PEIGFQIRTRVQDLGHGCI FLVQKAGALQVCPDTDSYTKRELIECARADVTEKVS
LALSALQAGNKQTQACITATAVSGI IADLDTTIFMATGLTNAENSETFADHRENILK
TAKALVEDTKLLVSGAASPTDKLAQAQSSAATITQLAEVVKLGASLGSDDPETQV
DLINAIKDVAKALSDLISATKGAASKPVDDPSMYQLKGAAKVMVTNVTSLKTVK
VADEATRGTRALEATIEICIQELTVFQSKDVPEKTSPEESIRMTKGTIMTATAKAV
AAGNSCRQEDVIATANLSRKAVSMDLTACKQASFHDPVSDVETRTRALRFGTECT
LGYLDLLEHVLVILQKPTPEFKQQLAAPSKRVAGAVTELIQAAEAMKGT
EWDPEDPTVIAETELLGAAASIEAAAKLEQLKPKRAKPKQADETLDFEEQILEAAS
IAAATSAVLSASAQAQRELVAQGVKSGIPANAADDGQWSQGLISAARMVAAATSS
LCEANASVQGHASEEKLISAKQVAASTAQLLVACKVKADQDSEAMRLQAA
GNAVKRASDNLVRAAQKAAFGKADDDVVVE TKFVGGAQIIAAQEEMLKKE
RELEEARKKLAQIRQQQYKFLPTLEDEG

Table 21B. Protein Sequence Properties NOV21a	
PSort analysis:	0.5964 probability located in mitochondrial matrix space; 0.3037 probability located in mitochondrial inner membrane; 0.3037 probability located in mitochondrial intermembrane space; 0.3037 probability located in mitochondrial outer membrane
SignalP analysis:	No Known Signal Sequence Predicted

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	(fragment).			
Q9VSL8	CG6831 PROTEIN (TALIN) - Drosophila melanogaster (Fruit fly), 2836 aa.	1..2532 1..2534	1197/2563 (46%) 1707/2563 (65%)	0.0
Q9Y4G6	KIAA0320 PROTEIN - Homo sapiens (Human), 949 aa (fragment).	1597..2545 1..949	947/949 (99%) 948/949 (99%)	0.0

PFam analysis predicts that the NOV21a protein contains the domains shown in the Table 21E.

Table 21E. Domain Analysis of NOV21a			
Pfam Domain	NOV21a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	64..88	8/27 (30%) 20/27 (74%)	4.3
Band_41: domain 1 of 1	123..316	67/211 (32%) 172/211 (82%)	1.3e-92
IRS: domain 1 of 1	312..404	19/109 (17%) 46/109 (42%)	1.2
I_LWEQ: domain 1 of 5	674..768	31/98 (32%) 59/98 (60%)	11
transport_prot: domain 1 of 1	667..814	24/182 (13%) 88/182 (48%)	10
I_LWEQ: domain 2 of 5	852..894	18/47 (38%) 31/47 (66%)	2.4e+02
Vinculin: domain 1 of 1	860..903	12/48 (25%) 30/48 (62%)	1.3
I_LWEQ: domain 3 of 5	925..984	21/62 (34%) 37/62 (60%)	5.9e+04
TP_methylase: domain 1 of 1	861..1036	26/226 (12%) 105/226 (46%)	8
Apolipoprotein: domain 1 of 1	981..1229	48/288 (17%) 141/288 (49%)	3.5
CAP: domain 1 of 1	917..1354	94/557 (17%) 209/557 (38%)	4.4

I_LWEQ: domain 4 of 5	1529..1545	10/17 (59%) 13/17 (76%)	56
STAT: domain 1 of 1	1660..1821	35/211 (17%) 95/211 (45%)	8.2
LEA: domain 1 of 1	1768..1834	15/76 (20%) 42/76 (55%)	7
Histone_HNS: domain 1 of 1	2232..2356	29/143 (20%) 63/143 (44%)	3.7
I_LWEQ: domain 5 of 5	2345..2536	100/202 (50%) 183/202 (91%)	2e-101

Example 22.

The NOV22 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 22A.

Table 22A. NOV22 Sequence Analysis			
	SEQ ID NO: 77	2214 bp	
NOV22a, CG57551-01 DNA Sequence	<div>ATTCTCTCCCTGCCCTCGTGAGCCGCTGCCATGGCCCAGACACTGCAGATGGAGATC CCGAACCTTCGGCAACAGCATCCTGGAGTGCCTCAATGAACAGCGGCTGCAGGGCCTGT ACTGTGACGTGTCACTGGTGGTCAAGGGCCATGCCTTCAAGGCCACCGGGCCGTGCT TGCTGCCAGCAGTCTCTACTTCCGGGACCTGTTCAACAACAGCCGACGCGCGTGGTG GAGCTGCCGGCGGCTGTGCAGCCCCAGTCTTCCAGCAGATCCTCAGCTTCTGCTACA CGGGCCGGCTGAGCATGAACGTGGGCGACCAAGTTCCTGCTCATGTACAGCGCTGGCTT CCTGCAGATCCAGGAGATCATGGAGAAGGGCACCGAGTTCTTCTCAAGGTGAGCTCC CCGAGTCTGCGACTCCAGGGCCTGCATGCGGAGGAGGGCCCCATCGTCGGAGCCCCAGA GCCCGTGGCGCAGACATCGGGCTGGCCAGCCTGTAGCACCCGCTCAGCGCTCGTGTG GCGGGTGAAGACGGAGCAGCAGGAGTCCGACTCCGTGCAGTGCATGCCCGTGGCCAAG CGGCTGTGGGACAGTGGCCAGAAGGAGGCTGGGGGCGGCGCAATGGCAGCCGCAAGA TGGCCAAGTTCTCCACGCCGACCTGGCTGCCAACCGGCCTCACCAGCCCCGCCACC CCAACAGGCTCCGGTGGTGGCAGCAGCCAGCCCGCGTGGTGCAGGAGCAGGGCAG CCAGCCGGTGGGGTGGCAGCAGCAGGGGGTGTGGTGAAGTGGCCAGCAGCTCGGAGC GGACCAGCCAGGCACCTCAAGCGCCTACACCAGCGACAGCCCTGGCTCCTACCACAA TGAGGAGGACGAGGAGGAGGATGGTGGCGAGGAGGGCATGGATGAGCAGTACCGGAG ATCTGCAACATGTACACCATGTACAGCATGATGAACGTGCGCCAGACAGCCGAGAAGG TGGAGGCCCTCCGGAGCAGGTAGCCCCGAGTCCCGAAATCGCATCCGGGTTCGGCA AGACCTGGCGTCTCTCCCGGCTGAACCTTATCAACCAGATTGGGAACCGCTGCCACCCC AAGCTCTACGACGAGGGCGACCCCTCTGAGAAGCTGGAGCTGGTGCAGGACCAACAG TGTACATCACAAGGGCGCAGCTGATGAACGTGCCAGCTCAGCGCAGGCACGCGGCACAA GGTCTACTGCGGCGGCTCCTGGCCTCCTTCTTTGACCGGAACACGCTGGCCAACAGC TGCGGCACCGGCATCCGCTCTTCTACCAACGATCCCCGTGCGGAAGCCCTGGACAGCC GCGTGTCTCCACGCTGTCAAGTACTACTGCCAGAACTTCGCCCCAACTTCAAGGAGAG CGAGATGAATGCCATCGCGGCCGACATGTGCACCAACGCCCGCGCGCTCGTGCGAAG AGCTGGATGCCCAAGGTCAAGGTGCTCAAGGCTGAGGATGACGCCTACACCACCTTCA TCAGTGAACCGGCAAGATCGAGCCGGACATGATGGGTGTGGAGCATGGCTTCGAGAC CGCCAGCCACGAGGGCGAGGCGGGTCCCATCGCTGAAGCCCTGCAGTAACCCGCCAG CCTCCCGCGGGCCGACACTTCCCTCCCAACACACACACACCTGCCATCTTGGT CATGAGCTACTGTCTGTCCCTCCCGAGGACCCGCGGTGGGTGCTGCATGTTCCGGCC CTCTGCCCTCTGTCTTACCCCTTTCGCCACCGAGAGCTGGGCCGGGAGAGGACCG CAGGCGAGGTGGCGTGAGGTCCGTGTTGCCTTCTTTAAACACACTCGTGCAAGTGGGG GAGTTCTGGCTCCCAACCTTAACCCCTAGCCGTCTATCCACACTCACCAGGCCACCC AGGGGAGGGGGTGGCCTGGGGGTCTTGGGAAGGCCCTCCCGAGGCCTTAGGCCACC TCGCGGAAGCCTTCAGCCTCCGCCCTCACTGCAGCCCTTGGGACTTGAGGGGGGCC CCAGGGGTTCTCAGGACCCCTCCCAACCTCCCAAGTGTCTCCACGTCTCCAAAAGCG CCTTCCTGTACCCCTCGTCTATCCTGCGCCTGGGGGTGGGGTAGGCGAGGCGGTGG GGACTACCCATTTATAGCTGGGGAACAGGCTCCGAGAAATGCACAACCGACCTCA GGTGGCCGGC</div>		
	ORF Start: ATG at 32	ORF Stop: TAA at 1613	
	SEQ ID NO: 78	527 aa	MW at 57283.8kD

	[WO9957144-A2, 11-NOV-1999]			
AAM41058	Human polypeptide SEQ ID NO 5989 - Homo sapiens, 804 aa. [WO200153312-A1, 26-JUL-2001]	7..291 2..271	84/295 (28%) 123/295 (41%)	2e-17

In a BLAST search of public sequence databases, the NOV22a protein was found to have homology to the proteins shown in the BLASTP data in Table 22D.

Table 22D. Public BLASTP Results for NOV22a				
Protein Accession Number	Protein/Organism/Length	NOV22a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RE7	NAC1 PROTEIN - Homo sapiens (Human), 527 aa.	1..527 1..527	526/527 (99%) 526/527 (99%)	0.0
O35260	NAC-1 PROTEIN - Rattus norvegicus (Rat), 514 aa.	1..527 1..514	462/530 (87%) 475/530 (89%)	0.0
Q9CZ72	4930511N13RIK PROTEIN - Mus musculus (Mouse), 514 aa.	1..527 1..514	462/530 (87%) 476/530 (89%)	0.0
Q96BF6	SIMILAR TO RIKEN CDNA 0610020I02 GENE - Homo sapiens (Human), 587 aa.	1..501 1..478	289/522 (55%) 335/522 (63%)	e-140
AAH22103	RIKEN CDNA 0610020I02 GENE - Mus musculus (Mouse), 586 aa.	1..485 1..459	281/502 (55%) 327/502 (64%)	e-139

PFam analysis predicts that the NOV22a protein contains the domains shown in the Table 22E.

Table 22E. Domain Analysis of NOV22a			
Pfam Domain	NOV22a Match Region	Identities/ Similarities for the Matched Region	Expect Value
BTB: domain 1 of 1	14..124	40/143 (28%) 88/143 (62%)	6.2e-23

5 Example 23.

The NOV23 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 23A.

Table 23A. NOV23 Sequence Analysis			
	SEQ ID NO: 79	1497 bp	
NOV23a, CG57411-01 DNA Sequence	ATGGCCACTGCACAGGTGGAACCTGGTGCAGGGTGGTCCCGGGCTCCAGTAGGGGAGA AGCTGGAGTCTCGTCTGTGCAACCTGCAGGCAGACGCTCTGGAGTTGCTGCTGGAGTT TGTCTACACGGGCTCCCTGGTCATCGACTCGGCCAACGCCAAGACACTGCTGGAGGCG GCCAGCAAGTTCAGTTCCACACCTTCTGCAAAGTCTGCGTGTCTTTCTCGAGAAGC AGCTGACGGCCAGCAACTGCCTGGGCGTGTGGCCATGGCCGAGGCCATGCAGTGCAG CGAGCTCTACCACATGGCCAAGGCCCTTCGCGCTGCAGATCTTCCCCGAGGTGGCCGCC CAGGAGGAGATCCTCAGCATCTCAAGGACGACTTCATCGCCTACGTTCTCCAACGACA GCCTCAACACCAAGGCTGAGGAGCTGGTGTACGAGACAGTCATCAAGTGGATCAAGAA GGACCCCGCGACACGCACACAGCTGCAGTACGCGGTGAGCTCTGGCCGTGGTCCGCC CTCCCTTTCATCCACCCAGCTACCTGCTCAATGTGGTTGACAATGAAGAGCTGATCA AGTCATCAGAAGCTGCGGGACCTGGTGAACGAGGCCAAACGCTACCATATGCTGCC CCACGCCCCGCCAGGAGATGCAGACGCCCCGAACCCGGCCGCGCGTCCCTGCAGGTGTG GCTGAGGTTCATCGTCTTGGTTGGGGGCCGTGAGTGGTGGGGATGACCCAGCGCTCGC TGGTGGCCGTCACTGTGTGGAACCCGAGAACCAACAAGTGGTACCCCTTGGCGTCTCGT GCCCTTCTATGACCGCGAGTTCTTCAGTGTAGTGAGTGCAGGGGACAACATCTACCTC TCAGGTGGGATGGAATCAGGGGTGACGCTGGCTGATGTCTGGTGCTACATGTCCCTGC TTGATAACTGGAACCTCGTCTCCAGAATGACAGTCCCCGCTGTCCGCACAATAGCCT CGCTACGATGGGAAGATTTACACCCTCGGGGGACTTGGCGTGGCAGGCAACGTGGAC CACGTGGAGGTCCCTGCAGGTGTGGCTGAGGTTCATCGTCTTGGTTGGGGCCGTGAGA TGGTGGGGATGACCCAGCGCTCGTGGTGGCCGTACCTGTGGAACCCGAGAACAA CAAGTGGTACCCCTTGGCGCTCGTGGGTGGGATGGAATCAGGGGTGACGCTGGCTGAT GTCTGGTGCTACATGTCCCTGCTTGATAACTGGAACCTCGTCTCCAGAATGACAGTCC CCCGCTGTCCGCACAATAGCCTCGTCTACGATGGGAAGATTTACACCCTCGGGGGACT TGGCGTGGCAGGCAACGTGGACACGTTGGAGGCCCTACGAGCCCAACCAACACATGG ACCCTCTCCCCACATGCCCTGCCCTGTGTTTACAGACCGGTGCGTCTGTGATAAAGA AATATATTCAAAGCGGTGACATCAGCAGAAAGCCACGATAAGACT		
	ORF Start: ATG at 1	ORF Stop: TGA at 1468	
	SEQ ID NO: 80	489 aa	MW at 54208.2kD
NOV23a, CG57411-01 Protein Sequence	MATAQVELVQGGPRAPVGEKLELVLSNLQADVLELLLEFVYTGSLVIDSANAKTLLEA ASKFQFHTFCKVCVSFLEKQLTASNCLGVLAMAEAMQCSSELYHMAKAFALQIFPEVAA QEEILLSISKDDFIAYVSNDSLNTKAEELVYETVIKWKDPATRTQLQYAAELLAVVR LPFIHPSYLLNVVDNEELIKSSEACRDLVNEAKRYHMLPHARQEMQTPRTRPRVPAGV AEVIVLVGGRQMVGMTQRLSLAVTCWNPQNNKWYPLASLPFYDREFFSVVSAGDNIYL SGGMESGVTLADVWCYMSLLDNWNLVSRMTVPCRHNLSLVYDGKIYTLGGLGVAGNV HVEVPAGVAEVIVLVGGRQMVGMTQRLSLAVTCWNPQNNKWYPLASLGGMESGVTLAD VWCYMSLLDNWNLVSRMTVPCRHNLSLVYDGKIYTLGGLGVAGNVHVEAYEPTTNTW TLLPHMPCPVFRHGCVVIKKYIQSG		

Further analysis of the NOV23a protein yielded the following properties shown in Table 23B.

Table 23B. Protein Sequence Properties NOV23a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.2271 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV23a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 23C.

Table 23C. Geneseq Results for NOV23a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB40940	Human ORFX ORF704 polypeptide sequence SEQ ID NO:1408 - Homo sapiens, 335 aa. [WO200058473-A2, 05-OCT-2000]	19..351 4..334	317/333 (95%) 320/333 (95%)	e-180
AAM38711	Human polypeptide SEQ ID NO 1856 - Homo sapiens, 574 aa. [WO200153312-A1, 26-JUL-2001]	22..472 78..559	151/488 (30%) 222/488 (44%)	2e-61
AAB43090	Human ORFX ORF2854 polypeptide sequence SEQ ID NO:5708 - Homo sapiens, 506 aa. [WO200058473-A2, 05-OCT-2000]	22..468 9..487	150/491 (30%) 241/491 (48%)	3e-59
AAM38956	Human polypeptide SEQ ID NO 2101 - Homo sapiens, 587 aa. [WO200153312-A1, 26-JUL-2001]	22..468 90..568	149/491 (30%) 240/491 (48%)	1e-58
AAM94018	Human stomach cancer expressed polypeptide SEQ ID NO 106 - Homo sapiens, 568 aa. [WO200109317-A1, 08-FEB-2001]	25..470 76..553	148/490 (30%) 231/490 (46%)	3e-56

In a BLAST search of public sequence databases, the NOV23a protein was found to have homology to the proteins shown in the BLASTP data in Table 23D.

Table 23D. Public BLASTP Results for NOV23a

Protein Accession Number	Protein/Organism/Length	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96CT2	HYPOTHETICAL 76.8 KDA PROTEIN - Homo sapiens (Human), 707 aa (fragment).	19..489 203..707	390/507 (76%) 406/507 (79%)	0.0
Q96PW7	KIAA1921 PROTEIN - Homo sapiens (Human), 545 aa (fragment).	19..489 41..545	390/507 (76%) 406/507 (79%)	0.0
Q96BF0	SIMILAR TO HYPOTHETICAL PROTEIN FLJ14106 - Homo sapiens (Human), 503 aa.	19..351 172..502	329/333 (98%) 330/333 (98%)	0.0

Q9D5K3	4930429H24RIK PROTEIN - Mus musculus (Mouse), 484 aa.	33..485 1..477	165/492 (33%) 248/492 (49%)	2e-66
Q9UH77	Kelch-like protein 3 - Homo sapiens (Human), 587 aa.	22..468 90..568	150/491 (30%) 241/491 (48%)	1e-58

PFam analysis predicts that the NOV23a protein contains the domains shown in the Table 23E.

Table 23E. Domain Analysis of NOV23a			
Pfam Domain	NOV23a Match Region	Identities/ Similarities for the Matched Region	Expect Value
BTB: domain 1 of 1	4..79	24/143 (17%) 53/143 (37%)	3.7
Kelch: domain 1 of 4	223..272	9/50 (18%) 28/50 (56%)	0.94
Kelch: domain 2 of 4	275..320	11/47 (23%) 27/47 (57%)	0.016
Kelch: domain 3 of 4	322..396	14/75 (19%) 44/75 (59%)	3.3e-05
Kelch: domain 4 of 4	426..471	19/47 (40%) 35/47 (74%)	7.2e-10

Example 24.

The NOV24 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 24A.

Table 24A. NOV24 Sequence Analysis		
	SEQ ID NO: 81	4268 bp
NOV24a, CG57399-01 DNA Sequence	<p>ATGACCTGGGACACAGCTCTCTGGACCTCAGTTTTTCTGATTGGGCTCCTTCCTACCC TTGGTTTCGCTAATTGCATCCTCCAGACTTCTGGTAAATGTGTACTTTAAGAGGTAG ATACCCCGACGCCCCACAACCACCTCTCTGCTTGTCTCCCTAGTCCACCAGCTCCGA CCAGCAGACATCAAAGTGGTGGCCGCTGGGTAATGATGAAACCTTCCAGGAAAGTG GTGCAGGCGAGCTAAGTGAGCCTGACCCAGGCAGTGGTCTGGCCACAGGCTGCTT GCCTGGGGTAAAAAGGAAATGCAAGATGTGGTAGGTGAGAGAACGCCGAGCCGTCGC CGCAGCCTCCGCGCCGAGAGGCCCTTGTTCGCGCTGCTGGGAAGGAGAGTCTGTGCC GACAAGATATTTTCATTTCCTTGTGGAAATTATCAAGCATTTTCCTCCCTCCCTCA GGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACACTCTTCATTGGGGTCAACGAC TTGTGTCACTTACTGTCCACTTGTTCAGGGCCCCGTTATAGACCTGGGTGGGATGGATA CCCTCCACTCCCTGCAGCTCCCAAGGCTTTCGTCAACGTGGTGGAGGTCTAGGAGCT GGCTAGCCTGTACAGGGCCAGGCGGAAATGTGCCATGCTGGCAGCTCAGGAAGCC TGGAACAGCCTCCTGGCCTCCAGCAGGTACAGTGAGCAGGAGTCTTCACCGTGGTTT TCCAGCCTTTCTCTATGAGACCACCCATCTGACCCCGACTCCAGGATTCTACCA GCTGGCCTGGCATCTCTGGAATAGGATGATGGAGCCAGCAGGAGAGAAAGATGAGCCA TTGAGTGTAAACACGGGAGGCCAATGAAGTGTCCCTCTCAGGAGAGCCCTATCTGT TCAGCTACAGAAACAGCAACTACCTGACCAGACTGCAGAAACCCCAAGACAAGCTTGT AAGAGAAGGAGCGGAAATCAGATGTCTGACAAAGACCCCTCCGATACGGTTCACACC TCAGTTTCATAGCTGAAGCCGCTGACATCAACGTAATTGGAGCCCTGGGTGACTCTC TCACGGCAGGCAATGGGGCCGGTCCACACCTGGGAACGCTCTGGACGCTCTTGACTCA GTACCGAGGCCTGTCTGGAGCGTCGGCGGAGATGAGAACATCGGCACCGTTACCACC</p>	

	<p>CTGGCAGACATCCTCCGGAATTCAACCCCTTCCCTGAAGGGCTTCTCTGTGGCACTG GGAAAGAAACCAAGTCCTAATGCCTTCTTAAACCAAGCTGTGGCAGGAGGCCGAGCTGA GCAGGCCAGGAGGCTGTGGACCTGATGAAGAATGACACGAGGATACACTTTCAGGAA GACTGGAAGATAATAACCTGTTTATAGGCGGCAATGACCTCTGTGATTCTGCAATG ATCTGGTACACTATTCTCCCCAGAACTTCACAGACAACATTGGAAGGCCCTGGACAT CCTCCATGCTGAGTCTCAGGTTCTCGGGCATTGTGAACCTGGTGACGGTGTCTGAG ATCGTCAACCTGAGGGAGCTGTACCAGGAGAAAAAGTCTACTGCCAAGGATGATCC TCAGGTCACTGTGTCTCTGTCTGAAGTTTGATGATAACTCAACAGAAGTTGCTAC CCTCATCGAATTCAACAAGAAGTTTCAGGAGAAGACCCCAACTGATTGAGAGTGGG CGATATGACACAAGGGGAAGATTCTACTGTGGTTGTGCAGCCGTTCTTTGAAAACGTGG ACATGCCAAAGACCCAGGAAGATTGCTGACAACTCTTTCTCGCTCCTGACTGTTT CCACTTCAGCAGCAAGTCTACTCCGAGCAGCCAGTGCTCTCTGGAAACAATATGCTG GAGCCTGTTGGCCAGAAGACGACTCGTCATAAGTTTGAAAACAAGATCAATATACAT GTCCGTACAGGTCCAGCCGTTCTGAGGACCTACAAGAACAGATGCAGGGTCATGG GACCTGGCTGCCATGCAGGGACAGAGCCCTTCTGCCTTGCAACCTACCTCAGTGCAT GCCCTGAGACCTGCAGACATCCAAGTTGTGGCTGCTCTGGGGGATTCTCTGACCGCTG GCAATGGAATTGGCTCCAAACCAGACGACCTCCCGATGTCAACACAGTATCGGGG ACTGTCATACAGTGCAGGAGGGGACGCTCCCTGGAGATGTGACCACTTACCTAGT TCTATCCTTCGGGAGTTTAAACAGAAACCTCACAGGCTACGCCGTGGGACGGGTGATG CCAATGACACGAATGCATTCTCAATCAAGCTGTTCCCGGAGCAAGGCTAGGGATCT TATGAGCCAAAGTCCAAACTCTGATGCAGAAGATGAAAGATGATCATAGAGTAAATTT CATGAAGACTGGAAGGTTCATCAGTGTGATCGGAGGCAGCGATTATGTGACTACT GCACAGATTGCAATCTGTATTCTGCAGCCAACCTTGTTCACCATTCCGCAATGCCTT GGACGCTCTGCATAGAGAGGTGCCAGAGTCTGGTCAACCTCGTGGACTTCTGGAAC CCCCTATCATGCGGCAGGTGTCTCTGGGAAACCCAGACAGTGGCCAGTGCAGCAGG CCAGCGTTTGTGTAAGTGCCTTCTGACCTGCGGGAGAACTCCAAGAGCTAGCCAG GCTGGAGGCTTACGCCGAGCCTACCAGAGCAGCATGCGCGAGCTGGTGGGCTCAGGC CGCTATGACACGCAGGAGGACTTCTCTGTGGTGTCTGAGCCCTTCTTCAGAACATCC AGCTCCCTGTCTGCAGGATGGGCTCCAGATACGTCCTTCTTGGCCAGAGTGCAT CCACCCAAATCAGAAATTCCTCTCCAGCTGGCCAGAGCCCTTGGACCAATATGCTT GAACCACTTGGAAAGCAAAACAGAGACCTGGACCTGAGAGCAGAGATGCCCATCACT GTCCACTCAGAATGAGCCCTTCTGAGAACCCTCGGAATAGTAATACAGTACCTACCC CATCAAGCCAGCATTGGAAGTGGGGCAGTGACTTCTGTGTACAGATGGAAGGCT TCCAATAGTGTTCACACCTCTGTCCACAGCTCCGACCAAGCAGATCAAGAGTGGTGG CCGCCCTGGGTGACTCTCTGACTACAGCAGTGGGAGCTCGACCAACAACCTCCAGTGA CCTACCCACATCTTGGAGGGGACTCTCTGGAGCATTGGAGGGGATGGGAACCTGGAG ACTCACACCACACTGCCCAGTATTCTGAAGAAGTTCAACCTTACTCTCTGGCTTCT CTACCAGCACCTGGGAGGGGACAGCAGGACTAAATGTGGCAGCGGAAGGGCCAGAGC TAGGAGGGACATGCCAGCCAGGCTGGGACCTGGTAGAGCGAATGAAAAACAGCCCC ATACACTTTCAGGAAGACTGGAAGATAATAACCTGTTTATAGGCGGCAATGACCTCT GTGATTTCTGCAATGATCTGGTAGGTGAATATGTTACAGCATCCAACAGGCCCTGGA CATCTCTCTGAGGAGCTCCCAAGGGCTTTCGTCAACGTTGGTGGAGGTGATGGAGCTG GCTAGCCTGTACAGGGGCAAGGCGGGAATGTGCCATGTGGCAGCTCAGAACAACT GCACTTGCTCAGACACTCGCAAAGCTCCCTGGAGAAGCAAGAACTGGAAGAAGTGAA CTGGAACCTCCAGCATGGCATCTCCAGTTTCTCTACTGGCACCATAACACAGCGT GAGGACTTTGCGGTTGTGGTGACGCTTCTTCCAAAACACACTACCCCACTGAACA GAGGGGACACTGACCTCACCTTCTTCTCCGAGGACTGTTTTCACCTCTCAGACCGCGG GCATGCCGAGATGGCCATCGCACTCTGGAACAACATGCTGGAACCAAGTGGGCCGCAAG ACTACCTCCAACAACCTCACCCACAGCCGAGCAAACTCAAGTGCCCTCTCTGTGA GTCTTACCTCTACACCTGCGGAACAGCCGATTGCTCCAGACAGGCTGAAGAAGC CCCCGAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGAGTGGCCCTTGTGGTGGGC ATCATCGGACAGTGGTCTGGAGGTGCAGGAGAGGTGGCCGAGGGAAGATCTCCAA TGAGCCTGCGCACTGTGGCCCTTAGGCCCGGG</p>
	<div>ORF Start: ATG at 1</div> <div>ORF Stop: TAG at 4258</div>
	<div>SEQ ID NO: 82</div> <div>1419 aa</div> <div>MW at 158435.1kD</div>
NOV24a, CG57399-01 Protein Sequence	<p>MTWDTALWTSVFLIGLLPTLGFANCI LQTSKMCITLRGRYPQPPQPLCLSPVLHQLR PADIKVVAALGNDETFOESGAGQLSEPDPRQSWPQACLPGVKKEMQDVVGERTPSRR RSLRRREALVPAAGKESLCRQDIFISLLEIKHFPSPQDINLEKDWLVTFLFVND LCHYCPLVQGPVIDLGGMDTLHSLQLPRAFNVVVEVMEASLYQGGGKCAMLAQA WNSLLASSRYSEQSFYVVFQFFYETTPSDPRLQDSTTLAWHLWNRMMEPAGEKDEP LSVKHGRPMKCPSESYPYFSYRNSNYLTRLQKPQDKLVREGAEIRCPDKDPSDVTPT SVHRLKPADINVIGALGDSLTAAGNAGSTPGNVLDVLTQYRGLSWSVGGDENIGTVTT LADILREFNPFLKGFVSGTGKETS PNAFLNQAVAGGRAEQARRVLDMKNDTRIHFOE DWKIITLFIGGNDLDCFNLDVHYSQNFNTDNIGKALDILHAESQVPRAFNVLVTLE IVNLRRELYQEKKYCPRLMLRSLCPVLKFDNSTELATLIEFNKKFQEKTHQLIESG RYDTREDFYVVFQFFENVDMPKTQGLPDNSFFAPDCFFHSSKSHSRAASALWNNML EPVGQKTRHKFENKINICPSQVQPLRTYKNSMQGHGTWLPDRAPSAHPTSVH ALRPADIQVVAALGDSLTAAGNIGSKPDDLDPVTTQYRGLSYAGGDSLENVITLPS SILREFNRNLTGYAVGTGDANDTNAFLNQAVPGAKARDLMSQVQTLQMKMKDHRVNF HEDWKVITVLIGGSDLCDYCTDSNLYSAANFVHHLRNALDVLHREVPRLVNLVDFLN PTIMRQVFLGNPKCPVQASVLCNVLTLRENSQELARLEAFSRAYSMSRELVGSG RYDTQEDFSVVLQFFQNIQLPVLQDGLPDTFFAPDCIHFNQKFHSQLARALWNNML EPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTPIKPAIENWGSDFLCTEWEKA SNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNSSDLPTSWRGLSWSIGGDGNLE</p>

	THTTLP SILKKFNPYLLGFSTSTWEGTAGLNVAEAGARRRDMPAQAWDLVERMKNSP IHQEDWKI IITLFIGGNDLDFCNDLVGEYVQHIQQALDI LSEELPRAFVNVEVMEL ASLYQGQGGKCAMLAAQNNCTCLRHSQS SLEKQELKKVNNWLQHG I SFSFYWHQYTOR EDFAVVVQPPFFQNTLTPLNRGDTDLTFFSEDCPHFSDRGHAEMAIALWNNMLEPVGRRK TTSNNFTHSRALKKCPSPVSPYLYTLRNSRLLPDQAEAEPEVLYWAVPVAAGVGLVVG IIGTVVWRCRRGGRREDPPMSLRVAL		
	SEQ ID NO: 83	1624 bp	
NOV24b, CG57399-02 DNA Sequence	<u>GCCGGCTGACATCAATGTAATTGGAGCCCTGGGTGACTCTCTCACGGCAGGCAATGGG</u> <u>GCCGGGTCCACACCTGGGAACGCTCTGGACGCTTGACTCAGTACCGAGGCTGTCTCT</u> <u>GGAGCGTCGGCGGAGATGAGAACATCGGCACCGTTACCAACCTGGCGGAACATCCTCCG</u> <u>GGAATTC AACCCCTTCCCTGAAGGGCTTCTCTGTTGGCACTGGGAAAGAAACCAGTCCT</u> <u>AATGCCCTTCTTAAACAGGCTGTGGCAGGAGGCCGAGCTGAGGATCTACCTGTCCAGG</u> <u>CCAGGAGGCTGGTGGACCTGATGAAGAATGACACGAGGATACACTTTCAGGAAGACTG</u> <u>GAAGATAATAACCCGTGTTTATAGGCGGCAATGACCTCTGTGATTTCTGCAATGATCTG</u> <u>GTCCACTATTCTCCCAGAACTTCACAGACAACATTGGAAGGCCCTGGACATCCTCC</u> <u>ATGCTGAGGTTCTCGGGCATTGTGAACCTGGTGACGGTGCTTGAGATCGTCAACCT</u> <u>GAGGGAGCTGTACCAGGAGAAAAAGTCTACTGCCAAGGATGATCCTCAGGTCTCTG</u> <u>TGTCCTCTGTGTCTGAAGTTTGATGATAACTCAACAGAACTTGCTACCTCATCGAAT</u> <u>TCAACAAGAAGTTTCAGGAGAAGACCCACCAACTGATTGAGATGGGCGATATGACAC</u> <u>AAGGGAAGATTTTACTGTGGTTGTGCAGCCGTTCTTTGAAAACGTGGACATGCCAAG</u> <u>ACCTCGGAAGGATTGCTGCAAACTCTTTCTTCGCTCCTGACTGTTTCCACTTCAGCA</u> <u>GCAAGTCTCACTCCCAGCAGCCAGTGCTCTCTGGAACAATATGCTGGAGCCTGTGG</u> <u>CCAGAAGACGACTCGTCATAAGTTTGAAAAACAAGATCAATATCACATGTCCGAACCAG</u> <u>GTCCAGCCGTTTCTGAGGACCTACAAGAACAGCATGCAAGGCTACGGGACCTGGCTGC</u> <u>CATGCAGGGACAGAGCCCTTCTGCCTTGCACCCTACCTCAGTGCATGCCCTGAGACC</u> <u>TGCAGACATCCAAGTTGTGGCTGCTCTGGGGGATTCTCTGACCGCTGGCAATGGAATT</u> <u>GGCTCCAAACAGACGACCTCCCGATGTCAACACACAGTATCGGGGACTGTATACATA</u> <u>GAGAAAGTAAACAGGGTTCTTATCAGACTCCTGGGTGAGCAATCCAACAGGAAATG</u> <u>CACCAGAAAAGCACCAAATCCCTGAATCTTCACTCCCGCTTGCAATGATACGTGTA</u> <u>CAGTGGTGTTTCTACGCTCTCTGTTTACTGTCTTTATGTGTTTATTCATGTTGTCTTG</u> <u>TAGTCACACAGCTGCCTTTACATATATGTACACATCTGCACAGAAAACCTCTGAAACC</u> <u>CATCGCACACTTCGAGAGGCCATAACCAAGACACAATCACAATCAGCCATGTCTTGAA</u> <u>AGATTAGCAATTCGACAAGAGGAAAGGGTGAGAAAGGGCATCCCGAACACGGAAGTGG</u> <u>AGAAGCTCAGGGTGTGTGAGCGAGCGGTTGCGTGTAGATATTCTCAAGTTTCTTTCT</u> <u>CTCCTAATAAAGTTCTCATTCTCTGAGGCTTCAAAGTAAGTGGCGAGTAGCTCAGAA</u>		
	ORF Start: ATG at 311	ORF Stop: TGA at 1241	
	SEQ ID NO: 84	310 aa	MW at 35240.6kD
NOV24b, CG57399-02 Protein Sequence	MKNDTRIHFQEDWKI IITLFIGGNDLDFCNDLVHYSQNFDTNIGKALDILHAEVPA FVNLVTVLEI VNLRELYQEKKVYCPRLILRSLCPCVLKFDNDSTELATLIEFNKKFQE KTHQLIESGRYDTREDFTVVVQPPFENVDMPKTSEGLPDNSFFAPDCPHFSSKSHSRA ASALWNNMLEPVGQKTTTRHKFENKINICTPNQVQPLRTYKNSMQGHGTWLP CRDRAP SALHPTSVHALRPADIQVVAALGDSLTAGNGIGSKPDDL PDVTQYRGLSYRESKPGF LSDSWVSKSNRKCTR KAPNP		
	SEQ ID NO: 85	4425 bp	
NOV24c, CG57399-03 DNA Sequence	<u>CTGGAGCATTCTGGCATGGGGCTGCGGCAGGCATTTTCTCCTGGAGCTGCTGCTGC</u> <u>TTCTGGGGCAAGGTACCCCTCAGATCCATACCTCTCCTAGAAAGAGTACATTGGAAGG</u> <u>GCAGCTATGGCCAGAGACAGTTCACTCTCTGAAGCCTTCTGATATTAAATTTGTGGCA</u> <u>GCCATTGGCAATCTGGAATTTGTGCCAGACCCAGGAGACGGGCGATCTGGAGAAGCAAG</u> <u>ACGAAAGGCCACAGCAGGTGTGCATGGGAGTGATGACAGTCTTTTCAGACATCATCAG</u> <u>ATATTTTCAGTCTTCTGTTCCAATGCCTGTGTGCCACACTGGAAGAGAGTCAATCCC</u> <u>CACGATGGTGCTGAGGACTTGTGGATTGAGGCTCAAGAACTGGTGAGAAACATGAAAG</u> <u>AGAACCAACTTGACTTTCAATTTGACTGGAAGCTCATCAATGTGTTCTTCAGTAATGC</u> <u>AAGCCAGTGTTACCTGTGCCCTCTGCTCAACAGAATGGGCTTGCGGCGGGCGGCGTG</u> <u>GATGAGCTGATGGGGGTGCTGGACTACCTGCAGCAGGAGGTGCCAGAGCATTGTAA</u> <u>ACCTGGTGGACCTCTCTGAGGTTGCAGAGGTCTCTCGTCAGTATCACGGCACTTGCT</u> <u>CAGCCCTGCACACAGAGCCCTGTAATTGCTCAGAGGAGACCACCGGCTGGCCAAGGTG</u> <u>GTGATGCAGTGGTCTTATCAGGAAGCCTGGAACAGCCTCCTGGCCTCCAGCAGGTACA</u> <u>GTGAGCAGGAGTCTTCAACCGTGGTTTTCCAGCCTTTCTTCTATGAGACCACCCATC</u> <u>TGACCCCGACTCCAGGATTCTACCACGCTGGCCTGGCATCTCTGGAATAGGATGATG</u> <u>GAGCCAGCAGGAGAGAAAGATGAGCCATTGAGTGTAACAAACAGGGAGGCCAATGAAGT</u> <u>GTCCCTCTCAGGAGAGCCCTATCTGTTTCACTACAGAAACAGCAACTACCTGACCAG</u> <u>ACTGCAGAAACCCCAAGACAAGCTTGAGGTAAGAGAAGGAGCGGAAATCAGATGTCTT</u> <u>GACAAAGACCCCTCCGATACGGTTCACCTCAGTTCATAGGCTGAAGCCGGCTGACA</u> <u>TCAACGTAATTTGAGCCCTGGGTGACTCTCTCACGGCAGGCAATGGGGCCGGTCCAC</u> <u>ACCTGGGAACGTCTTGGACGTCTTGACTCAGTACCGAGGCCTGTCTCTGGAGCGTCGGC</u> <u>GGAGATGAGAACATCGGCACCGTTACCACTTGGCGGACATCTCCGGGAATTCACCC</u> <u>CTTCCCTGAAGGGCTTCTCTGTTGGCACTGGGAAAGAAACAGTCTTAATGCCTTCTT</u> <u>AAACCAAGGCTGTGGCAGGAGGCCGAGCTGAGCAGGCCAGGAGGCTGGTGGACCTGATG</u> <u>AGAATGACACGAGGATACACTTTCAGGAAGACTGGAAGATAATAACCTGTTTATAG</u> <u>GCGGCAATGACCTCTGTGATTTCTGCAATGATCTGGTACACTATTCTCCCAGAACTT</u>		

	<p>CACAGACAACATTGGAAGGCCCTGGACATCCTCCATGCTGAGGTTCTCGGGCATT GTGAACCTGGTGACGGTGCTTGAGATCGTCAACCTGAGGGAGCTGTACCAGGAGAAAA AAGTCTACTGCCAAGGATGATCCTCAGGTCAGTGTGCTGCTGAGTTTGA TGATAACTCAACAGAACTTGCTACCCTCATCGAATTCAACAAGAGTTTCAGGAGAAG ACCCACCAACTGATTGAGAGTGGGCGATATGACACAAGGGAAGATTTTACTGTGGTTG TGCAGCCGTTCTTTGAAAACGTGGACATGCCAAAGACCCAGGAAGGATTGCTGACAA CTCTTTCTTCGCTCCTGACTGTTTCCACTTCAGCAGCAAGTCTCACTCCCGAGCAGCC AGTGCTCTCTGGAACAATATGCTGGAGCCTGTTGGCCAGAAGACGACTCGTCATAAGT TTGAAAACAAGATCAATATCACATGTCCGAACAGGTAGAGTGGCCGTTTCTGAGGAC CTACAAGAACAGCATGCAGGGTCATGGGACCTGGCTGCCATGCAGGGACAGAGCCCTC TCTGCCTTGACCCCTACCTCAGTGCATGCCCTGAGACCTGCAGACATCCAAGTTGTGG CTGCTCTGGGGGATTCTTGACCGCTGGCAATGGAATTGGCTCCAAACCAGACGACCT CCCCGATGTCAACACACAGTATCGGGGACTGTATACAGTGCAGGAGGGGACGGCTCC CTGGAGAAATGTGACCACTTACCTGATATCCTTCGGGAGTTTAAACAGAACTCACAG GCTACGCCGTGGGCACGGGTGATGCCAATGACACGAATGCATTCTCAATCAAGCTGT TCCCGGAGCAAAAGGCTAGGGATCTTATGAGCCAAGTCCAAACTCTGATCAGAAAGATG AAAGATGATCATAGAGTAAATTTCCATGAAGACTGGAAGGTCATACAGCTGCTGATCG GAGGCAGCGATTATGTGACTACTGCACAGATTGGAATCTGTATTCTGCAGCCAACTT TGTTCAACATCTCCGCAATGCCTTGGACGTCCTGCATAGAGAGGTGCCAGAGTCCCTG GTCAACCTCGTGGACTTCTGAACCCCACTATCATGCGGAGGTGTTCTGCGGAAACC CAGACAAGTGCCAGTGCAGCAGGCCAGCGTTTTGTGTAAGTGCCTTCTGACCTGCG GGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCCCTCAGCCGAGCCTACGAGCAGC ATGCGCGAGCTGTGGGTGAGGCCGCTATGACACGAGGAGGAGTCTCTGTGGTGC TGCAGCCCTTCTTCCAGAACATCCAGCTCCTGTCTGCTGAGGATGGGCTCCAGATAC GTCCTTCTTGGCCCCAGACTGCATCCACCCAAATCAGAAATTCAGTCCAGCTGGCC AGAGCCCTTTGGACCAATATGCTTGAACCACTTGAAGCAAAAACAGAGACCTGGACC TGAGAGCAGAGATGCCCATCACTGTCCCACTCAGAATGAGCCCTTCTGAGAACCCC TCGGAATAGTAACTACACGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCAGTGAC TTCCTGTGTACAGAGTGAAGGCTTCCAATAGTGTCCAACCTCTGTCCACAGCTCC GACCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTGTGGCAGTGGG AGCTCGACCAAACTCCAGTGACCTACCCACATCTTGGAGGGGACTCTCTTGGAGC ATTGGAGGGGATGGAACTTGGAGACTCACACCACACTGCCCGACATTTCTGAAGAAGT TCAACCCCTTACCTCCTTGGCTTCTCTACCAGCACCTGGGAGGGGACAGCAGGACTAAA TGTGGCAGCGGAAGGGGCCAGAGCTAGGGACATGCCAGCCAGGCCCTGGGACCTGGTA GAGCGAATGAAAAACAGCCCCCAGGACATCAACCTGGAGAAAGACTGGAAGCTGTGCA CACTCTTCAATGGGGTCAACGACTTGTGTCTTACTGTGAGAATCCGGTAGGCGAATA TGTTGAGCAGATCCAACAGGCCCTGGACATCCTCTCTGAGGAGCTCCCAAGGGCTTTC GTCAACGTGGTGGGAGCTATGGAGCTGGCTAGCCTGTACAGGGCCAGGCCGCGGAAAT GTGCCATGTCTGGCAGCTCAGAACAACTGCCTTGCCTCAGACACTCGCAAAGCTCCCT GGAGAAGCAAGAACTGAAGAAAGTGAAGTGAACCTCCAGCATGGCATCTCCAGTTTC TCCTACTGGCACCAATACACACAGCGTGAGGACTTGGCGTTGTGGTGCAGCCTTCT TCCAAAACACACTACCCCCACTGAACAGAGGGGACACTGACCTCACCTTCTTCTCGA GGACTGTTTCACTTCTCAGACCGCGGGCATGCCGAGATGGCCATCGCATCTGGAAC AACATGCTGGAACCACTGGGGCCGAAGACTACCTCCAACAACCTACCCACAGCCGAG CCAAACTCAAGTGCCCTCTCTCTGAGAGCCCTTACCTCTACACCTGCGGAACAGCCG ATTGCTCCAGACAGGCTGAAGAAGCCCCGAGGTGCTCTACTGGGCTGTCCAGTG GCAGCGGAGTCGGCCTTGTGGTGGGCATCATCGGACAGTGTCTGAGGTGAGGA GAGGTGGCGGAGGGAAGATCCTCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCG GGGGTGGGTCTCACCTTAACTCCCTATAGCCACTCTCTTACCGCCCTCTGCCCCA GCCACTCCCGGCCACAGGACATGCTTCAATGCCTGGTGCCATAGGAAGCCAGGGGA CAGTCACAACTTCTTGG</p>
	<div>ORF Start: ATG at 16</div> <div>ORF Stop: TAG at 4285</div>
	<div>SEQ ID NO: 86</div> <div>1423 aa</div> <div>MW at 159352.7kD</div>
<p>NOV24c, CG57399-03 Protein Sequence</p>	<p>MGLRPGIFLLELLLLLQGGTPQIHTSPRKSTLEGQLWPETVHSLKPSDIKFVAAIGNL EIVPDPGTGDLKQDERPQQVCMGVMTVLSDIIRYFSPSPVMPVCHTGRKRVIPHDGAE DLWIQAQELVRNMKENQLDFQDWKLINVFFSNASQCYLCPAQNGNLAAGGVDELGM VLDYLQQEVPRAFVNLVDLSEAEVSRQYHGTWLSPAPEPCNCSEETRLAKVVMQWS YQEAWSLLASSRYSEQESFTVVFPFFYETTPSDPRLQDSTTLAWHLWNRMMEPAGE KDEPLSVKHGRPMKCPSEQESPYLFSYRNSNYLTRLQKPKQDKLEVREGAIEIRCPDKDPS DTVPTSVHRLKPADINVIGALGDSLTAGNGAGSTPGNVLDVLTQYRGLSWSVGGDENI GTVTTLADILREFNPSLKGFPSVGTGKETSPNAFLNQAVAGGRAEQARRLVDLMKNDTR IHFQEDWKIITLIGGNDLDCFCNDLVHYSPONFDTNIGKALDILHAEVPRAFVNLVT VLEIVNLRELYQEKVYCPRMILRLSLCPCVLKFDNDNSTELATLIEFNKKFQEKTHQLI ESGRYDTRDFTVVVQPFENVDMPKTQEGLPDNSFFAPDCFHSSKSHSRAASALWN NMLEPVGQKTRHFKENKINITCPNQVEWPFLRTYKNSMQGHGTWLPDRDRAPSALHP TSVHALRPADIQVVAALGDSLTAGNGIGSKPDDLDPVTTQYRGLSYSAGGDSLENVT TLPDILREFNRNLTGYAVGTGDANDTNAFLNQAVPGAKARDLMSQVQTLQMKMKDDHR VNFHEDWKVITVLIGGSDLCYCTDSNLYSAANFVHLLRNALDVLHREVPRVNLVND FLNPTIMRQVFLGNPDKCPVQASVLCNCVLTLENSQELARLEAFSRAYSQSMRELV GSGRYDTEQDFSVVLQPFQNIQLPVLQDGLPDTSSFFAPDCIHPNQKFHSQLARALWT NMLEPLGSKTETDLRAEMPICTPTQNEPFLRTPRNSNYTPIKPAIENWGSDFLCTE WKASNSVPTSVHQLRPADIKVVAALGDSLTVAVGARPNNSDLPSTSWRGLSWSIGGDK NLEHTTLPDILKFNPYLLGFSTSTWEGTAGLNVAEGARARDMPAQAWDLVERMKN SPQDINLEKDWLVTFLFIGVNDLCHYCENPVGEYVQHIQALDILSEELPRAFPVNVVE</p>

<p> VMELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQ YTQREDFAVVVQPFQNTLTPLNRGDTDLTFSEDCFHFSDRGHAEMAIALWNNMLEP VGRKTTSNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEAEVLYWAVPVAAGVG LVVGIIGTVVWRCRRGGRRREDPEMSLRTVAL </p>
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 24B.

Table 24B. Comparison of NOV24a against NOV24b through NOV24c.		
Protein Sequence	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV24b	454..748	283/295 (95%)
	1..293	285/295 (95%)
NOV24c	27..1419	1211/1426 (84%)
	23..1423	1261/1426 (87%)

- Further analysis of the NOV24a protein yielded the following properties shown in
- 5 Table 24C.

Table 24C. Protein Sequence Properties NOV24a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1080 probability located in nucleus
SignalP analysis:	Likely cleavage site between residues 24 and 25

A search of the NOV24a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 24D.

Table 24D. Geneseq Results for NOV24a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW30751	Rat phospholipase-B/lipase - Rattus rattus, 1450 aa. [JP09248190-A, 22-SEP-1997]	50..1403 60..1447	911/1404 (64%) 1077/1404 (75%)	0.0
ABB11053	Human phospholipase B	985..1203 45..267	205/224 (91%) 213/224 (94%)	e-117

Protein Accession Number	Protein/Organism/Length	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q05017	Phospholipase ADRAB-B precursor (EC 3.1.-.-) - <i>Oryctolagus cuniculus</i> (Rabbit), 1458 aa.	6..1416 2..1456	1042/1466 (71%) 1179/1466 (80%)	0.0
O70320	PHOSPHOLIPASE B - <i>Cavia porcellus</i> (Guinea pig), 1463 aa.	7..1414 3..1458	965/1474 (65%) 1135/1474 (76%)	0.0
O54728	PHOSPHOLIPASE B - <i>Rattus norvegicus</i> (Rat), 1450 aa.	50..1403 60..1447	911/1404 (64%) 1077/1404 (75%)	0.0
Q96DP9	CDNA FLJ30866 FIS, CLONE FEBRA2004110, HIGHLY SIMILAR TO PHOSPHOLIPASE ADRAB-B PRECURSOR (EC 3.1.-.-) - <i>Homo sapiens</i> (Human), 270 aa.	454..714 1..259	257/261 (98%) 258/261 (98%)	e-151
Q9N2Z4	HYPOTHETICAL 41.4 KDA PROTEIN - <i>Caenorhabditis elegans</i> , 377 aa.	343..673 37..369	130/343 (37%) 202/343 (57%)	1e-59

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Pfam analysis predicts that the NOV24a protein contains the domains shown in the Table 24F.

Table 24F. Domain Analysis of NOV24a			
Pfam Domain	NOV24a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Lipase_GDSL: domain 1 of 3	360..484	54/147 (37%) 116/147 (79%)	4.8e-42
Lipase_GDSL: domain 2 of 3	705..834	57/147 (39%) 116/147 (79%)	4.5e-44
SecA_protein: domain 1 of 1	834..851	10/20 (50%) 17/20 (85%)	4.9
Vitellogenin_N: domain 1 of 1	1107..1124	8/18 (44%) 17/18 (94%)	3.8
Lipase_GDSL: domain 3 of 3	1062..1185	48/147 (33%) 114/147 (78%)	6.3e-37

Example 25.

- 5 The NOV25 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 25A.

Table 25A. NOV25 Sequence Analysis		
	SEQ ID NO: 87	1348 bp
NOV25a, CG59311-01 DNA Sequence	CTGGGTCGCCCCGTGTTCTACCCAGATGGGATGGCAGCGACGCTGATCCTGGAGCCCG CGGGCCGCTGCTGCTGGGACGAGCCGCTGCGCATCGCAGTGCAGCGGCTGGCCCCGGA GCAGCCAGTCACGCTGCGCACGTCCCTGCGCGACGAAGAGGGCCGCTCTTCCGGGCC CACGCGCGTACCGTGCAGCGCCCGCGACGAGCTGGACCTGGAGCGCGCGCCCGCGC TGGGAGGCAGCTTCGCGGGGCTCCAGCCCATGGGGCTGCTGTGGGCGTTGGAGCCCGA GAAAGCCTTGGTGCAGGCTGGTGAAGCGCGACGTGCGGACGCCCTTCGCGGTGGAGCTG GAAGTGCTGGACGCCACGACACCGAGCCCGGGCGGCTGCTGTGCCTGGCGCAGAACA AGCGCGACTTTCTCCGGCCGGGGGTGCGCGCGAGCCGGTGCGCGCGGGCCCGGTGCG CGCCGCGCTCTTCTGCGCGCGGATAGGGGGCCCTTCTGGGATCATTGATCTGTTT GGGAGCAGCAGGGCCCTTTGTGAATACAGGGCCAGCCTCCTGGCGGACATGTTTTG CTGTGCTTGCCCTGGCTTATTTAGATTTGAAGACCTCCCCGAAGATCTGAATGATGT ACATCTGGAGTACTTTGAAGAAGCCGTGGACTTTATGCTGCAGCATCCAAAGGTGAAA GGTCTAGTATTGCGCTTCTTGGATTTCCAAAGGAGGTGACCTGTGTCTCTCAATGG CTTCTTTCTGAAGGGCATCACAGCCACTGTACTTATCAATGCCTGTGTAGCCAACAC AGTAGCTCCTCTACATTACAAGGATATGATTATTCCTAACTTGTGATGATCTAGGA AAAGTAAATCACTAAGTCAGGATTTCTCACTTTATGGACACTTGGAGCAATCCAC TGGAGGAACACAATCACCAAAGTCTTGTTCCATTGGAAGGCGCAGGTGCCCTTCTT GTTATTGTGGCATGGATGATCAAAGCTGGAAGAGTGAATTCTATGCTCAGATAGCC TCTGAAAGGCTACAAGCTCATGGGAAAGAAAGACCCAGATAATCTGTTACCCAGAAA CTGGTCACTGTATTGACCCACCTTATTTCTCCTTCTAGAGCTTCTGTGCAGCGCTGT TTTGGGTGAGGCAATATTCTATGGAGGTGAGCCAAAGGCTCACTCAAAGGCACAGGTA GATGCCTGGCAGCAAATCAAACCTTCTTCATAAACATCTCAATGGTAAAAAATCTG TCAAGCAGCAAAATATAACATTGTAGCCACAGACCAGATACCATTAATAAAAAATCC TATTCATACAACCTT	
	ORF Start: ATG at 31	ORF Stop: TAA at 1294

	SEQ ID NO: 88	421 aa	MW at 46815.4kD
NOV25a, CG59311-01 Protein Sequence	MAATLILEPAGRCWDEPLRIAVRGLAPEQPVTLRSLRDEEGALFRAHARYRADARD ELDLERAPALGGSFAGLQPMGLLWALEPEKALVRLVKRDVRTPFAVELEVLDGHDTEP GRLLCLAQNKRDFLRPGVRREPVRAGPVRAALFLPPDRGPFPGIIDLFGSSRGLCEYR ASLLAGHGFVALLAYFRFEDLPEDLNDVHLEYFEEAVDFMLQHPKVKGPSIALLGFS KGGDLCLSMASFLKGITATVLINACVANTVAPLHYKDMIIPKLVDLGLKVKITKSGFL TFMDTWSNPLEEHNHQSIVPLEKAQVPFLFIVGMDQSWKSEFYAQIASERLQAHGKE RPQIIICYPETGHCIDPPYFPPSRASVHAVLGEAIFYGGEPAKSKAQVDAWQQIQTF HKHLNGKKS VKHSKI		
	SEQ ID NO: 89	1021 bp	
NOV25b, CG59311-02 DNA Sequence	AGATTGGGATGGCAGCGACGCTGATCCTGGAGCCCGCGGCCGCTGCTGCTGGGACGA GCCGCTGCGCATCGCAGTGCGCGGCCCTGGCCCGGAGCAGCAGTCACGCTGCGCACG TCCCTGCGCGACGAAGAGGGCGCGCTCTTCCGGGCCACGCGCGCTACCGTGCCGACG CCTCTAATCCCGGCACCTTGGGGGGCCAAAGCAGGGGGCCCTTCTGGGATCATTGA TCTGTTTGGGAGCAGCAGGGGCCCTTGTGAATACAGGGCCAGCCTCCTGGCCGGACAT GGTTTTGCTGTGCTTGCCCTGGCTTATTTTCAAGATTGGAAGACCTCCCGAAGATCTGA ATGATGTACATCTGGAGTACTTTGAAGAAGCCGTGGACTTTATGCTGCAGCATCCAAA GGTGAAAGGTCCTAGTATTGCGCTTCTTGGATTTTCCAAAGGAGGTGACCTGTGTCTC TCAATGGCTTCTTCTTGAAGGGCATCACAGCCACTGTACTTATCAATGCTGTGTAG CCAAACACAGTAGCTCCTCTACATTACAAGGATATGATTATTCCTAAACTGTGCGATGA TCTAGGAAAAGTAAAAATCACTAAGTCAGGATTTCTCACTTTTATGGACACTTGGAGC AATCCACTGGAGGAACACAATCACCAGAGTCTTGTTCATTGGAAAAGGCGCAGGTGC CCTTCTTGTATTATGTTGGCATGGATGATCAAAGCTGGAAGAGTGAATTCTATGCTCA GATAGCCTCTGAAAGGCTACAAGCTCATGGGAAAGAAAGACCCAGATAATCTGTTAC CCAGAACTGGTCACTGTATTGACCCACCTTATTTTCTCTCTAGAGCTTCTGTGC ACGCTGTTTGGGTGAGGCAATATTCTATGGAGGTGAGCCAAAGGCTCACTCAAAGGC ACAGGTAGATGCCTGGCAGCAAATTCAACTTTCTCCATAAACATCTCAATGGTAAA AAATCTGTCAAGCACAGCAAATATAACATTGTAG		
	ORF Start: ATG at 9	ORF Stop: TAA at 1011	
	SEQ ID NO: 90	334 aa	MW at 36926.0kD
NOV25b, CG59311-02 Protein Sequence	MAATLILEPAGRCWDEPLRIAVRGLAPEQPVTLRSLRDEEGALFRAHARYRADASN PGLGGQGRGPFPGIIDLFGSSRGLCEYRASLLAGHGFVALLAYFRFEDLPEDLNDV HLEYFEEAVDFMLQHPKVKGPSIALLGFSKGGDLCLSMASFLKGITATVLINACVANT VAPLHYKDMIIPKLVDLGLKVKITKSGFLTTFMDTWSNPLEEHNHQSIVPLEKAQVPFL FIVGMDQSWKSEFYAQIASERLQAHGKERPQIIICYPETGHCIDPPYFPPSRASVHAV LGEAIFYGGEPAKSKAQVDAWQQIQTFHKLNGKKS VKHSKI		
	SEQ ID NO: 91	1021 bp	
NOV25c, CG59311-03 DNA Sequence	AGATTGGGATGGCAGCGACGCTGATCCTGGAGCCCGCGGCCGCTGCTGCTGGGACGA GCCGCTGCGCATCGCAGTGCGCGGCCCTGGCCCGGAGCAGCAGTCACGCTGCGCACG TCCCTGCGCGACGAAGAGGGCGCGCTCTTCCGGGCCACGCGCGCTACCGTGCCGACG CCTCTAATCCCGGCACCTTGGGAGGCCAAGCAGGGGGCCCTTCTGGGATCATTGA TCTGTTTGGGAGCAGCAGGGGCCCTTGTGAATACAGGGCCAGCCTCCTGGCCGGACAT GGTTTTGCTGTGCTTGCCCTGGCTTATTTTCAAGATTGGAAGACCTCCCGAAGATCTGA ATGATGTACATCTGGAGTACTTTGAAGAAGCCGTGGACTTTATGCTGCAGCATCCAAA GGTGAAAGGTCCTAGTATTGCGCTTCTTGGATTTTCCAAAGGAGGTGACCTGTGTCTC TCAATGGCTTCTTCTTGAAGGGCATCACAGCCACTGTACTTATCAATGCCCTGTGTAG CCAAACACAGTAGCTCCTCTACATTACAAGGATATGATTATTCCTAAACTGTGCGATGA TCTAGGAAAAGTAAAAATCACTAAGTCAGGATTTCTCACTTTTATGGACACTTGGAGC AATCCACTGGAGGAACACAATCACCAGAGTCTTGTTCATTGGAAAAGGCGCAGGTGC CCTTCTTGTATTATGTTGGCATGGATGATCAAAGCTGGAAGAGTGAATTCTATGCTCA GATAGCCTCTGAAAGGCTACAAGCTCATGGGAAAGAAAGACCCAGATAATCTGTTAC CCAGAACTGGTCACTGTATTGACCCACCTTATTTTCTCTCTAGAGCTTCTGTGC ACGCTGTTTGGGTGAGGCAATATTCTATGGAGGTGAGCCAAAGGCTCACTCAAAGGC ACAGGTAGATGCCTGGCAGCAAATTCAACTTTCTCCATAAACATCTCAATGGTAAA AAATCTGTCAAGCACAGCAAATATAACATTGTAG		
	ORF Start: ATG at 9	ORF Stop: TAA at 1011	
	SEQ ID NO: 92	334 aa	MW at 36926.0kD
NOV25c, CG59311-03 Protein Sequence	MAATLILEPAGRCWDEPLRIAVRGLAPEQPVTLRSLRDEEGALFRAHARYRADASN PGLGGQGRGPFPGIIDLFGSSRGLCEYRASLLAGHGFVALLAYFRFEDLPEDLNDV HLEYFEEAVDFMLQHPKVKGPSIALLGFSKGGDLCLSMASFLKGITATVLINACVANT VAPLHYKDMIIPKLVDLGLKVKITKSGFLTTFMDTWSNPLEEHNHQSIVPLEKAQVPFL FIVGMDQSWKSEFYAQIASERLQAHGKERPQIIICYPETGHCIDPPYFPPSRASVHAV LGEAIFYGGEPAKSKAQVDAWQQIQTFHKLNGKKS VKHSKI		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 25B.

Table 25B. Comparison of NOV25a against NOV25b through NOV25c.		
Protein Sequence	NOV25a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV25b	154..421 67..334	268/268 (100%) 268/268 (100%)
NOV25c	154..421 67..334	268/268 (100%) 268/268 (100%)

Further analysis of the NOV25a protein yielded the following properties shown in Table 25C.

Table 25C. Protein Sequence Properties NOV25a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3630 probability located in microbody (peroxisome); 0.1958 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV25a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 25D.

Table 25D. Geneseq Results for NOV25a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV25a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41490	Human polypeptide SEQ ID NO 6421 - Homo sapiens, 494 aa. [WO200153312-A1, 26-JUL-2001]	1..421 74..494	288/421 (68%) 347/421 (82%)	e-175
AAM39704	Human polypeptide SEQ ID NO 2849 - Homo sapiens, 483 aa. [WO200153312-A1, 26-JUL-2001]	1..421 63..483	288/421 (68%) 346/421 (81%)	e-175

	(Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) - Mus musculus (Mouse), 419 aa.			
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Pfam analysis predicts that the NOV25a protein contains the domains shown in the Table 25F.

Table 25F. Domain Analysis of NOV25a			
Pfam Domain	NOV25a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 26.

- 5 The NOV26 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 26A.

Table 26A. NOV26 Sequence Analysis			
	SEQ ID NO: 93	1375 bp	
NOV26a, CG59309-01 DNA Sequence	GGGACGCGGACGCGCTCCGGACATTCCGGCGCGCTTGCCACGATCTTGGACGGGTCTC GGGCTCGACCTTTGAATTCCTCCGCTCCGGCTCCAAGATGTGACGAACGCTGATCCTG GAGCCCCAGGCGCTGCTGCTGGAACGAGCCGGTGCGCATTGCGGTGCGCGGCCTGG CCCCGGAGCAGCGGGTTACGCTGCGCGCGCTCCCTGCGCGACGAGAAGGCGCGCTCTT CCGGGCCACGCGCGCTACTGCGCGGACGCCGCGGCGAGCTGGACCTGGAGCGCGCA CCCGCGCTGGGCGGCAGCTTCGCGGGACTCGAGCCCATGGGGCTGCTCTGGGCGCTGG AACCCGAGAAGCCTTTTGGCGCTTCTGAAGCGGGACGTACAGATTCTCTTTGTGCTG GGAGTTGGAGGTGCTGGACGGCCACGACCCGAGCCTGGACGGTGCTGTGCCAGGCG CAGCATTGAGCGCCACTTCCTCCCGCCAGGGGTGCGGCGCCAGTCCGTGCGAGCGGGCC GGGTGCGCGCCACGCTCTTCTGCCGCCAGGTGAGCCTGGACCTTCCAGGGGATCAT TGACATCTTTGGTATTGGAGGGGGCTCTTGAATATCGAGCCAGCCTCTTGTCTGGC CATGGCTTTGCCACGTTGGCTCTAGCTTATTATAACTTTGAAGATCTCCCCAATAACA TGGACAACATATCCCTGGAGTACTTCGAAGAAGCCGTATGTACATGCTTCAACATCC CCAGGTTAAAGGCCCAGGCATTGGGCTTTTGGGCATTCTCTAGGAGCTGATATTTGT CTCTCAATGGCCTCATTTCTGAAGAATGTCTCAGCCACAGTTTCCATCAATGGATCTG GGATCAGTGGGAACACAGCCATCAACTATAAGCACAGTAGCATTCACCATTTGGGCTA TGACCTGAGGAGAATCAAGGTAGCTTTCTCAGGCCTCGTGGACATTGTGGATATAAGG AATGCTCTCGTAGGAGGTACAAGAACCCAGCATGATTCCAATAGAGAAGGCCCAGG GGCCCATCTGCTCATTTGTTGGTCAGGATGACCATAACTGGAGAAGTGAGTTGTATGC CCAAACAGTCTCTGAACGGTTACAGGCCCATGGAAAGGAAAAACCCAGATCATCTGT TACCCTGGGACTGGGCATTACATCGAGCCTCCTTACTTCCCCTGTGCCAGCTTCCC TTCACAGATTACTGAACAAACATGTTATATGGGGTGGGGAGCCAGGGCTCATTCTAA GGCCAGGAAGATGCCTGGAAGCAAATTCTAGCCTTCTTCTGCAACACCTGGGAGGT ACCCAGAAAACAGCTGTCCCTAAATTGTAATGCATTGTCT		
	ORF Start: ATG at 96	ORF Stop: TAA at 1362	
	SEQ ID NO: 94	422 aa	MW at 46455.1kD
NOV26a, CG59309-01 Protein Sequence	MSATLILEPPGRCCWNEPVRIVRGLAPEQVRVTLRASLRDEKALFRAHARYCADARG ELDLERAPALGGSFAGLEPMGLLWALEPEKPFWRFLKRDVQIPFVVELEVLDGHDPEP GRLLCQAOHERHFLPPGVRRQSVRAGRVRATLFLPPGEPGPPGIIDIFGIGGGLLEY RASLLAGHGFATLALAYNFEDLPNNMDNISLEYFEEAVCYMLQHPQVKGPGLGLGI SLGADICLSMASFLKNVSATVISINGSIGNTAINYKHSSIPLGYDLRRIKVAFSGL VDIVDIRNALVGGYKNPSMPIEKAQGPILLIVGQDDHNWRSELYAQTVSERLQAHGK EKPQIICYPGTGHYIEPPYFPLCPASLHRLLNKHVIVGGEPRAHSAQEDAWKQILAF FCKHLGGTQKTAVPKL		

Further analysis of the NOV26a protein yielded the following properties shown in Table 26B.

Table 26B. Protein Sequence Properties NOV26a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.2585 probability located in lysosome (lumen); 0.1940 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

5 A search of the NOV26a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 26C.

Table 26C. Geneseq Results for NOV26a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41490	Human polypeptide SEQ ID NO 6421 - Homo sapiens, 494 aa. [WO200153312-A1, 26-JUL-2001]	1..422 74..494	296/422 (70%) 341/422 (80%)	e-179
AAM39704	Human polypeptide SEQ ID NO 2849 - Homo sapiens, 483 aa. [WO200153312-A1, 26-JUL-2001]	1..422 63..483	296/422 (70%) 341/422 (80%)	e-179
AAY71112	Human Hydrolase protein-10 (HYDRL-10) - Homo sapiens, 483 aa. [WO200028045-A2, 18-MAY-2000]	1..422 63..483	296/422 (70%) 341/422 (80%)	e-179
AAB93479	Human protein sequence SEQ ID NO:12766 - Homo sapiens, 483 aa. [EP1074617-A2, 07-FEB-2001]	1..422 63..483	295/422 (69%) 340/422 (79%)	e-178
AAY07932	Human secreted protein fragment encoded from gene 81 - Homo sapiens, 182 aa. [WO9918208-A1, 15-APR-1999]	242..422 1..181	93/181 (51%) 123/181 (67%)	2e-48

In a BLAST search of public sequence databases, the NOV26a protein was found to have homology to the proteins shown in the BLASTP data in Table 26D.

Table 26D. Public BLASTP Results for NOV26a				
Protein Accession Number	Protein/Organism/Length	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9QYR8	PEROXISOMAL LONG CHAIN ACYL-COA THIOESTERASE IB - Mus musculus (Mouse), 421 aa.	1..422 1..421	312/422 (73%) 362/422 (84%)	0.0
P49753	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (EC 3.1.2.2) (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128) - Homo sapiens (Human), 421 aa.	1..422 1..421	296/422 (70%) 341/422 (80%)	e-178
Q9QYR7	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (EC 3.1.2.2) (Peroxisomal long-chain acyl-coA thioesterase 2) (PTE-Ia) - Mus musculus (Mouse), 432 aa.	1..422 12..432	281/424 (66%) 333/424 (78%)	e-163
O55137	Cytosolic acyl coenzyme A thioester hydrolase, inducible (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) - Mus musculus (Mouse), 419 aa.	1..422 1..419	275/423 (65%) 330/423 (78%)	e-162
O88267	Cytosolic acyl coenzyme A thioester hydrolase, inducible (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) (LACH2) (ACH2) - Rattus norvegicus (Rat), 419 aa.	1..422 1..419	276/423 (65%) 329/423 (77%)	e-162

PFam analysis predicts that the NOV26a protein contains the domains shown in the Table 26E.

Table 26E. Domain Analysis of NOV26a			
Pfam Domain	NOV26a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DLH: domain 1 of 2	144..188	17/52 (33%) 32/52 (62%)	63
DLH: domain 2 of 2	394..411	9/18 (50%) 13/18 (72%)	2.6

Example 27.

The NOV27 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 27A.

Table 27A. NOV27 Sequence Analysis			
	SEQ ID NO: 95	1333 bp	
NOV27a, CG57364-01 DNA Sequence	CCTGGCCCCCAAGCTCCCCACTCTGGTGCCCCGAGCAGCCCTGTGGGCAAGCAGCCGC CGCCATGGCCGAGCACCTGGAGCTGCTGGCAGAGATGCCCATGGTGGGCAGGATGAGC ACACAGGAGCGGCTGAAGCATGCCAGAAGCGGCGCGCCAGCAGGTGAAGATGTGGG CCCAGGCTGAGAAGGAGGCCAGGGCAAGAAGGGTCTTGGGGAGCGTCCCCGGAAGGA GGCAGCCAGCCAAGGGCTCCTGAAGCAGGTCTCTTCCCTCCCAGTGTTGTCTCTCTG GAGGCGGCTGCCCCGAAATGACCTGGAAGAAGTCCGCCAGTTCTTGGGAGTGGGGTCA GCCCTGACTTGGCCAACGAGGACGGCCTGACGGCCCTGCACCAAGTGTGCTGATTGATGA TTTCCGAGAGATGGTGCAGCAGCTCCTGGAGGCTGGGGCCAACATCAATGCCCTGTGAC AGTGAGTGTGGACGCCTCTGCATGCTGCGGCCACCTGCGGCCACCTGCACCTGGTGG AGCTGCTCATCGCCAGTGGCGCCAATCTCCTGGCGGTCAACACCGACGGGAACATGCC CTATGACCTGTGTGATGATGAGCAGACGCTGGACTGCCTGGAGACTGCCATGGCCGAC CGTGGCATACCCAGGACAGCATCGAGGCGCGCCGGGCGGTGCCAGAACTGCGCATGC TGGACGACATCCGAGCGCGGTGCAGGCCGGGGCAGACCTCCATGCCCCCTGGACCA CGGGGCCACGCTGCTGCAGCTGCAGCGCCCAACGGGTTACGCGAGGCGGGCTGCCCTG CTGCTGGAACACCGAGCCAGCCTGAGCGCTAAGGACCAAGACGGCTGGGAGCCGCTGC ACGCCGCGGCTACTGGGGCCAGGTGCCCTGGTGGAGCTGCTCGTGGCGCACGGGGC CGACCTGAACGCAAAGTCCCTGATGGACGAGACGCCCTTGATGTGTGCGGGGACGAGC GAGGTGCGGGCCAAGCTGCTGGAGCTGAAGCACAAGCACGACGCCCTCTGCGCGCCC AGAGCCGCCAGCGCTCCTTGTGCGCCGCGCACCTCCAGCGCCGGCAGCCGCGGGAA GGTGGTGAGGCGGGATGAGCCTAACCCAGCGCAGCGGCTGACGCATGTCCCAAGCGG GCGCGCCAGCAGGTGAAGATGTGGGCCAGGCTGAGAAGGAGGCCAGGGCAAGAAG GGTCTCTGGGGAGCGTCCCGGAAGGAGGCAGCCAGCCAAGGGCTCCTGAAGCAGGTCC TCTTCCCTCCCAGTGTTGTCTCTTGGAGGCGCTGCCCGAAATGACCTGGAAGAAG		
	ORF Start: ATG at 63	ORF Stop: TGA at 1194	
	SEQ ID NO: 96	377 aa	MW at 41019.9kD
NOV27a, CG57364-01 Protein Sequence	MAEHELLEAEMPVMGRMSTQERLKHAKRRRAQQVKMWAQAEKEAQKKGPGERPRKEA ASQGLLKQVLFPPSVVLLLEAAARNDLLEVRQFLGSGVSPDLANEDGLTALHQCCIDDF REMVQQLLEAGANINACDSECWTPHAAATCGHLHLVELLIASGANLLAVNTDGNMPY DLCDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSLQAGADLHAPLDHG ATLLHVAAANGFSEAAALLLEHRASLSAKDQDGEPLHAAAYWGQVPLVELLVAHGAD LNAKSLMDETPLDVCGDEEVRAKLELKHKHDALLRAQSRQSLRRRTSSAGSRGKV VRRDEPNPAQRLTHVPEARPAGEDVGPG		

Further analysis of the NOV27a protein yielded the following properties shown in Table 27B.

Table 27B. Protein Sequence Properties NOV27a	
PSort analysis:	0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1547 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV27a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 27C.

In a BLAST search of public sequence databases, the NOV27a protein was found to have homology to the proteins shown in the BLASTP data in Table 27D.

Protein Accession Number	Protein/Organism/Length	NOV27a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96I34	UNKNOWN (PROTEIN FOR MGC:14333) - Homo sapiens (Human), 528 aa.	1..351 1..351	351/351 (100%) 351/351 (100%)	0.0
Q923M0	MYOSIN PHOSPHATASE TARGETING SUBUNIT 3 MYPT3 - Mus musculus (Mouse), 524 aa (fragment).	1..351 1..351	301/351 (85%) 320/351 (90%)	e-171

AAL62093	PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 16B - Mus musculus (Mouse), 568 aa.	1..351 1..348	210/351 (59%) 266/351 (74%)	e-118
Q95N27	CAAX BOX PROTEIN TIMAP - Bos taurus (Bovine), 568 aa.	1..351 1..348	210/351 (59%) 266/351 (74%)	e-118
Q96T49	CAAX BOX PROTEIN TIMAP - Homo sapiens (Human), 567 aa.	1..351 1..348	209/351 (59%) 265/351 (74%)	e-117

PFam analysis predicts that the NOV27a protein contains the domains shown in the Table 27E.

Table 27E. Domain Analysis of NOV27a			
Pfam Domain	NOV27a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ank: domain 1 of 5	70..102	8/33 (24%) 20/33 (61%)	99
ank: domain 2 of 5	103..135	16/33 (48%) 26/33 (79%)	7.1e-08
ank: domain 3 of 5	136..168	15/33 (45%) 26/33 (79%)	2.9e-07
ank: domain 4 of 5	231..263	16/33 (48%) 24/33 (73%)	2e-06
ank: domain 5 of 5	264..296	16/33 (48%) 27/33 (82%)	2.7e-08

Example 28.

The NOV28 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 28A.

Table 28A. NOV28 Sequence Analysis		
	SEQ ID NO: 97	1719 bp
NOV28a, CG59348-01 DNA Sequence	CGGGCACAGGCTCACCCTCGAGTGGCACAGGAATCCCAGGTAGATGACGGCGGCCGCG GCTGGTGCTGCAGGGTCGGCAGCTCCCGGGCAGCGGCCGGCGCCCGGGATCTGGGG GCGCACCTCAGGGTCGACGGGGTGCTGATCGGGACAGGCTGTACTCCGGGGTGCT CATCACTTGGAGAACTGCCTCCTGCCTGACGACAAGCTCCGTTTCACGCCGTCCATG TCGAGCGGCCTCGACACCGACACAGAGACCGACCTCCGCGTGGTGGGCTGCGAGCTCA TCCAGGCGGCCGTATCCTGCTCCGCTGCCGAGGTGGCCATGGCTACCGGGCAGGT GTGTTCCAGCGGTTCTTTTATACCAAGTCCTTCGTGAAGCACTCCATGGAGCATGTG TCAATGGCCTGTGTCCACCTGGCTTCCAAGATAGAAGAGGCCCAAGACGCATACGGG ACGTCATCAATGTGTTTCACCGCCTTCGACAGCTGAGAGACAAAAGAAGCCGTGCC TCTACTACTGGATCAAGATTATGTTAATTAAAGAACCAAAATTATAAAGGCGGAAAGA CGAGTTCTCAAGAGTTGGGTTTCTGCGTCCATGTGAAGCATCCTCATAAGATAATCG TTATGTACCTTCAGGTGTTAGAGTGTGAGCGTAACCAACACCTGGTCCAGACCTCATG GAATTACATGAACGACAGCCTTCGACCGACGCTTTCGTGCGGTTCCAGCCAGAGAGC ATCGCCTGTGCCTGCAATTTATCTTGCTGCCCGGACGCTGGAGATCCCTTTGCCCAATC GTCCCATTTGGTTCTTTTGGAGCAACTGAAGAAGAAATTCAGGAAATCTGCTT	

	AAAGATCTGCAGCTTTATGCTCGGAAAAAGGTTGATCTCACACACCTGGAGGGTGAA GTGGAAAAAGAACGCTATCGAAGAGGCAAAGGCCAAGCCGGGGCCTGTTGC CTGGGGGCACACAGGTGCTGGATGGTACCTCGGGGTTCTCTCTGCCCCCAAGCTGGT GGAATCCCCCAAGAGAGTTAAAGGGAGCAAGCCTTCCCCACTGTCTGTGAAGAACACC AAGAGGAGGCTGGAGGGCGCCAAGAAAGCCAAGGCGGACAGCCCGTGAACGGCTTGC CAAAGGGGCGAGAGAGTCGGAGTCGGAGCCGGAGCCGTGAGCAGAGCTACTCGAGGTC CCCATCCCGATCAGCGTCTCCTAAGAGGAGGAAAAGTGACAGCGGCTCCACATCTGGT GGGTCCAAGTCGAGAGCCGCTCCCGAGCAGGAGTGACTCCCCACCGAGACAGGCC CCCGCAGCGCTCCCTACAAAGGCTCTGAGATTCCGGGGCTCCCGGAAGTCCAAGGACTG CAAGTACCCCGAAGCCACACAAGTCTCGAGCCGGAGTTCTTCCCGTTCTCGAAGC AGGTCACGGGAGCGGGCGGATAATCCGGGAAAATACAAGAAGAAAAGTCATTACTACA GAGATCAGCGACGAGAGCGCTCGAGGTCGTATGAACGCACAGGCCGTGCTATGAGCG GGACCACCTGGGCACAGCAGGCATCGGAGGTGACACGTGCTTCAGACCGGCTGCGGG TGGCGGCACACCTGGGCCGTCAGGGCTCAGCTCGGCAGCAGCTCTGAGGCGAGCT CAATGAAAAAGTGAATGCACACGCCCTTGTGGCGTG		
	ORF Start: ATG at 44	ORF Stop: TGA at 1598	
	SEQ ID NO: 98	518 aa	MW at 58034.5kD
NOV28a, CG59348-01 Protein Sequence	MTAAAAGAAGSAAPAAAAGAPSGGAPSGSGVLIQDRLYSGVLITLLENCLLPDDKLR FTPSMSSGLDITDTEDLRVVGCLELIQAAGILLRLPQVAMATQVLFQRFYTKSFVKH SMEHVSMACVHLASKIEEAPRRIRDVINVFHLRLQRLDKKPVPLLLDQDYVNLKNQI IKAERRVLKELGFCVHVHKPHKIIVMYLQVLECCERNQHLVQTSWNMNDLSLRTDVFVR FQPESIACACIYLAARTLEIPLPNRPHWFLFLFGATEEEIQEICLKILQLYARKKVDLT HLEGEVEKRKHAIIEAKAQARGLLPGGTQVLDGTSGFSPAPKLVESPKEGKGSKPSPL SVKNTKRRLEGAKKAKADSPVNGLPKGRESRSRSRSREQSYRSRSPRSASPKRKSDS GSTSGGSKSQRSRSDSPPRQAPRSAPYKGEIRGSRKSKDCKYPQKPHKSRSSRS SRSRSRSRERADNPGYKKKSHYYRQRRERSRSYERTGRRYERDHPGHSRHR		

Further analysis of the NOV28a protein yielded the following properties shown in Table 28B.

Table 28B. Protein Sequence Properties NOV28a	
Psort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.2400 probability located in nucleus; 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV28a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 28C.

Table 28C. Geneseq Results for NOV28a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM94028	Human stomach cancer expressed polypeptide SEQ ID NO 126 - Homo sapiens, 298 aa. [WO200109317-A1, 08-FEB-2001]	221..518 1..298	298/298 (100%) 298/298 (100%)	e-172

AAG64403	Human paneth cell enhanced expression-like protein - Homo sapiens, 298 aa. [WO200138372-A1, 31-MAY-2001]	221..518 1..298	298/298 (100%) 298/298 (100%)	e-172
AAB94641	Human protein sequence SEQ ID NO:15526 - Homo sapiens, 298 aa. [EP1074617-A2, 07-FEB-2001]	221..518 1..298	298/298 (100%) 298/298 (100%)	e-172
AAM78533	Human protein SEQ ID NO 1195 - Homo sapiens, 526 aa. [WO200157190-A2, 09-AUG-2001]	2..518 8..526	316/526 (60%) 390/526 (74%)	e-168
AAB94371	Human protein sequence SEQ ID NO:14909 - Homo sapiens, 526 aa. [EP1074617-A2, 07-FEB-2001]	2..518 8..526	316/526 (60%) 390/526 (74%)	e-168

In a BLAST search of public sequence databases, the NOV28a protein was found to have homology to the proteins shown in the BLASTP data in Table 28D.

Table 28D. Public BLASTP Results for NOV28a				
Protein Accession Number	Protein/Organism/Length	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96S94	HYPOTHETICAL 58.1 KDA PROTEIN - Homo sapiens (Human), 520 aa.	3..518 5..520	516/516 (100%) 516/516 (100%)	0.0
Q9JJA7	BRAIN CDNA, CLONE MNCB-5160, SIMILAR TO MUS MUSCULUS PANETH CELL ENHANCED EXPRESSION PCEE MRNA - Mus musculus (Mouse), 518 aa.	1..518 1..518	466/519 (89%) 482/519 (92%)	0.0
Q9UK58	CYCLIN L ANIA-6A - Homo sapiens (Human), 526 aa.	2..518 8..526	316/526 (60%) 390/526 (74%)	e-167
Q9R1Q2	CYCLIN ANIA-6A - Rattus norvegicus (Rat), 527 aa.	2..518 9..527	312/526 (59%) 391/526 (74%)	e-165
Q9WV44	CYCLIN ANIA-6A - Mus musculus (Mouse), 531 aa.	3..518 15..531	314/526 (59%) 385/526 (72%)	e-162

PFam analysis predicts that the NOV28a protein contains the domains shown in the Table 28E.

Table 28E. Domain Analysis of NOV28a

Pfam Domain	NOV28a Match Region	Identities/ Similarities for the Matched Region	Expect Value
cyclin: domain 1 of 1	46..190	28/163 (17%) 86/163 (53%)	0.0022
Srg: domain 1 of 1	221..230	4/10 (40%) 10/10 (100%)	6.7
transcript_fac2: domain 1 of 1	235..253	12/19 (63%) 15/19 (79%)	0.86
cyclin_C: domain 1 of 1	196..311	22/139 (16%) 65/139 (47%)	2.6

Example 29.

The NOV29 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 29A.

Table 29A. NOV29 Sequence Analysis

Table 29A. NOV29 Sequence Analysis			
	SEQ ID NO: 99	1069 bp	
NOV29a, CG59245-01 DNA Sequence	CGGGGCCCTGGTCGGCAGCTGGGCCGCCATGGAGTCCACGCTGGGCGCGGGCATCGTGA TAGCCGAGGCGCTACAGAACCAGCTAGCCTGGCTGGAGAACGTGTGGCTCTGGATCAC CTTTCTGGGCGATCCCAAGATCCTTTCTGTTCTACTTCCCGCGGCCTACTACGCC TCCGCGCGTGTGGGCATCGCGGTGCTCTGGATCAGCCCTCATACCGAGTGGCTCAACC TCATCTTCAAGTGGTTTCTTTTGGAGACAGGCCCTTTTGGTGGGTCCATGAGTCTGG TTACTACAGCCAGGCTCCAGCCCAGGTTACCAGTTCCTCCTTCTTGTGAGACTGGT CCAGGTGGCAGCCCTTCTGGACACTGCATGATCACAGGAGCAGCCCTCTGGCCCATAA TGACGGCCCTGTCTTCGCAGGTGCGCTGGGTAAGGGTGATGCCTAGCCTGGCTTATTG CACCTTCCTTTGGCGGTTGGCTTGTGCGGAATCTTCATCTTAGCACATTTCCCTCAC CAGGTGCTGGCTGGCCATAAATACTGGTTGGCTGATGACTCCCCGAGTGCCTATGGAGC GGGAGCTAAGCTTCTATGGGTTGACTGCACTGGCCCTCATGCTAGGCACCAGCCTCAT CTATTGGACCCTCTTACACTGGGCGTGGATCTTCTTGGTCCATCAGCCTAGCCTTC AAGTGGTGTGAGCGGCTGAGTGGATACACGTGGATAGCCGGCCCTTGGCTCCCTGA CGCGTGACTCAGGGGCTGCCTGGGCGTGGGCATTGCCTTGCACTCTCCCTGCTATGC CCAGGTCGCTCGGGCAGACGCTGGGAAATGCCAGAAAGATAGCCTGCCCTTGTCTGGCC ATGGGGCTGCTGGGCCCCCTGGACTGGCTGGGGCACCCCCCTCAGATCAGCCTCTTCT ACATTTTCAATTTCCCTCAAGTACACCTCTGGCCATGCCTAGTCTTGCCCTCGTGCC CTGGGATGTCACATGTTCACTGCCAGGAAGCACGCCCATCCACTCTTCTGCTGACTT CTTGTGTGCTCCCTTTCCCTTCCC		
	ORF Start: ATG at 28	ORF Stop: TGA at 1039	
	SEQ ID NO: 100	337 aa	MW at 37808.0kD
NOV29a, CG59245-01 Protein Sequence	MESTLGAGIVIAEALQNQLAWLENVWLWITFLGDPKILFLFYFPAAYYASRRVGI AVL WISLITEWLNLI FKWFLFGDRPFVWVHESGYYSQAPAQVHQFPSSCETPGGSPSGHC MITGAALWPI M TALSSQVRWVRVMPSLAYCTFLLAVGLSRIFILAHFPHQVLAGLITG WLMTPRVPMERELSFYGLTALALMLGTSLSIYWLFTLGLDLSWSISLAFKWCERPEWI HVDSRPFASLSRDSGAALGLGIALHSPCYAQVRRQAQLGNQKIAICLVAMGLLGLPLDW LGHPPQISLFYIFNFLKYTLWPCLVLALVPWAVHMFSAQEAPEPIHSS		
	SEQ ID NO: 101	1386 bp	
NOV29b, CG59245-02 DNA Sequence	TGAGTCTGTACTTCCGCCCTGGAGCAAGCCGGGGCGCTGGTCGGCAGCTGGGCCGCCA TGGAGTCCACGCTGGGCGCGGGCATCGTGATAGCCGAGGCGCTACAGAACCAGCTAGC CTGGCTGGAGAACGTGTGGCTCTGGATCACCTTCTTGGGCGATCCCAAGATCCTCTTT CTGTTCTACTTCCCGCGGCTACTACGCCTCCGCGGTGTGGGCTCGCGGTGCTCT GGATCAGCCTCATCACCAGTGGCTCAACCTCATCTTCAAGTGGTTTCTTTTGGAGA CAGGCCCTTTTGGTGGGTCCATGAGTCTGGTTACTACAGCCAGGCTCCAGCCAGGTT CACCACTTCCCCTCTTCTTGTGAGACTGGTCCAGGCAGCCCTTCTGAGCATGCATGA		

	<p>TCACAGGAGCAGCCCTCTGGCCCATATGACGGCCCTGTCTTCGAGGTGGCCACTCG GGCCCGCAGCCGCTGGGTAAGGGTGATGCCTAGCCTGGCTTATTGCACCTTCCTTTTG GCGGTTGGCTTGTGCGGAATCTTCATCTTAGCACATTTCCCTCACCAGGTGCTGGCTG GCCTAATAACTGGCGCTGTCTGGGCTGGCTGATGACTCCCGAGTGCTATGGAGCG GGAGCTAAGCTTCTATGGGTTGACTGCACTGGCCCTCATGCTAGGCACCAGCCTCATC TATTGGACCCTCTTACACTGGGCCTGGATCTTTCTTGGTCCATCAGCCTAGCCTTCA AGTGGTGTGAGCGGCCTGAGTGGATACAGTGGATAGCCGGCCCTTTGCCTCCCTGAG CCGTGACTCAGGGGCTGCCCTGGGCCTGGGCATTGCCTTGCACTCTCCCTGCTATGCC CAGGTGCGTCGGGCACAGCTGGGAAATGGCCAGAAGATAGCCTGCCTTGTGCTGGCCA TGGGGCTGCTGGGCCCTGGACTGGCTGGGCCACCCCTCAGATCAGCCTCTTCTA CATTTCAATTTCTCAAGTACACCCTCTGGCCATGCCAGTCCCTGGCCCTCGTGCC TGGGCAGTGCACATGTTCAAGTGCAGGAAGCACGCCCATCCACTCTTCCTGACTTC TTGTGTGCTCCCTTTCTTTCCCTCCCAAGCCAACTCTGTGACCACCACACT CCAGGAGGCAGCCCATCCCTTCCAGCCCTAAGTAGGCCCTCCCTCCCTAAATCT GCTTCGACACCTGGTCTTAGCCCCAAGATGGGCCTTCTCTCTCCAGATAAGTT GGTCTCCTCTGCTTCTCTCAAGCCCCAAGAGCAAGGCAACAGCAAGACCA GCGGGTCTTGCAACTGTGAGGGCAGCCAGGCGGAAAGTACAGACTCA</p>		
	ORF Start: ATG at 58 ORF Stop: TGA at 1096		
	SEQ ID NO: 102	346 aa	MW at 38718.0kD
NOV29b, CG59245-02 Protein Sequence	<p>MESTLGAGIVIAEALQNQLAWLENVWLWITFLGDPKILFLFYFPAAYASRRVGI AVL WISLITEWLNLIKFkwFLGDRPFVWVHESGYYSQAPVHQFPSSCETGPGSPSGH CM ITGAALWPIMTALSSQVATRARSRWVRVMPSLAYCTFLAVGLSRIFILAHFPHQVLA GLITGAVLGWLMTPRVPMERELSFYGLTALALMLGTS LIYWTFLGLDLWSISLAF KW CERPEWIHVDSRPFASLSRDSGAALGLGIALHSPCYAQRRAQLGNGOKIACLVL A MGLGLPLDWLGHPPIQLFYIFNFKYTLWPCVLA LVPWAVHMFSAQEAPPIHSS</p>		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 29B.

Table 29B. Comparison of NOV29a against NOV29b.		
Protein Sequence	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV29b	1..337	335/347 (96%)
	1..346	335/347 (96%)

Further analysis of the NOV29a protein yielded the following properties shown in Table 29C.

Table 29C. Protein Sequence Properties NOV29a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 41 and 42

- 5 A search of the NOV29a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 29D.

O42153	Glucose-6-phosphatase (EC 3.1.3.9) (G6Pase) (G-6-Pase) - <i>Haplochromis nubilus</i> , 352 aa.	8..323 8..339	127/333 (38%) 184/333 (55%)	1e-59
Q98UF8	GLUCOSE-6-PHOSPHATASE - <i>Sparus aurata</i> (Gilthead sea bream), 350 aa.	8..323 8..337	123/333 (36%) 185/333 (54%)	2e-57
Q9Z186	GLUCOSE-6-PHOSPHATASE - <i>Mus musculus</i> (Mouse), 355 aa.	7..325 7..345	128/343 (37%) 188/343 (54%)	5e-56

PFam analysis predicts that the NOV29a protein contains the domains shown in the Table 29F.

Table 29F. Domain Analysis of NOV29a			
Pfam Domain	NOV29a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PAP2: domain 1 of 1	51..190	38/175 (22%) 95/175 (54%)	0.00037

Example 30.

- 5 The NOV30 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 30A.

Table 30A. NOV30 Sequence Analysis		
	SEQ ID NO: 103	1624 bp
NOV30a, CG59241-01 DNA Sequence	<p>ATGGAAGTGAAGCCGAGGAGGAGGAGGTGGGTGGCGTCCAGCCGGTGGACTTGGTGG CCTTTGCCAACAGCTGCACCCCTCCATGGCACCACACATTTTGTGGAGGGGGTCC AGGGCCAGGCAGGTGCTGTGGGCGGTGGCCTTTGTCTGGCACTGGGTGCCTTCCTG TGCCAGGTAGGGACCGGTGCTTATTACCTCAGCTACCCACAGTACCCCTCTAA ACGAAGTGGCCACACGGAGCTGGCCTTCCCGGCAGTACCCCTCTGCAACACTAATGC TGTGCGGCTGTCCAGCTCAGCTACCTGACTTGTCTTATTTGGCCCCATGCTGGGA CTGGATGAAAGTGATGACCCCGGGGTGCCCTCGCTCCACCGGCCCTGAGGCCTTCT CTGGGGAGCCCTTTAACTGCACCGCTTCTACAATCGCTCCTGCCACCGGCTGGAGGA CATGCTGCTCTATTGCTCCTACCAAGGGGGACCTGCGGCCCTCACAACTTCTCAGTG GTGTTACACAGCTATGGAAGTGCTACACGTTCAACTCGGGCCGAGATGGGCGGCCGC GGCTGAAGACCATGAAGGGTGGGACGGGCAATGGGCTGGAAATCATGCTGGACATCCA GCAGGACGAGTACCTGCTGTGTGGGGGAGACTGACGAGACGTCCTTCGAAGCAGGC ATCAAAGTGCAGATCCATAGTCAGGATGAACCTCCTTTTCATCGACAGCTGGGCTTTG GCGTGGCCCCAGGCTTCCAGACCTTTGTGGCCTGCCAGGAGCAGCGGATCTACCTGCC CCACCCCTGGGGCACCTGCAAGCTGTTACCATGGACTCGGATTTCTTCGACTCCTAC AGCATCACTGCTGCGCATCGACTGTGAGACGCGCTACTGTGGAGAACTGCAACT GCCGATGGTGCACATGCCAGGTGATGCCCATACTGTACTCCAGAGCAGTACAAGGA GTGTGCAGATCCTGCTCTGGACTTCTGTGGGAGAAAGGACAGGAGTACGCTGTGT GAAATGCCTTGCAACCTGACCCGCTATGGCAAAGAGCTGTCCATGGTCAAGATCCCCA GCAAAGCCTCAGCCAAGTACCTGGCCAAGAAGTTCAACAAATCTGAGCAATACATAGG GGAGAATCCTGGTGTCTGGACATTTCTTTGAAGTCTCAACTATGAGACCATTTGAA CAGAAGAAGGCCTATGAGATTGCAGGGCTCCTGGGTGACATCGGGGCGCAGATGGGGC TGTTTCATCGGGGCGAGCATCCTCAGGGTGTGGAGCTCTTTGACTACGCTACGAGGT AGTCATTAAGCACAAGCTGTGCCGACGAGGAAAATGCCAGAAGGAGGCCAAAGGAGC AGTGCGGACAAGGGCTGGCCCTCAGCCTGGACGACGTCAAAGACACAACCGTGC AGAGCCTTCGGGGCCACCTGCGGGATGACATACGCTGCCAACATCTACCTACCA TCCGGCCCGAGGCACGTTTCGAGGACTTTACCTGCTGAGCCCCGAGGCGCTGAACCA AAGGCCTAGATGGGGAGGACTAGGAGAGCGAGGGGGCCCCAGCTGCCTCCTCACATC</p>	

	ORF Start: ATG at 1	ORF Stop: TGA at 1543	
	SEQ ID NO: 104	514 aa	MW at 57221.7kD
NOV30a, CG59241-01 Protein Sequence	MELKAE EEEVGGVQPVDLVAFANSCTLHGTNHFVEGGPGPRQVLWAVFVLALGAFL CQVGDRVAYYLSYPHTLLNEVATTELAFPAVTLCNTNAVRLSQLSYPDLLYLAPMLG LDESDDPGVPLAPPGPEAFSGEPFNLHRFYNRSCRLEDMLLYCSYQGGPCGPHNFSV VFTRYGKCYTFNSGRDGRPLKTMKGGTGNGLEIMLDIQDEYLPVWGETDETSFEAG IKVQIHSQDEPPFIDQLGFGVAPGFQTFVACQEQR IYLPWPWGCKAVTMDSDFFDSY SITACRIDCETRYLVENCNCRMVHMPGDAPYCTPEQYKECADPALDFLVEKDQEYCVC EMPCNLTRYGKELSMVKIPSKASAKYLAKKFNKSEQYIGENILVLDIFFEVLNYETIE QKKAYE IAGLLDIGQMGLFIGASILTVLELFDYAYEVVIKHKLCRRGKCQKEAKRS SADKGVALLDDVKRHNPCESLRGHPAGMTYAANILPHHPARGTFEDFTC		

Further analysis of the NOV30a protein yielded the following properties shown in Table 30B.

Table 30B. Protein Sequence Properties NOV30a	
PSort analysis:	0.7900 probability located in plasma membrane; 0.3000 probability located in Golgi body; 0.2000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 60 and 61

A search of the NOV30a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 30C.

Table 30C. Geneseq Results for NOV30a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AA Y69178	A rat acid-sensitive cationic channel 1B (rASIC1B) - Rattus sp, 559 aa. [WO200008149-A2, 17-FEB-2000]	1..514 47..559	488/515 (94%) 497/515 (95%)	0.0
AA Y03186	Rat Acid sensitive ion channel protein sequence - Rattus sp, 513 aa. [WO9911784-A1, 11-MAR-1999]	1..514 1..513	488/515 (94%) 498/515 (95%)	0.0
AA W68507	Rat acid sensing ionic channel 1B - Rattus sp, 559 aa. [WO9835034-A1, 13-AUG-1998]	1..514 47..559	488/515 (94%) 497/515 (95%)	0.0
AA Y69175	A rat acid-sensitive cationic	1..514 1..526	416/527 (78%) 445/527 (83%)	0.0

	526 aa. [WO200008149-A2, 17-FEB-2000]			
AAY03188	Rat Acid sensitive ion channel alpha protein sequence - Rattus sp, 526 aa. [WO9911784-A1, 11-MAR-1999]	1..514 1..526	416/527 (78%) 445/527 (83%)	0.0

In a BLAST search of public sequence databases, the NOV30a protein was found to have homology to the proteins shown in the BLASTP data in Table 30D.

Table 30D. Public BLASTP Results for NOV30a				
Protein Accession Number	Protein/Organism/Length	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q91YB8	ION CHANNEL - Rattus norvegicus (Rat), 559 aa.	1..514 47..559	489/515 (94%) 498/515 (95%)	0.0
O88762	ASIC-BETA - Rattus norvegicus (Rat), 513 aa.	1..514 1..513	488/515 (94%) 498/515 (95%)	0.0
P55926	Amiloride-sensitive brain sodium channel BNaC2 (Amiloride-sensitive cation channel neuronal 2) (Proton gated cation channel ASIC1) - Rattus norvegicus (Rat), 526 aa.	1..514 1..526	416/527 (78%) 445/527 (83%)	0.0
P78348	Amiloride-sensitive brain sodium channel BNaC2 (Amiloride-sensitive cation channel neuronal 2) - Homo sapiens (Human), 574 aa.	1..514 1..574	421/575 (73%) 447/575 (77%)	0.0
Q99NA1	PROTON-GATED CATION CHANNEL SUBUNIT ASIC-BETA2 - Rattus norvegicus (Rat), 425 aa.	175..514 86..425	334/341 (97%) 337/341 (97%)	0.0

PFam analysis predicts that the NOV30a protein contains the domains shown in the

5 Table 30E.

Table 30E. Domain Analysis of NOV30a			
Pfam Domain	NOV30a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ASC: domain 1 of 2	21..118	34/106 (32%) 79/106 (75%)	1.6e-29
ASC: domain 2 of 2	145..442	133/351 (38%) 281/351 (80%)	2.1e-139

Example 31.

The NOV31 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 31A.

Table 31A. NOV31 Sequence Analysis			
	SEQ ID NO: 105	1949 bp	
NOV31a, CG58602-01 DNA Sequence	TGCCTGGCTATGGCCCGACTGCTCAGGTCTGCAACCTGGGAGCTGTTCCCCTGGAGGG GCTACTGCTCCCAGTCCCTGCAGGGAGAGCTCTGCAGGGAATTTCGTAGAGGCTCTGAA GGCCGTGGTGGGCGGCTCCACGTGTCCACTGCCGCGGTGGTCCGAGAGCAGCACGGG CGCGATGAGTCGGTGACAGGTGCGAACCTCCTGATGCTGTGGTGTGGCCCCAGAACG TGGAGCAGGTGAGCCGGCTGGCAGCCCTGTGCTATCGCCAAGGTGTGCCCATCATCCC ATTCCGCCACCGGCACCGGCTTGAGGGTGGCGTCTGTGCTGTGCAGGGCGGCGTCTGC GTTAACCTGACGCATATGGACCGAATCCTGGAGCTGAACCAGGAGGACTTCTCTGTGG TGGTGGAGCCAGGTGTCAACCGCAAAGCCCTCAACGCCACCTGCGGGACAGCGGCTCT CTGGTTTCTCTCAGACCCAGGCGCGGACGCCTCTCTCTGTGGCATGGCGGCCACCGGG GCGCTCGGGGACCAACGCGGTCCGCTACGGCACCATGCGGGACAACGTGCTCAACCTGG AGGTGGTGTGCTCCCGCAGGGCGGCTGTGTCACACGGCGGGCCAGGCTCATCACAGA TTCCACTGCTGCATTCCCCACATCAGCCCCACTGAGTGCTTTTCCAGGGGCCAGGG CCTCATGTCAAATTCTCTCAACCTGCCCTGAGGCCACAGTGGCCGCCACGTGTGCGCT TCCCCAGTGTCCAGGCTGCTGTGGACAGCACTGTACACATCTCCAGGCTGCAGTGCC CGTAGCCCGCATTGAGTTCCTGGATGAAGTCATGATGGATGCTGCAACAGGTACAGC AAGCTGAATTGCTTAGTGGCGCCACACTCTTCTCTGGAGTTCATGGCTCCAGCAGG CACTGGAGGAGCAGCTGCAGCGCACAGAGGAGATAGTCCAGCAGAACGGAGCTCTGA CTTCTCCTGGGCCAAGGAGGCCGAGGAGCGCAGCCGGCTTTGGACAGCACGGCACAAT GCCTGGTACGCAAGCCCTGGCCACGCGGCCAGGCTGCAAGGGCTACTCCAGGATGTGT GTGTGCCCATCTCCCGCTGCGGAGATCGTGGTGACAGCAAGGAGGATCTGAATGC CTCAGGACTCACAGGAAGCATTGTGCGGCATGTGGGTGACGGCAACTTCCACTGCATC CTGCTGGTCAACCTGATGACGCCGAGGAACCTGGGCAGGGTCAAGGCTTTTTCGAGAAC AGCTGGGCGAGCGGGCACTGGCTCTCCACGGAACGTGCACGGGGAGCATGGCATCGG AATGGGCAAGCGGCAGCTGTGTCAGGAGGAGGTGGGCGCGGTGGCGCTGGAGACCATG CGGCAGCTCAAGGCCGTGCTAGACCCCCAAGGCCCTCATGAATCCAGGCAAAGTGCTGT GAAGGGGGTCTGAGCACTTAGCCCCACAAGTTCCCTGACTACGGAGCCGGTTCTGGAAC TTTTTCTTCATGCCACGCCCCCTGCAAGGAAATAGATGCTGAGGCAGTCTTCTCGCCAG CGAGCCCACTGTATCTGGGCCAAGGCCAGAGGGCCAGAGAGAAGCTGAGCACCGT GTTACCTCCCTGGCCCTCTGGCTGGCCCCAGGAGCCTTTGGTTACAGTAAACGACCCAG GGTGGTTCCTCCAGCAAAGCTGCTTCTCTCTGCTCCTACGCATCTCTGCTCGGGGAA GAGAGCGTCTGGGTCCATTCAAGACTCTGATGACACCCCTCCCCGAGGCCTCCCACTG CCGGGGTCCCAGGACCTTCCCCCTTCACTGGTGACAGGAACACTCTTCTCTGGTA TGAACGTGAGCTCCCGTGACATGATGATAGGTCTTCTCTTGGGGCTCCCCAATA AATCTGTAATAAACCCTGAAACCCACCTACAGCTAA		
	ORF Start: ATG at 10	ORF Stop: TGA at 1450	
	SEQ ID NO: 106	480 aa	MW at 51629.1kD
NOV31a, CG58602-01 Protein Sequence	MARLLRSATWELFPWRGYCSQSLQGLCRDFVEALKAVVGGSHVSTAADVREQHGRDE SVHRCEPPDAVWVPQNVQVSRLLAALCYRQGVPIIPFGTGTLEGGVCAVQGGVCVNL THMDRIELNQEDFSVVVEPGVTRKALNAHLRDSGLWFPDPGADASLCGMAATGASG TNAVRYGTMRDNLNLEVLDPGRLLHTAGRLITDSTAAPHISPTFCFSQGPVPHV NSPHPAPEATVAATCAFPVQAAVDSTVHILQAAVPVARIIEFLDEVMMDACNRYSKLN CLVAPTFLFLEHGSQQALEEQLQRTTEIVQNGASDFSWAKEAERSRLWTAHNAWY		

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Table 31B. Protein Sequence Properties NOV31a	
PSort analysis:	0.6574 probability located in mitochondrial matrix space; 0.3502 probability located in mitochondrial inner membrane; 0.3502 probability located in mitochondrial intermembrane space; 0.3502 probability located in mitochondrial outer membrane
SignalP analysis:	Likely cleavage site between residues 20 and 21

5

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB10446	Human cDNA SEQ ID NO: 754 - Homo sapiens, 115 aa. [WO200154474-A2, 02-AUG-2001]	1..96 15..110	91/96 (94%) 92/96 (95%)	8e-49
AAE09597	Human gene 5 encoded novel protein HDPMT22, SEQ ID NO:33 - Homo sapiens, 115 aa. [WO200155311-A2, 02-AUG-2001]	1..96 15..110	91/96 (94%) 92/96 (95%)	8e-49
AAM52368	GIP12-C4 protein - Arabidopsis thaliana, 159 aa. [FR2806095-A1, 14-SEP-2001]	66..203 3..140	69/138 (50%) 98/138 (71%)	9e-34
AAG92286	C glutamicum protein fragment SEQ ID NO: 6040 - Corynebacterium glutamicum, 948 aa. [EP1108790-A2, 20-JUN-2001]	46..477 25..502	108/486 (22%) 186/486 (38%)	2e-22
AAB79309	Corynebacterium glutamicum SMP protein sequence SEQ ID NO:134 - Corynebacterium glutamicum, 945 aa. [WO200100844-A2, 04-JAN-2001]	46..477 22..499	108/486 (22%) 186/486 (38%)	2e-22

In a BLAST search of public sequence databases, the NOV31a protein was found to have homology to the proteins shown in the BLASTP data in Table 31D.

Table 31D. Public BLASTP Results for NOV31a				
Protein Accession Number	Protein/Organism/Length	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9D635	4733401P21RIK PROTEIN - Mus musculus (Mouse), 481 aa.	1..480 1..481	394/483 (81%) 423/483 (87%)	0.0
Q19965	F32D8.4 PROTEIN - Caenorhabditis elegans, 912 aa.	20..480 445..909	221/466 (47%) 307/466 (65%)	e-121
CAD16371	PUTATIVE D-LACTATE DEHYDROGENASE (CYTOCHROME) OXIDOREDUCTASE PROTEIN (EC 1.1.2.4) - Ralstonia solanacearum (Pseudomonas solanacearum), 472 aa.	32..479 20..469	226/454 (49%) 300/454 (65%)	e-119
A89201	protein F32D8.4 [imported] - Caenorhabditis elegans, 870 aa.	30..480 399..867	214/469 (45%) 296/469 (62%)	e-115
AAL51780	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4) - Brucella melitensis, 468 aa.	41..480 28..467	209/444 (47%) 286/444 (64%)	e-114

- 5 PFam analysis predicts that the NOV31a protein contains the domains shown in the Table 31E.

Table 31E. Domain Analysis of NOV31a			
Pfam Domain	NOV31a Match Region	Identities/ Similarities for the Matched Region	Expect Value
FAD_binding_4: domain 1 of 1	33..214	70/208 (34%) 154/208 (74%)	3.7e-56
FAD-oxidase_C: domain 1 of 1	206..479	91/307 (30%) 210/307 (68%)	1.3e-58

Example 32.

The NOV32 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 32A.

Table 32A. NOV32 Sequence Analysis			
	SEQ ID NO: 107	698 bp	
NOV32a, CG58468-01 DNA Sequence	CTCCTTCCTGTGCTCTTTATATGGACCAACAACCTCTCGTCCTTGGGGTCTCTGTGCA AATATCAATTTTTTACATTATCTTTCTCCACAGACATGAGAGGGAAGGCATTTATT TTCCCTCAAGAATCAGCTACAGTCTATGTGTCCCTGATCCCCAAGGTGAAGAAGCCCC TGAAGAACTTCAAGCTTTGCCGTGAAAACCTTCACAGACTTCACCTGCCCTTATAGCCT CTTCTACAGCACTCGGTCCCAGGACAATGAGCTGCTTCTCCTTGTCACAAAAATGGGA ATGTATCTGCTGCACATTGGAAATGCTGCGGTCACTTTCAATGGCCCCACCCCTGCC CTCGATCTCCTTATGCTTCGACCCATGTCAATGTGAGCTGGGAGTCTGCCTCTGGAAT TGCTACACTCTGGGCAAATGGGAAGCTGGTGGGGAGGAAGGGTGTGTGGAAGGGGTAC TCTGTGGGAGAAGAGGCTAAGATCATCCTGGGACAAGAGCAGGATTCCTTTGGGGGAC ATTTTGATGAAAATCAATCCTTTGTTGGGGTGATATGGGATGTGTTTTGTGGGATCA TGTGCTCCCTCCAAAGGAGATGTGTGACTCCTGTTACAGCGGCAGCCTCCTGAATCGG CATACCCTGACTTATGAAGATAATGGCTATGTGGTAACTAAGCCCAAGGTGTGGGCTT AA		
	ORF Start: ATG at 21	ORF Stop: TAA at 696	
	SEQ ID NO: 108	225 aa	MW at 25265.8kD
NOV32a, CG58468-01 Protein Sequence	MDQQLLVLGVSQISIFSHYLFSTDMRGKAFIPQESATVYVSLIPKVKPLKNFKLC LKTFTDFTCPYSLFYSTRSQDNELLLVNKMGMYLLHIGNAAVTENGPTPCPRSPYAS THVNVSWESASGIATLWANGKLVGRKGVWKGYSVGEEAKIILGQEQDSFGGHFDENQS FVGVIWDVFLWDHVLPPKEMCDSCYSGSLNLRHTLTIEDNGYVVTKPKVWA		

Further analysis of the NOV32a protein yielded the following properties shown in Table 32B.

Table 32B. Protein Sequence Properties NOV32a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.3200 probability located in microbody (peroxisome); 0.2368 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

- A search of the NOV32a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
- 5 several homologous proteins shown in Table 32C.

Table 32C. Geneseq Results for NOV32a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV32a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR74763	Sermun amyloid P component, promoter sapm - Homo sapiens, 204 aa. [WO9505394-A, 23-FEB-1995]	24..224 2..203	98/207 (47%) 136/207 (65%)	4e-48

AAR29923	SAP - Homo sapiens, 223 aa. [WO9221364-A, 10-DEC-1992]	7..224 5..222	101/224 (45%) 143/224 (63%)	3e-47
AAR29922	CRP - Homo sapiens, 225 aa. [WO9221364-A, 10-DEC-1992]	14..224 11..224	100/218 (45%) 132/218 (59%)	2e-43
AAR74769	Female hamster protein, 1fhp - Cricetus cricetus, 210 aa. [WO9505394-A, 23-FEB-1995]	24..222 1..199	95/206 (46%) 132/206 (63%)	6e-43
AAV76844	Human C reactive protein (CRP) sequence - Homo sapiens, 206 aa. [JP2000014388-A, 18-JAN-2000]	24..224 2..205	98/208 (47%) 128/208 (61%)	1e-42

In a BLAST search of public sequence databases, the NOV32a protein was found to have homology to the proteins shown in the BLASTP data in Table 32D.

Table 32D. Public BLASTP Results for NOV32a				
Protein Accession Number	Protein/Organism/Length	NOV32a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9D8J8	1810030J14RIK PROTEIN - Mus musculus (Mouse), 219 aa.	6..224 4..218	130/220 (59%) 166/220 (75%)	5e-72
Q9D8V2	1810030J14RIK PROTEIN - Mus musculus (Mouse), 200 aa.	6..190 20..200	110/186 (59%) 139/186 (74%)	2e-58
Q63913	SERUM AMYLOID P - Cricetulus migratorius (Armenian hamster), 223 aa.	1..224 1..222	109/231 (47%) 152/231 (65%)	4e-51
P23680	Serum amyloid P-component precursor (SAP) - Rattus norvegicus (Rat), 228 aa.	6..224 4..223	105/224 (46%) 145/224 (63%)	7e-50
P15697	Female protein precursor (FP) (Serum amyloid P-component) - Cricetulus migratorius (Armenian hamster), 231 aa.	1..222 1..220	108/229 (47%) 151/229 (65%)	7e-50

PFam analysis predicts that the NOV32a protein contains the domains shown in the

5 Table 32E.

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Table 32E. Domain Analysis of NOV32a

Pfam Domain	NOV32a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pentaxin: domain 1 of 1	29..221	103/214 (48%) 156/214 (73%)	8e-76

Example 33.

The NOV33 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 33A.

Table 33A. NOV33 Sequence Analysis

	SEQ ID NO: 109	3350 bp
NOV33a, CG58183-01 DNA Sequence	<p>TAATGAGGAGACTGAGTTTGTGGTGGCTGCTGAGCAGGGTCTGTCTGCTGTTGCGGCC GCCCTGCGCACTGGTGTGGCCGGGGTGCCAGCTCCTCCTCGCACCCGCGAGCCCTGC CAGATCCTCAAGCGCATCGGGCAGCGGTGAGGGTGGGCGCGGTGCACTTGACGCCCT GGACCACCGCCCCCGCGCGGCCAGCGCGCTCCGGACGACAGCCGAGCAGGAGCCCA GAGGGATGAGCCGGAGCCAGGGACTAGGCGGTCCCCGGCGCCCTCGCCGGGCGCACGC TGGTTGGGGAGCACCTGCATGGCCGGGGGCGCCGGGCTCCCGTAAGCCCGGGGAGG GCGCCAGGGCGGAGGCCCTGTGGCCACGGGACGCCCTCCTATTTGCCGTGGACAACCT GAACCGCGTGGAAGGGCTGTACCCCTACAACCTGTCTTTGGAAGTAGTGATGGCCATC GAGGCAGGCCTGGGCGATCTGCCACTTTTGCCCTTCTCCTCCCTAGTTTCGCCATGGA GCAGTGACCCCTTCTCCTTCTGCAAAGTGTGTGCCATACCGTGGTGGTGCAAGGGGT GTCGGCGCTGCTCGCCTTCCCCCAGAGCCAGGGCGAAATGATGGAGCTCGACTTGGTC AGCTTAGTCTGCAATTCAGTGATCAGCATCGTGCGCCACGAGTTCCACGGGAGA GTCAGAATCCCTTCACTACAAGTGTAGTTAGAAAATTCATTAAGTTCTGATGCTGA TGTCAGTGTCTCAATCCTGACCATGAACAAGTGTGCAATTTAGCTTGTGTGTGTC CAGGAAGACTGGAACATCACGACTTCTCCTCCTTACCCAGAATAATTCAGTTCC ACCTTGGTTCTATCATCAACATCACCGCTAACCTCCCTCCACCAGGACCTCTTGAG CTTCTACAGATCCAGCTTGAGAGTATTAAGAACAGCACACCCACAGTGGTGATGTTT GGCTGCGACATGGAAGTATCCGGCGGATTTTCGAAATTACAACCAAGTTTGGGGTCA TGCCCCCTGAACCTTCGTTGGGTGCTGGGAGATTCCAGAATGTGGAGGAAGTGGAGAC AGAGGGTCTGCCCTTAGGGCTCATTGCTCATGGAAGAACACACAGTCTGTCTTTGAG CACTACGTACAAGATGCTATGGAGCTGGTCGCAAGAGCTGTGAGAGTGGTTACCTGATG TCCAACCAAGAACTTGCTCTCATTCCAGCAGCATGAAGTGCATGGAGGTGGAAGTAC AAATCTCACTTCAGGACAATATTTATCAAGGTTTCTAGCCAATACCCTTTCAGAGGC CTCAGTGGTTCCATCAGAGTAAAAGTTCCACCATGCTCAGCTCAGAAAACAATTTT TCATCTGGAATCTTCAACATGACCCCATGGGAAAGCCAATGTGGACCCGCTTGGGCAG CTGGCAGGGGGGAAAGATTGTGATGAGTATGGAATATGGCCAGAGCAGGCCAGAGA CACAAAACCACTTCCAACATCCAAGTAAGCTACACTTGAGAGTGGTTACCTGATTG AGCATCCTTTTGTCTTCAAGGGAGGTAGATGATGAAGCTTGTGCCCTGTGGCCA ACTCTGTCTAGACCCCATGACTAATGACTCTCCACATTGGACAGCCTTTTATGACG TCCCATAGCAGTAATGATACAGTGCCCATTAATCAAGAAGTGTGCTATGGATATT GCATTGATCTGCTGGAAGATAGCAGAAGACATGAACCTTGACTTCGACCTATATAT TGAGGGGATGGAAGATATGGAGCATGGAAGAAATGGGCACTGGAGCTAGTGGGT GATCTCCTGAGAGGACTGCCACATGGCAGTCACTTCTTAGCATCAATACACTGCAC GGAGCCAGGTGATAGATTTACACAGCCCTTCTTCTCCACAGCTTGGGCATCTTAGT GAGGACCCGAGATACAGCAGCTCCCATTTGGAGCCTTCATGTGGCCACTCCACTGGACA ATGTGGCTGGGGATTTTGTGGCTCTGCACATCACTGCCGTCTTCTCACTCTGTATG AATGGAAGAGTCCATTGGTTTGACTTCCAAGGGGCGAAATAGAAGTAAAGTCTTCTC CTTTTCTTCAGCTTGAACATCTGTATGCCCTCTGTTTGGCAGAACAGTGGCCATC AAACCTCCAAATGTTGGACTGGAAGGTTTCTAATGAACCTTTGGGCCATTTTCTGTA TGTTTGGCTTCCACATACACGGCAAACTTGGCTGCTGTGATGGTAGGTGAGAGAT CTATGAAGAGCTTTCTGGAATACATGACCCCAAGTTACATCATCTTCCCAAGGATT CGCTTTGGAACGTCCGAGAAAGCAGTGTGAAGATTATGTGAGACAAAGTTTCCAG AGATGCATGAATATATGAGAAGGTACAATGTTCAGCCACCCCTGATGGAGTGGAGTA TCTGAAGAAATGATCCAGAGAACTAGACGCTTTCATGAGACAAAGCCCTTCTGGAT TATGAAGTGTCAATAGATGCTGACTGCAAACTTCTCACTGTGGGGAAGCCATTGGCCA TAGAAGTTACGGCATTTGGCTCCACCCCACTTCCATTGACCGCCCAACATATCCGA GCTAATCAGTCAATACAAGTCATGGGTTTATGGATATGCTCCATGACAAGTGGTAC</p>	

	AGGGTGGTTCCTGTGGCAAGAGAAGTTTTGCTGTACGAGACTTTGCAATGGGCA TCAAACACTTCTCTGGGCTCTTGTGCTGTGTGCATTGGATTGGTCTGTCCATTTT GACCACCATTTGGTGAGCACATAGTATACAGGCTGCTGTACCACGAATCAAAACAAA TCCAAGCTGCAATACTGGCTCCACACGAGCCAGAGATTACACAGAGCAATAAATACAT CATTATAGAGGAAAGCAGCAGCATTTCAAGACCAACGCTGTGGAAGAGATCTAA TGTGGGACCCCGTCAGCTTACCGTATGGAATACTTCCAATCTGAGTCATGACAACCGA CGGAAATACATCTTTAGTGATGAGGAAGGACAAACAGCTGGGCATCCGGATCCACC AGGACATCCCCCTCCCTCCAAGGAGAAGAGAGCTCCCTGCCTTGCGGACCACCAATGG GAAAGCAGACTCCCTAAATGTATCTCGGAACTCAGTGATGCAGGAACCTCTCAGAGCTC GAGAAGCAGATTGAGTGATCCGTGAGGAGCTGCAGCTGGCTGTGAGCAGGAAACCG AGCTGGAGGAGTATCAAAGGACAAGTCGGACTTGTGAGTCCTAG		
	ORF Start: ATG at 3 ORF Stop: TAG at 3348		
	SEQ ID NO: 110	1115 aa	MW at 125453.7kD
NOV33a, CG58183-01 Protein Sequence	MRRLSLWLLSRVCLLLPPPCALVLAVPSSSSHPQPCQILKRIGHAVRVGAVHLQPW TTAPRAASRAPDDSRAGAQRDEPEPGTRRSPPAPSPGARWLGSTLHGRGPPGSRKPGEG ARAEALWPRDALLFAVDNLRVEGLLPYNLSLEVMAIEAGLGDPLLPFSSPSPWS SDPFSFLQSVCHTVVVQGVSAALLAFPSQSGEMMELDLVSLVLHI PVISIVRHEFPRES QNPLHLQLSLENSLSSDADVTVSILTMNNWYNFSLLLCQEDWNI TDFLLLTQNNSKFH LGSINITANLPSTQDLSFLQIQLESIKNSTPTVVMFGCDMESIRRIFEITTFQFGVM PPELRWVLGDSQNVVELRTEGLPLGLIAHGKTTQSVFEHYVDAMELVARAVATATMI QPELALIPSTMNMEVETTNLTSGQYLSRFLANTTFRGLSGSIRVKGSTIVSSENNFF IWNLQHDPMGKPMWTRLGSSWQGGKIVMDYGIWPEQAQRHKTHFQHPSKLHLRVVTLIE HPFVFTREVDDGLCPAGQLCLDPMTNDSSTLDSLFSSLSHSSNDTVPIKFKKCCYGYC IDLEKIAEDMNFDFDLYIVGDGKYGAWKNGHWTLVGLDRLRGTAHMAVTSFSINTAR SQVIDFTSPFFSTSLGILVRTRDTAAPIGAFMWPLHWTMWLGI FVALHITAVFLTLYE WKSPPFGLTSKGRNRSKVFSSALNICYALLFGRTVAIKPPKCTGRPLMNLWAI FCM FCLSTYTANLAAMVGEKIYEELSGIHDPKLHHP SQGFRFGTVRESSAEDYVRQSFPPE MHEYMRRYNVPATPDGVEYLKNDPEKLDAPIMDKALLDYEVSIDADCKLLTVGKPFPI EGYGIGLPPNSPLTANISELISQYKSHGFMMDLHDKWYRVVPCGKRSPAVTETLQMG KHFSGLFVLLCIGFGLSILTTIGEHIYVRLLLPRIKNKSKLQYWLHTSQRLHRAINTS FIEEKQHFKTKRVEKRSNVGPRQLTVWNTSNLSDHNRKRYIFSDEEQGNQLGIRIHQ DIPPPRRRELPAVRTNGKADSLNVSRSVMQELSELEKQIQVIRQELQLAVSRKTE LEEYQRTSRTCES		

Further analysis of the NOV33a protein yielded the following properties shown in Table 33B.

Table 33B. Protein Sequence Properties NOV33a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 34 and 35

A search of the NOV33a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 33C.

Table 33C. Geneseq Results for NOV33a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU02199	Human glutamate receptor-like protein, MEM4 - Homo sapiens, 1043 aa. [WO200144473-A2, 21-JUN-2001]	95..1103 6..1007	508/1047 (48%) 680/1047 (64%)	0.0
AAB42494	Human ORFX ORF2258 polypeptide sequence SEQ ID NO:4516 - Homo sapiens, 901 aa. [WO200058473-A2, 05-OCT-2000]	95..985 6..885	484/912 (53%) 635/912 (69%)	0.0
AAU02198	Human glutamate receptor-like protein, MEM3 - Homo sapiens, 971 aa. [WO200144473-A2, 21-JUN-2001]	532..1103 362..935	361/579 (62%) 448/579 (77%)	0.0
AAU02197	Human glutamate receptor-like protein, MEM2 - Homo sapiens, 965 aa. [WO200144473-A2, 21-JUN-2001]	532..1103 362..929	352/579 (60%) 437/579 (74%)	0.0
AAR44192	Rat NMDA receptor subunit, NR2A - Rattus rattus, 1464 aa. [DE4216321-A, 18-NOV-1993]	175..1023 77..911	245/873 (28%) 425/873 (48%)	2e-83

In a BLAST search of public sequence databases, the NOV33a protein was found to have homology to the proteins shown in the BLASTP data in Table 33D.

Table 33D. Public BLASTP Results for NOV33a

Protein Accession Number	Protein/Organism/Length	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL40734	N-METHYL-D-ASPARTATE RECEPTOR 3A - Homo sapiens (Human), 1115 aa.	1..1115 1..1115	1110/1115 (99%) 1112/1115 (99%)	0.0
Q62800	IONOTROPIC GLUTAMATE RECEPTOR - Rattus norvegicus (Rat), 1115 aa.	1..1115 1..1115	1032/1115 (92%) 1083/1115 (96%)	0.0

Q9R1M7	N-METHYL-D-ASPARTATE RECEPTOR SPLICE VARIANT NR3A-2 - Rattus norvegicus (Rat), 1135 aa.	1..1115 1..1135	1032/1135 (90%) 1083/1135 (94%)	0.0
CAC69380	SEQUENCE 7 FROM PATENT WO0144473 - Homo sapiens (Human), 1043 aa.	95..1103 6..1007	508/1047 (48%) 680/1047 (64%)	0.0
Q91ZU9	NMDA-TYPE GLUTAMATE RECEPTOR SUBUNIT NR3B PRECURSOR - Mus musculus (Mouse), 1003 aa.	112..1103 34..980	510/1001 (50%) 669/1001 (65%)	0.0

Pfam analysis predicts that the NOV33a protein contains the domains shown in the Table 33E.

Table 33E. Domain Analysis of NOV33a			
Pfam Domain	NOV33a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lig_chan: domain 1 of 1	674..952	81/323 (25%) 232/323 (72%)	4e-95

Example 34.

The NOV34 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 34A.

Table 34A. NOV34 Sequence Analysis		
	SEQ ID NO: 111	1253 bp
NOV34a, CG59315-01 DNA Sequence	<p>CCCAGCGCCATGGGGAGTGGGCGTTCCTGGGCTCGCTGCTGGACGCCGTGCAGCTGC AGTCGCCGCTCGTGGGCGGCTCTGGCTGGTGGTCATGCTGATCTTCGCCATCCTGGT GCTGGCCACGGTGGGCGGCGCGGTGTTCGAGGACGAGCAAGAGGAGTTCTGTGCAAC ACGCTGACGCCGGGCTGTGCGCAGACCTGCTACGACCGCGCCTTCCCGGTCTCCCACT ACCGCTTCTGGCTCTTCCACATCCTGCTGCTCTCGGCGCCCCGGGTGCTGTTCTGCTCGT CTACTCCATGCACCGGGCAGGCAAGGAGGCGGGCGGCGCTGAGGCGGCGCGCAGTGC GCCCCCGGACTGCCGAGGCCAGTGCGCGCGTGGCGCCTGCGCGCCCGCGCGCGCG GCCGCTGCTACCTGCTGAGCGTGGCGCTGCGCCTGCTGGCCGAGCTGACCTTCCTGGG CGGCCAGGCGCTGCTTACGGCTTCGCGTGGCCCCGCACTTCGCGTGGCCGGTCCG CCCTGCCCGCACACGGTGCAGTCTTCTGAGCGGCCCCACGAGAAGACCGTCTTCG TGCTCTTCTATTTCGGGTGGGGCTGCTGTGCGGCTGCTCAGCGTAGCCGAGCTGGG CCACCTGCTCTGGAAGGGCGCCCGCGCGCGGGGAGCGTGACAACCGCTGCAACCGT GCACACGAAGAGGCGCAGAAGCTGCTCCCGCCGCGCCCGCCGACCTCCGCCACCGG CCCTGCCCTCCGCGCGCCCCGCGCCGAGCCGTGCGCCCGCGGCTATGCGCACCC GGCGCCGCGCAGCCTCCGCGAGTGGCGCAGCGCGCGCGGAGGAATGCGCAATGGCT CCCAGATGTGGAGCCACCGCTTAACCCCTTACCCCGAGCCGCGCTCCCCAAGGGC CTTCAGCCTGAGCCCCGCCAACAGCAGGAGCTCTGCCAGGTGAGAACCAGCCAG GACTGGAGTCAGCGCCAGCCCGCCCTAGTGCCACGGACACCTCCCAACCTAGATCC TACCTGTCTTCTTCTTCTGAGGCTGGAGGGGAAGGCTCATGGACACAAGAATGCAAGC ATGCATGCACACAGTACACTGCCTCCCATCCCCCTCCGCGCCAGCGTGGCAGGGTGCC CCTCCCTCGCTCCCATCCTGGCAGGGCGGGCGCGCAGAGCGCTCCACTCCGATTCC CCACGCCCCCGAGCCGTTTCGAGGCTCGACAAG</p>	

	ORF Start: ATG at 10	ORF Stop: AG at 1252
	SEQ ID NO: 112	414 aa MW at 44773.0kD
NOV34a, CG59315-01 Protein Sequence	MGEWAFGLSLLDAVQLQSPVLVGRWLWVMLIFRIILVLTAVGGAVFEDEQEFEVCNTLQ PGCRQTCYDRAPFVSHYRFWLFHILLSSAPPVLFVVYSMHRAGKEAGGAEAAAQCAPG LPEAQCAPCALRARRARRCYLLSVALRLLAELTFLGGQALLYGFRVAPHFACAGPPCP HTVDCFVSRPTEKTVFVLFYFAVGLLSALLSVAELGHLLWKGRPRAGERDNRNRAHE EAQKLLPPPPPPPPALPSRRPGPEPCAPPAYAHAPASLRECGSGRGNAPMAPRC GRHRLTPYPPAALPQGPSSLSPANRELCPGENQPRTGVSASPLVPTDTSQPRSYLS SFLEAGGEGSWTQECKHACTQLHCLPSPADAARVPLPRSPSWQGGRRRALHSGFPTP PSRSQART	

Further analysis of the NOV34a protein yielded the following properties shown in Table 34B.

Table 34B. Protein Sequence Properties NOV34a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 39 and 40

A search of the NOV34a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 34C.

Table 34C. Geneseq Results for NOV34a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW49009	Mouse alpha 3 connexin protein - Mus sp, 417 aa. [WO9830677-A1, 16-JUL-1998]	1..296 1..327	121/334 (36%) 169/334 (50%)	5e-52
AAW23968	Connexin protein Cx40 - Homo sapiens, 358 aa. [WO9802150-A1, 22-JAN-1998]	1..215 1..232	93/233 (39%) 133/233 (56%)	9e-46
AAW23970	Connexin protein Cx45 - Homo sapiens, 396 aa. [WO9802150-A1, 22-JAN-1998]	4..212 3..253	93/252 (36%) 137/252 (53%)	3e-43
AAW23969	Connexin protein Cx43 - Homo sapiens, 382 aa. [WO9802150-A1, 22-JAN-1998]	1..216 1..235	86/235 (36%) 130/235 (54%)	1e-42
AAM93194	Human polypeptide, SEQ ID NO:	7..384 7..360	129/409 (31%) 169/409 (40%)	8e-38

	[EP1130094-A2, 05-SEP-2001]			
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In a BLAST search of public sequence databases, the NOV34a protein was found to have homology to the proteins shown in the BLASTP data in Table 34D.

Table 34D. Public BLASTP Results for NOV34a				
Protein Accession Number	Protein/Organism/Length	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q91YD1	CONNEXIN30.2 - Mus musculus (Mouse), 278 aa.	1..283 1..265	228/283 (80%) 240/283 (84%)	e-129
I46053	connexin44 - bovine, 402 aa.	1..397 1..396	151/418 (36%) 207/418 (49%)	1e-62
P41987	Gap junction alpha-3 protein (Connexin 44) (Cx44) - Bos taurus (Bovine), 401 aa.	2..397 1..395	150/417 (35%) 206/417 (48%)	4e-62
AAA50954	CONNEXIN44 - Bos taurus (Bovine), 407 aa.	1..398 1..402	154/429 (35%) 214/429 (48%)	1e-60
Q9TU17	GAP JUNCTION PROTEIN (CONNEXIN) - Ovis aries (Sheep), 413 aa.	1..398 1..408	147/415 (35%) 204/415 (48%)	1e-60

5 PFam analysis predicts that the NOV34a protein contains the domains shown in the Table 34E.

Table 34E. Domain Analysis of NOV34a			
Pfam Domain	NOV34a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF26: domain 1 of 1	107..152	12/56 (21%) 27/56 (48%)	1.4
connexin: domain 1 of 1	1..212	101/247 (41%) 150/247 (61%)	6.5e-75

Example 35.

The NOV35 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 35A.

Table 35A. NOV35 Sequence Analysis			
	SEQ ID NO: 113	724 bp	
NOV35a, CG59203-01 DNA Sequence	<u>TAAATTCGCGGCCGCTCGACCTTCGCGAGACTCAACTGAGAAGTCAGCCTCTGCGGC</u> <u>AGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCT</u> <u>GCGGGCATCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACA</u> <u>CTCGTTGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTT</u> <u>CAGCCTTGGAAGCTGGATCTGCATGGCGTATTATGAGAGCGGCTACAACACCACAGCC</u> <u>CAGACGGTCTCTGGATGACGGCAGCATCGACTACGGCATCTTCAGATCAACAGCTTCG</u> <u>CGTGGTGACAGCGCGGAAAGCTGAAGGAGAAACAACCACTGCCACGTGCGCTGCTCAGC</u> <u>CTTGGTCACTGATGACCTCACAGATGCGATTATCTGTGCCAAGAAAATTGTTAAAGAG</u> <u>ACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACACTGTGAGGGGAGAGACCTGT</u> <u>CCGACTGGAAAAAAGACTGTGAGGTTTCCTAAACTGGAAGTGGACCCAGGATGCTTTG</u> <u>CAGCAACGCCCTAGGGTTTGAGTGAATGTCCAAATGCCTGTGTATCTGTCCCGTT</u> <u>TCCTCCCAATATTCTTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAA</u> <u>AATAAATATTTCCATTAAATGTCAAAA</u>		
	ORF Start: ATG at 108	ORF Stop: TAA at 552	
	SEQ ID NO: 114	148 aa	MW at 16655.9kD
NOV35a, CG59203-01 Protein Sequence	MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYN TTAQTVLDDGSIDYGIQINSFAWCRRGKLENNHCHVACSALVTDDLDAIICAKKI VKETQGMNYWQGWKKHCEGRDLSDWKKDCEVS		
	SEQ ID NO: 115	453 bp	
NOV35b, CG59203-02 DNA Sequence	<u>CATTCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGT</u> <u>TGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCC</u> <u>TTGGAACCTGGATCTGCATGGCGTATTATGAGAGCGGCTACAACACCACAGCCAGAC</u> <u>GGTCTGGATGACGGCAGCATCGACTACGGCATCTTCAGATCAACAGCTTCGCGTGG</u> <u>TGCAGACGCGGAAAGCTGAAGGAGAAACAACCACTGCCACGTGCGCTGCTCAGCCTTG</u> <u>TCCTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACA</u> <u>AGGAATGAATTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAC</u> <u>TGGAAAAAAGGCTGTGAGGTTTCCTAAACTGGAAGTGGACCCAGGAT</u>		
	ORF Start: ATG at 134	ORF Stop: TAA at 431	
	SEQ ID NO: 116	99 aa	MW at 11288.6kD
NOV35b, CG59203-02 Protein Sequence	MAYYESGYNNTAQTVLDDGSIDYGIQINSFAWCRRGKLENNHCHVACSALVTDDL DAIICARKIVKETQGMNYWQGWKKHCEGRDLSDWKKGCEVS		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 35B.

Table 35B. Comparison of NOV35a against NOV35b.		
Protein Sequence	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV35b	50..148 1..99	97/99 (97%) 98/99 (98%)

Further analysis of the NOV35a protein yielded the following properties shown in Table 35C.

Table 35C. Protein Sequence Properties NOV35a	
Psort analysis:	0.3700 probability located in outside; 0.1697 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 20 and 21

A search of the NOV35a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 35D.

Table 35D. Geneseq Results for NOV35a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY57399	Human lysoenzyme LYC2 polypeptide - Homo sapiens, 148 aa. [WO200012722-A1, 09-MAR-2000]	1..148 1..148	143/148 (96%) 147/148 (98%)	3e-86
AAU29169	Human PRO polypeptide sequence #146 - Homo sapiens, 148 aa. [WO200168848-A2, 20-SEP-2001]	1..148 1..148	143/148 (96%) 146/148 (98%)	6e-86
AAB66145	Protein of the invention #57 - Unidentified, 148 aa. [WO200078961-A1, 28-DEC-2000]	1..148 1..148	143/148 (96%) 146/148 (98%)	6e-86
AAY99396	Human PRO1278 (UNQ648) amino acid sequence SEQ ID NO:203 - Homo sapiens, 148 aa. [WO200012708-A2, 09-MAR-2000]	1..148 1..148	143/148 (96%) 146/148 (98%)	6e-86
AAY71109	Human Hydrolase protein-7 (HYDRL-7) - Homo sapiens, 194 aa. [WO200028045-A2, 18-MAY-2000]	1..148 47..194	142/148 (95%) 146/148 (97%)	1e-85

- 5 In a BLAST search of public sequence databases, the NOV35a protein was found to have homology to the proteins shown in the BLASTP data in Table 35E.

Table 35E. Public BLASTP Results for NOV35a

Protein Accession Number	Protein/Organism/Length	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96LF2	BA14C22.1 (NOVEL PROTEIN SIMILAR TO LYSOZYME) - Homo sapiens (Human), 148 aa.	1..148 1..148	148/148 (100%) 148/148 (100%)	7e-88
Q9H1R9	BA534G20.1.1 (NOVEL PROTEIN SIMILAR TO LYSOZYME C-1 (1,4-BETA-N-ACYLMURAMIDASE C, EC 3.2.1.17) (ISOFORM 1)) - Homo sapiens (Human), 148 aa.	1..148 1..148	144/148 (97%) 147/148 (99%)	4e-86
AAH21730	HYPOTHETICAL 21.6 KDA PROTEIN - Homo sapiens (Human), 194 aa.	1..148 47..194	143/148 (96%) 146/148 (98%)	2e-85
Q9CPX3	1700038F02RIK PROTEIN - Mus musculus (Mouse), 148 aa.	1..148 1..148	110/148 (74%) 127/148 (85%)	3e-66
Q9H1R8	BA534G20.1.2 (NOVEL PROTEIN SIMILAR TO LYSOZYME C-1 (1,4-BETA-N-ACYLMURAMIDASE C, EC 3.2.1.17) (ISOFORM 2)) - Homo sapiens (Human), 106 aa (fragment).	20..125 1..106	104/106 (98%) 106/106 (99%)	1e-59

Pfam analysis predicts that the NOV35a protein contains the domains shown in the Table 35F.

Table 35F. Domain Analysis of NOV35a

Pfam Domain	NOV35a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lys: domain 1 of 1	20..145	68/129 (53%) 107/129 (83%)	8e-58

Example 36.

- 5 The NOV36 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 36A.

Table 36A. NOV36 Sequence Analysis			
	SEQ ID NO: 117	712 bp	
NOV36a, CG58662-01 DNA Sequence	GCAGCTATTGCACTTAATCGCGGCTGCTAGCACCATGTCCC GCGT TTTGGTGCCTTGC CATGTGAAAGGCACCGTAGCCCTGCAGGTGGGGGACGTATGGACCTCCCAAGGCCGGC CTAGTGTGCTGGTCATTGATGTCACCTTCCCCTGTGTCACTCCGTTTCGAGGGGATCAC ATTTAAGAATTATTACACAGCGTTTTTTGAGCATCCTGTCTGTGACGACACCTCAGCA CACACACCGGCCAAGTGGGTGACCTGCCTGTGGGACTACTGTCTGATGCCCGACCCAC ACAGTGAGGAGGGAGCCAGGAGTATGTGTCGCTGTTCAAGCAACAGATACTGTGTGA CATGGCCAGAATATCGGAGCTACACCTGATTCTGCAGCAGCCATCACCCTGTGGCTG TCTTTTCACAGTGGAGGAGCTGCAGATCTATCAGCAGGGACCAAGAGCCCTCCATGA TCTTCCCCAAGTGGCTCTCCACCCAGTGCCCTGTGAGCAACCTGCACCTCCTCATGA GGGTCTCCAGACCCAGCAGGGTATCCTCTGAGGTGCAGCAGATGTGGGCACTGACA GAGATGATCCGGGCCAGTCAACCTCCGCGAGGATAGGCCACTTTGATGTAGATGGCT GTTATGACCTGAACCTTACTCTCTACACTTGAGTGGTGGCTCCTAGCCAAGATGTTGG CCTTCTGTGCCCACT		
	ORF Start: ATG at 35	ORF Stop: TGA at 668	
	SEQ ID NO: 118	211 aa	MW at 23932.3kD
NOV36a, CG58662-01 Protein Sequence	MSRVLVPCHVKGTV ALQVGDVWTSQGRPSVLVIDVTFPCVTFPEGITFKNYYTAF FEH PVCQHTSAHTPAKWVTC LWDYCLMPDPHSEEGAQEVSLFKQQLCDMARISELHLIL QQPSPLWLSFTVEELQIYQQGPKSPSMIFPKWLSHPVPCQEPALLHEGLPDPSPRSSE VQQMWALTE MIRASHTSARIGHFDVDGICYDLNLLSYT		
	SEQ ID NO: 119	843 bp	
NOV36b, CG58662-02 DNA Sequence	CTGGCCTGAAGCCATGTCCC GCGT TCTAGCACCATGTCCC GCGTCTAGCACCATGTCC CGCGTCTAGCACCATGTCCC GCGT TCTAGCACCATGTCCC GCGTCTAGCACCATGTCC CCGCGT TCTAGCACCATGTCCC GCGT TTTGGTGCCTTGCCATGTGAAAGGCTCCGTAG CCCTCCAGGTGGGCGACGTGCGGACCTCCCAAGGCCGCGCTGGCGTGTGGTTCATCGA TGTCACCTTCCCGAGCGTCGCTCCCTTCGAGTTGCAGGAAATCACGTTTAAGAATTAC TACACAGCTTTTTGAGCATCCGTGTCCGTGAGTACACCTCAGCACACACACCTGCCA AGTGGGTGACCTGCCTTCGGGACTACTGCCTGATGCCTGACCCACACAGTGAAGAGGG AGCCAGGAGTATGATCGCTGTTCAAGCATCAGATGCTATGTGACATGGCTAGAATA TCGGAGCTACGCCTGATTCTGCGGCAGCCATCACCCTGTGGCTGTCTTTCACAGTGG AGGAGCTGCAGATCTATCAGCAGGGACCAAGAGCCCTCCGTGACCTTTCCTCAAGTG GCTCTCCACCCAGTGCCTGTGAGCAACCTGCACTCCTCCGTGAGGGTTTCCAGAC CCCAGCAGGGTATCCTCCGAGGTGCAGCAGATGTGGGCACTGACAGAGATGATCCGGG CCAGTCAACCTCCGCAAGGATCGGCGCTTTGATGTGGATGGCTTTATGACCTGAC CTTGCTCTCCTACACTTGAATGGTTGCTCTTAGCCAAGATGTTGGCCTTTTGTGGGC ACAGAAAGGCCAACGCGGGACATGGTGCTAG		
	ORF Start: ATG at 132	ORF Stop: TGA at 771	
	SEQ ID NO: 120	213 aa	MW at 24222.6kD
NOV36b, CG58662-02 Protein Sequence	MSRVLVPCHVKG SVALQVGDVRTSQGRPGVLVIDVTFPSVAPFELQEITFKNYYTAF L SIRVRQYTSHTPAKWVTC LRDYCLMPDPHSEEGAQEVSLFKHQLCDMARISELRL ILRQPSPLWLSFTVEELQIYQQGPKSPSVTFPKWLSHPVPCQEPALLREGFPDPSPRSV SEVQQMWALTE MIRASHTSARIGHFDVDGICYDLTLLSYT		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 36B.

Table 36B. Comparison of NOV36a against NOV36b.		
Protein Sequence	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV36b	1..211	188/213 (88%)
	1..213	193/213 (90%)

Further analysis of the NOV36a protein yielded the following properties shown in Table 36C.

Table 36C. Protein Sequence Properties NOV36a	
PSort analysis:	0.5666 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1562 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV36a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 36D.

Table 36D. Geneseq Results for NOV36a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG04038	Human secreted protein, SEQ ID NO: 8119 - Homo sapiens, 115 aa. [EP1033401-A2, 06-SEP-2000]	1..103 1..105	82/105 (78%) 85/105 (80%)	1e-39

In a BLAST search of public sequence databases, the NOV36a protein was found to have homology to the proteins shown in the BLASTP data in Table 36E.

Table 36E. Public BLASTP Results for NOV36a				
Protein Accession Number	Protein/Organism/Length	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BSH3	SIMILAR TO RIKEN CDNA 1500032A17 GENE - Homo sapiens (Human), 213 aa.	1..211 1..213	190/213 (89%) 195/213 (91%)	e-107
Q9CQM0	1500032A17RIK PROTEIN - Mus musculus (Mouse), 213 aa.	1..211 1..213	174/213 (81%) 183/213 (85%)	4e-97

PFam analysis predicts that the NOV36a protein contains the domains shown in the Table 36F.

Table 36F. Domain Analysis of NOV36a			
Pfam Domain	NOV36a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 37.

The NOV37 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 37A.

Table 37A. NOV37 Sequence Analysis			
	SEQ ID NO: 121	520 bp	
NOV37a, CG58584-01 DNA Sequence	<u>CATTGCTGTCTCCTCTGCTCACCAGCAGCTGTACTGGAGCCACCCGCGAAAATTCGG</u> CCAGGGTTCTCGCTCTTGTCTGTCTGTTCAAACCGGCACGGTCTGATCCGGAATAT GGCCTCAATATGTGCCGCCAGTGTTCCGTCAGTACGCGAAGGATATCGGTTTCATTA AGAAAGACCTGAGCTGTCTTCCTTGGCACTGCCTATGGAGGTGACACCCATCTCCTCC ATCATGGCCATCCTGAGACCGCTCGCGAAGCCCAAGATCATCAAAAAGAGCACCAGT TCACTGGGAACCACTCAGACTGATATGTCAAAATTAAGGGTAACCTGGTGGAAACACAG AGGTATTGACAACAGGGTTCATAGAAGGTTTGAGGGCCAGATCTATGCCCAACATTGG TTATGGGAGAAACAAAAGACAAAGCACATACTGCCCAGTGGCTTCTGGAAGTTCCTG GTCCACAACGTTAAGGAGCTGGAAGTACTGCTGGTGAGCAGAGGAGACAGCAATG		
	ORF Start: TTT at 3	ORF Stop: TGA at 216	
	SEQ ID NO: 122	71 aa	MW at 8461.8kD
NOV37a, CG58584-01 Protein Sequence	FAVSSAHQQLYWSPRKFGQGSRSRVCNHRGLIRKYGLNMCRCQPRQYAKDIGFIK KDLSCLPWHCLWR		

Further analysis of the NOV37a protein yielded the following properties shown in
5 Table 37B.

Table 37B. Protein Sequence Properties NOV37a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV37a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 37C.

Table 37C. Geneseq Results for NOV37a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV37a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG76128	Human colon cancer antigen protein SEQ ID NO:6892 - Homo sapiens, 80 aa. [WO200122920-A2, 05-APR-2001]	7..60 2..55	46/54 (85%) 48/54 (88%)	4e-24
AAM79084	Human protein SEQ ID NO 1746 - Homo sapiens, 56 aa. [WO200157190-A2, 09-AUG-2001]	7..60 3..56	39/54 (72%) 43/54 (79%)	2e-18
AAG39921	Arabidopsis thaliana protein fragment SEQ ID NO: 49464 - Arabidopsis thaliana, 637 aa. [EP1033405-A2, 06-SEP-2000]	7..63 3..58	40/57 (70%) 45/57 (78%)	2e-18
AAM80068	Human protein SEQ ID NO 3714 - Homo sapiens, 74 aa. [WO200157190-A2, 09-AUG-2001]	7..58 22..73	38/52 (73%) 42/52 (80%)	5e-18
AAG34802	Arabidopsis thaliana protein fragment SEQ ID NO: 42406 - Arabidopsis thaliana, 56 aa. [EP1033405-A2, 06-SEP-2000]	7..58 3..54	37/52 (71%) 42/52 (80%)	1e-17

In a BLAST search of public sequence databases, the NOV37a protein was found to have homology to the proteins shown in the BLASTP data in Table 37D.

Table 37D. Public BLASTP Results for NOV37a

Protein Accession Number	Protein/Organism/Length	NOV37a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
BAB79485	RIBOSOMAL PROTEIN S29 - Homo sapiens (Human), 56 aa.	7..60 3..56	53/54 (98%) 53/54 (98%)	1e-27
P30054	40S ribosomal protein S29 - Homo sapiens (Human), 55 aa.	7..60 2..55	53/54 (98%) 53/54 (98%)	1e-27
Q90YP2	40S RIBOSOMAL PROTEIN S29 - Ictalurus punctatus (Channel catfish), 56 aa.	7..60 3..56	52/54 (96%) 53/54 (97%)	2e-27
AAL62474	RIBOSOMAL PROTEIN S29 - Spodoptera frugiperda (Fall armyworm), 56 aa.	7..60 3..56	41/54 (75%) 48/54 (87%)	6e-21
Q9VH69	CG8495 PROTEIN - Drosophila melanogaster (Fruit fly), 56 aa.	10..60 6..56	41/51 (80%) 46/51 (89%)	3e-20

Pfam analysis predicts that the NOV37a protein contains the domains shown in the Table 37E.

Table 37E. Domain Analysis of NOV37a

Pfam Domain	NOV37a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Ribosomal_S14: domain 1 of 1	7..61	17/60 (28%) 51/60 (85%)	7.5e-20

Example 38.

- 5 The NOV38 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 38A.

Table 38A. NOV38 Sequence Analysis

	SEQ ID NO: 123	2039 bp
NOV38a, CG58538-01 DNA Sequence	GCAGCACCTGCTCTGTGACTGACACTCTTGCAGAAGTGGGGCCACTTCAGGGACAT GGACAAGGTGTTGTACCTGCTGTACAGAGCCTGTTATCTGTTTCAGAAATGACCGAAGA AGCATGCCGAACACGGAGTCAGAAACGAGCGCTTGAACGGGACCCAAACAGAGGACGAT GTGGAGAGCAAGAAAATAAAATGGAGAGAGGATTGTTGGCTTCAGATTTAAACACTG ACGGAGACATGAGGGTGACACCTGAGCCGGGAGCAGGTCCAACCCAGGATTGCTGAG GGCAACAGAGGCCACGGCCATGGCCATGGGCAGAGGCGAAGGGCTGGTGGGCGATGGG CCCGTGGACATGCGCACCTCACACAGTGACATGAAGTCCGAGAGGAGACCCCTCAC CTGACGTGATTGTGCTCTCCGACAACGAGCAGCCCTCGAGCCGAGAGTGAATGGGCT GACCACGGTGGCCTTGAAGGAGACTAGCACCGAGGCCCTCATGAAAAGCAGTCCTGAA	

	GAACGAGAAAGGATGATCAAGCAGCTGAAGGAAGAATTGAGGTTAGAAGAAGCAAAAC TCGTGTTGTTGAAAAAGTTGCGGCAGAGTCAAATACAAAAGGAAGCCACCGCCAGAA GCCCCACAGGTTCTGTTGGGAGCACCGTGACCAACCCCTCCCCGCTTGTTCGGGGCACT CAGAACATTCCTGCTGGCAAGCCATCACTCCAGACCTCTTCAGCTCGGATGCCCGGCA GTGTCATACCCCCGCCCTGGTCCGAGGTGGGCAGCAGGCGCTCCTCGAAGCTGGGGCC ACAGGCGAGCTCACAGGTCGTATGCCCCCACTCGTCAGGGGGGCTCAGCAAAATCCAC AGCATTAGGCAACATTCCAGCACAGGGCCACCGCCCTCTCTGGCCCCCGGGCGT CGGTGCCAGTGTGAGATTGAGGACAGAGGATCATCCAGCAGGGCCTCATCCGCGT CGCCAATGTTCCCAACACAGCCTGCTCGTCAACATCCACAGGCCACCCAGCATCA CTGAAGGGGACAACAGCCACCTCCGCTCAGGCCAACTCCACCCCACTAGTGTGGCCT CTGTGGTCACCTCTGCCGAGTCTCCAGCAAGCCGACAGGCGGCCGCAAGCTGGCGCT GCCGAAACAGCTGGAGAAGACGCTACTCGAGATCCCCCAACCAAGCCCCAGCCCCA GAGATGAACCTTCTGCCAGCGCCGCAACAACGAGTTCATCTACCTGGTCCGCGCTGG AGGAGGTGGTGACAACCTACTGGAGACACAAGCAGGCAGGATGTCGGCCGCCACTGT GCTGTCCCGGGAGCCCTACATGTGTGCACAGTGCAGGAGCGGATTCACGTGCCGCTGG CGGGAGGAGAAGAGCGCGCCATCATGTGTGAGAACTGCATGACAACCAACCAAGA AGGCGCTCAAGGTGGAGCACACCAGCCGGCTGAAGGCCGCTTTGTGAAGGCGCTGCA GCAGGAACAGGAGATTGAGCAGCGGCTCCTGCAGCAGGGCAGGCCCTGCACAGGCC AAGCCGAGCCACCGCTGCCCCACACCCCGTGCTGAAGCAGGCTCCAGCCAGCTGT CCCCGGGTTCCGCCACGACGCCCCGAGGTGCTGTCACAGCTTCAGTCCGTACCCAA ACTGCAGAACTCAGCCTCGGCCACAGCCCTGGTCAGCAGGACCGGCAGACATTCTGAG AGAACCGTGAGCGCCGCAAGGGCAGCGCCACCTCCAACCTGGAAGAAGACGCCCTCA GCACAGGCGGGACCCTTGCGTTTGTGAGCCCAAGCCTGGCGGTGCACAAGAGCTCCTC GGCCGTGGACCGCCAGCGAGAGTACCTCCTGGACATGATCCCAACCCCGCTCCATCCCC CAGTCAGCCACGTGGAATAAGTGCAGGCCAGGCCCGCTGGAAGACGGGCTCCCTCCTC CCCCACCTGGCCCTGGTCTAGAAGGACCACTGCACCACCCTCCGCTGGCTCGGGAA GACACCGTG		
	ORF Start: ATG at 106	ORF Stop: TAG at 1933	
	SEQ ID NO: 124	609 aa	MW at 65295.8kD
NOV38a, CG58538-01 Protein Sequence	MTEACRTRSQRALERDPTEDDVESKKIKMERGLLASDLNTDGMVTPPEAGPTQ GLLRATEATAMAMGRGEGLVGDGPVDMRTSHSDMKSERPPSPDVIVLSDNEQSSPR VNGLTVALKETSTEALMKSSPEERERMIKQLKEELRLEAKLVLLKKLRQSQIQKEA TAQKPTGSGVSTVTPPLVVRGTQNI PAGKPSLQTSSARMPSVIPPPLVRGGQQASS KLGPQASSQVMPPLVRGAQQIHSIRQHSSTGPPPLLLAPRASVPSVQIQGQRIIQG LIRVANVPNTSLVNIPOPTPASLKGTTATSAQANSTPTSVASVTSAESPASRQAAA KLALRKQLEKTLLEIPPKPPAPEMNFPLPSAANNEFIYLVGLEEVQNLETOAGRMS AATVLSREPYMCAQCKTDFTCRWREEKSGAIMCENMTTNQKKALKVEHTSRLKAAPV KALQQEQEIEQRLQQGTAPAQAQAEPTAAPHVPLKQASSQLSRGSATTPRGVLHTFS PSPKLQNSASATALVSRTGRHSERTVSAGKGSATSNWKKTPLSTGGTLAFVSPSLAVH KSSAVDRQREYLLDMIIPRSIPQSATWK		

Further analysis of the NOV38a protein yielded the following properties shown in Table 38B.

Table 38B. Protein Sequence Properties NOV38a	
PSort analysis:	0.4404 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1257 probability located in mitochondrial inner membrane; 0.1257 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV38a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 38C.

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A search of the NOV39a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 39C.

Table 39C. Geneseq Results for NOV39a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV39a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB92925	Human protein sequence SEQ ID NO:11576 - Homo sapiens, 231 aa. [EP1074617-A2, 07-FEB-2001]	170..392 1..223	222/223 (99%) 222/223 (99%)	e-122
AAG75490	Human colon cancer antigen protein SEQ ID NO:6254 - Homo sapiens, 165 aa. [WO200122920-A2, 05-APR-2001]	1..67 99..165	64/67 (95%) 64/67 (95%)	1e-28
AAM78520	Human protein SEQ ID NO 1182 - Homo sapiens, 990 aa. [WO200157190-A2, 09-AUG-2001]	6..394 515..929	96/421 (22%) 182/421 (42%)	3e-12
AAM41000	Human polypeptide SEQ ID NO 5931 - Homo sapiens, 1988 aa. [WO200153312-A1, 26-JUL-2001]	70..420 852..1203	90/384 (23%) 161/384 (41%)	3e-12
AAM40999	Human polypeptide SEQ ID NO 5930 - Homo sapiens, 1988 aa. [WO200153312-A1, 26-JUL-2001]	70..420 852..1203	90/384 (23%) 161/384 (41%)	3e-12

In a BLAST search of public sequence databases, the NOV39a protein was found to have homology to the proteins shown in the BLASTP data in Table 39D.

Table 39D. Public BLASTP Results for NOV39a				
Protein Accession Number	Protein/Organism/Length	NOV39a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96H32	SIMILAR TO RIKEN CDNA 1200008O12 GENE - Homo sapiens (Human), 464 aa.	1..464 1..464	458/464 (98%) 458/464 (98%)	0.0
Q9DBZ8	1200008O12RIK PROTEIN - Mus musculus (Mouse), 462 aa.	1..464 1..462	348/464 (75%) 401/464 (86%)	0.0

Q9NVS7	CDNA FLJ10540 FIS, CLONE NT2RP2001245 - Homo sapiens (Human), 231 aa.	170..392 1..223	222/223 (99%) 222/223 (99%)	e-122
Q9CZP8	2700032M20RIK PROTEIN - Mus musculus (Mouse), 189 aa.	1..176 1..176	121/176 (68%) 150/176 (84%)	3e-63
Q9VJE5	CLIP-190 PROTEIN - Drosophila melanogaster (Fruit fly), 1690 aa.	4..439 675..1118	108/461 (23%) 203/461 (43%)	2e-16

PFam analysis predicts that the NOV39a protein contains the domains shown in the Table 39E.

Table 39E. Domain Analysis of NOV39a			
Pfam Domain	NOV39a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 40.

The NOV40 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 40A.

Table 40A. NOV40 Sequence Analysis		
	SEQ ID NO: 127	3955 bp
NOV40a, CG59346-01 DNA Sequence	TGACCCCTCGTGCCCTCCTTCCATGCTGCTGGATCTGGCGAGCTGGGGTGATT AATTGGCTATGATGATGAACGTCCCCGCGGAGGAGCGGCGCGGTGATGATGACGGG CTACAATAATGGTCGCTGTCCCCGGAATTCTCTACAGTGACTGCATTATTGAGGAG AAGACGGTGGTCCTGCAGAAAAAGACAATGAGGGCTTTGGATTCTGCTTCGAGGGG CCAAAGCTGACACACCCATTGAAGAATTCACACCAACACCGGCTTTCCAGCCCTACA GTACCTGGAGTCCCGTGGATGAAGTGGGGTGGCGTGGCAAGCCGACTAAGGACCGGG GACTTCTTGATTGAGGTAAACAATGAGAATGTGTCAAAGTCGGCCACAGGCAGGTGG TGAACATGATCCGGCAGGGAGGGAATCACCTGGTCTTAAGGTGGTCACGGTGACCAG GAATCTGGACCCCGACGACACCGCCAGGAAGAAAGCTCCCCCGCTCCAAAGCGGGCA CCGACCACAGCCCTACCTGCGCTCCAAGTCCATGACCTCGGAGCTGGAGGAGCTCG ATAAACCCGAGGAGATAGTCCCGGCTCCAAGCCCTCCCGCGCTGCTGAGAACATGGC TGTGGAACCGAGGTGGCGACCATCAAGCAGCGGCCAGCAGCCGCTTCCCGGCG GGCTCAGACATGAACGTGAGTGGCGGTACCTTGGGACACGAGGGCGGGGCGACGG TGCCCCCTAGGCTCTCTGGTTTGAGTCTGTGTACGAACGCCAAGGAATCGCCGTGAT GACGCCCCTGTTCTTGGGAGCCCAAAGCCCGTTCTGGGCATCCCTCGAGGTACG ATGCGAAGGCAGAAATCAATAGGAATAACAGAGGAAGAGCGGAGTTTCTGGCTCTTC CAATGTGAAGTTTACCAGAAGCTGTCCATGCCGACACCTCTGAGGACATCCCCC TCCACCGCAGTCTGTGCCCCCGTCCCCACCAACCTTCCCCAACCACTTACAATGC CCCAAGTCCCAACTCCAAGAGTCTACGGGACGATTAAGCTGCGTTCAATCAGATT CTGCCGCCAAGGTGTCCTCCCGCCACAGGTCCGACACCGTGGCCACCATGATGAGGGA GAAGGGGATGTAATTCAGGAGAGAGCTGGACCGCTACTCCTTGGACTCTGAAGACCTC TACAGTCGGAATGCCGGCCCGCAAGCCAATTCGCAACAGAGAGGCCAGTGCCAG AAAACCCATACTCAGAGGTGGGGAAGATCGCCAGCAAAAGCCGTCTACGTCCCCGCCAA GCCCCGAGCGGAAAGGGGATGCTGGTGAAGCAGTCCAACGTGGAGGACAGCCCCGAG AAGACGTGCTCCATCCCTATCCCGACCATCATCGTAAGGAGCCGTCACACGACGCA GCGGCAAGAGCAGCCAGGCGAGCATGGAGATCGACCCCGAGGCCCGGAGCCACC GAGCCAGCTCGGGCTGACGAAAGCCTGACCGTCAGCAGCCCCCTTTGCCGCCGCCATC GCCGGAGCCGTCCCGACCGTGAGAAGCGGCTGGAAGCCAGGAGGAATCCCCGGCCT TCCTCTCCACAGACTGGGGGATGAGGATGTGGGCTGGGGCCACCCGCCCCAGGAC GCGGCCCTCATGTTCCCCGAGGAGGGGATTTGCTGACGAGGACAGCGCTGAGCAG CTGTATCCCCATGCCAGTGCCACGCCAGGGAGCCGAAAACCATTTCTGGGTG GCGCCGAGGCCAGTGCTCCGGGTGAGGTGGGAGGCCGCTGAATTCACGCTCAAAGC	

	CCAGGGGCCCGAGAGCAGCCAGCAGTGCCTCCGCGAGCAGCGGCACAGCCGGCCCC GGGAATTATGTCCACCCACTCACAGGGCGGCTGCTTGATCCAGCTCCCCGCTGGCCC TGGCACTCTCCGCAAGGGACCGAGCCATGAAGGAGTCTCAACAGGGACCCAAAGGGGA GGCCCCAAGGCCGACCTCAACAACCTCTTTACATTGATACCAAAATGCGGCCAGC CTGGATGCCGGCTTCCCTACGGTCACAGGCAGAACCCCGGGGACCCTGAGGCGGC AGGAGACGGAGAACAGTACGAGACCGACTGGGCCGAGACCGGAAGGCGATGACAA GAAGAACATGCTGATCGACATCATGGACACGTCCAGCAGAAGTCCGCTGGCTGCTG ATGGTGACACCGTGGACGCCACTAAGCTGGACAAACCCCTGCAGGAAGAGGACGAGA AGGCAGAGGTGGAGATGAAGCCAGACAGCTCGCCGTCGAGGTGCCAGAAGGTGTTTC CGAAACCGAAGGTGCTTTACAGATCTCCGCTGCCCGGAGCCACCACCGTCCCGGC AGAACCATCGTCGGGTGGCTCCATGGAAGAGGCGGTGATTTTGCCATTCCGCATCC CTCCTCCCCCTCGGCATCCGTGGACTTGGATGAGGATTTTATTTTACAGAGCCATT GCCTCCTCCCCTGGAATTTGCAAATAGTTTGTATATCCCCGATACCGGGGAGCTTCT GTCCCCGCTCTCTCAGACTTAGTGAAGCAGAAGAAAAGCGACACCCCTCAGTCCCCTT CGTTGAACTCCAGCCAACCAACCACTCTGCAGACAGCAAGCCAGCCAGTCTTTTC AAACTGTCTGCCTGCCTCATCTCTGCCACCCCTGAAAGCTTTGACGCCGTGCGCGAC TCTGGGATCGAGGAGGTGGACAGCCGGAGTAGCAGCGACCACCCTCGAGACGACCA CGACTATCTCCACCGTGTCTAGCATCTCCACCTGTCTTCCGAAGGTGGAGGAATGT GGACACCTGCACAGTCTATGCAGATGGGCAAGCATTTATGGTTGACAAACCCCAAGTA CCTCCTAAGCCAAAATGAAGCCCATATTACAAAAGCAATGCACCTTTATCAAGACG CGCTCGTGAAGAAGATGTAGATAGCTTTGTTATCCCCCGCCCGCTCCCGCCCTCC GCCGGGAGTGCCAGCCTGGGATGGCAAGGTTCTCCAGCAAGGACCTCCAAGTTG TGGGGCGACGTCACAGAGATCAAAGCCCGATTCTCTCAGGCCCAAAGGCAACGTTA TTAGTGAATTGAACTCTATCTACAGCAAATGAACCGAGAGAGAATTCGAGGAGGAG GGAAGGACTGGATTACCAATGGGAGCCAAGTCCGCCAGCCTCGCTCCAAGAGCCCG GAGATCATGAGCACCATCTCAGGTACACGGAGCAGCAGGTCACCTTCACTGTTCCGC CGGCACCTCCAGCCCATCACCTGCAGAGCCGGCCCGCCCGATGGAAGAGCCGAC CTCAGGAACAAGACGTGCCCAAGCCCTGTGGTCTCGCAACAGAGATGAACAAAGAG ACCCTGCCCGCCCCCTGTCTGTCTGCCACCGCTCTCCTTCTCCCGCTCTCTCAGATG TCTTTAGCTTCCAAGCAGCCCCCTTCTGGGGATCTATTGGCTTGAACCGCGGG ACGCAGTAGGTGCGCATCCCCCTCGATACTGCAACAGCCAATCTCAAATAAGCCTTTT ACAACTAAACCTGTCCACCTGTGGACTAAACAGATGTGGCCGATTGGCTGGAAAGTC TAAACTTGGGTGAACATAAAGAGGCCCTCATGGACAATGAGATCGATGGCAGTCACTT ACCAAACCTGCAGAAGGAGGACCTCATCGATCTTGGGGTAATCGAGTCGGGCACAGA ATGAACATAGAAAGGGCTTTGAAACAGCTGCTGGACAGATAAGGACGGCTGCTCTCCA CCTCGCAGACTGCTCTTGTATAGTAGATGGGCTCGTGCTGAACATCTGAATGC CAAGCGAAGTC		
	ORF Start: ATG at 67	ORF Stop: TAA at 3868	
	SEQ ID NO: 128	1267 aa	MW at 136108.7kD
NOV40a, CG59346-01 Protein Sequence	MMMNVPGGGAAAVMMTGYNNGRCPRNSLYSDCIIEEKTVVVLQKDNNEGFGFVLRGAKA DTPIEEFTPTPAFPALQYLESVDEGGVAVQAGLRTGDFLIEVNNENVVKVGHRRQVNM IRQGGNHLVLKVVTVTRNLDPDDTARKKAPPPKRAPTTALTLRSKSMTSELELDKP EEIVPASKPSRAAENMAVEPRVATIKQRPSSRCFPAGSDMNVSGRTLGRPRGRPTVPP RLSGLQSVYERQGIAMVPTVPSPKAPFLGIPRGTMRRQKSIGITEERQFLAPML KFTRSLMPDTSEDI PPPPQSVPPSPPPSPPTTYNCPKSPTPRVYGTIKPAFNQNSAA KVSPATRSDTVATMMREKGMVFRRRLDRYSLDSEDLYSRNAGPQANFRNKRQMPENP YSEVGKIASKAVYVPAKPARRKGMVLVKQSNVEDSPEKTCIPIPTIIIVKEPSTSSSGK SSQGSSMEIDPQAPPEPSSQLRPDES LTVSSPFAAAIAGAVRDREKRLREARRNSPAFLS TDLGDEVDVGLPPAPRTRPSMFPEEGDFADEDSAEQLSSPMPSPATPREPENHFVGGAE ASAPGEAGRPLNSTSKAQPESSPAVPSASSGTAGPGNYVHPLTGRLLDPSSPLALAL SARDRAMKESQGGPKGEAPKADLNKPLYIDTKMRPSLDAGFPVTTRQNTGRPLRRQET ENKYETDLGRDRKGGDDKKNMLIDIMDTSQQKSAGLLMVHTVDATKLDNALQEEDEKAE VEMKPDSSPSEVPEGVSETEGALQISAAPEPTTVPGRTIVAVGSMEEAVILPFRIPPP PLASVDLDEDIFITEPLPPPLEFANSFDIPDDRAASVPALS DLVKQKSDTPQSPSLN SSQPTNSADSKKPAASLNCPLPASFLPPPESSFDAVADSGIEEVDSSSSDHHLETTSTI STVSSISTLSSEGGENVDTCTVYADGQAFMVDKPPVPPKPKMKPIIHKSNALYQDALV EEDVDSFVI PPPAPPPPGSAQPGMAKVLQPRTSKLWGDVTEIKSPI LSGPKANVISE LNSILOQMNRKLAKEGGLDSPMGAKSASLAPRSPPEIMSTISGTRSTTVTFTVRPGT SQPITLQSRPPDYESTSGTTRRAPSPVVSPTENMKETLPAPLSAATASPSALSDFVS LPSQPPSGDLFGLNPAGRSRSPSPSILQQPISNKPFTTKPVHLWTKPDVADWLESNLN GEHKEAFMDNEIDGSHLPNLQKEDLIDLGVTRVGHMNIERALKQLLDR		

Further analysis of the NOV40a protein yielded the following properties shown in Table 40B.

Table 40B. Protein Sequence Properties NOV40a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV40a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 40C.

Table 40C. Geneseq Results for NOV40a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79240	Human protein SEQ ID NO 1902 - Homo sapiens, 1248 aa. [WO200157190-A2, 09-AUG-2001]	14..1267 1..1248	1231/1271 (96%) 1231/1271 (96%)	0.0
AAB31518	Amino acid sequence of the rat Shank2 polypeptide - Rattus sp, 1470 aa. [WO200078921-A2, 28- DEC-2000]	30..1267 240..1470	1078/1255 (85%) 1132/1255 (89%)	0.0
AAM80224	Human protein SEQ ID NO 3870 - Homo sapiens, 1161 aa. [WO200157190-A2, 09-AUG-2001]	172..1267 82..1161	1071/1103 (97%) 1071/1103 (97%)	0.0
AAB31517	Amino acid sequence of the rat Shank3a polypeptide - Rattus sp, 1740 aa. [WO200078921-A2, 28- DEC-2000]	18..1264 550..1737	496/1349 (36%) 673/1349 (49%)	0.0
AAY83017	Rat shank 3a - Rattus rattus, 1740 aa. [WO200011204-A2, 02- MAR-2000]	18..1264 550..1737	496/1349 (36%) 673/1349 (49%)	0.0

- 5 In a BLAST search of public sequence databases, the NOV40a protein was found to have homology to the proteins shown in the BLASTP data in Table 40D.

Table 40D. Public BLASTP Results for NOV40a				
Protein Accession Number	Protein/Organism/Length	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UPX8	KIAA1022 PROTEIN - Homo sapiens (Human), 1131 aa (fragment).	124..1267 1..1131	1121/1154 (97%) 1121/1154 (97%)	0.0
Q9QX93	PROLINE RICH SYNAPSE ASSOCIATED PROTEIN 1 - Rattus norvegicus (Rat), 1252 aa.	2..1267 1..1252	1103/1276 (86%) 1158/1276 (90%)	0.0
O70470	CORTACTIN-BINDING PROTEIN 1 - Rattus norvegicus (Rat), 1252 aa.	2..1267 1..1252	1102/1276 (86%) 1158/1276 (90%)	0.0
Q9WUV9	PROLINE RICH SYNAPSE ASSOCIATED PROTEIN 1 - Rattus norvegicus (Rat), 1259 aa.	2..1267 1..1259	1103/1283 (85%) 1158/1283 (89%)	0.0
Q9WUW0	PROLINE RICH SYNAPSE ASSOCIATED PROTEIN 1 - Rattus norvegicus (Rat), 1250 aa.	2..1267 1..1250	1095/1276 (85%) 1151/1276 (89%)	0.0

PFam analysis predicts that the NOV40a protein contains the domains shown in the Table 40E.

Table 40E. Domain Analysis of NOV40a			
Pfam Domain	NOV40a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PDZ: domain 1 of 1	38..131	23/97 (24%) 70/97 (72%)	1e-07
SAM: domain 1 of 1	1202..1265	27/68 (40%) 53/68 (78%)	9.8e-22

Example 41.

- 5 The NOV41 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 41A.

Table 41A. NOV41 Sequence Analysis

	SEQ ID NO: 129	2069 bp
NOV41a, CG57814-01 DNA Sequence	<p>GGACACTGACATGGACTGAAGGAGTAGAAAGCACTATAAATGTCTTTCTTATCTGTG TGACTCTTATCTCACTGTTCTATTTTCTCCTCATTATATTAACCTTTCTTACC TTTTTTTCTGAACCTTAGGCCTTCTCTTCCAGAACTGGTGGAAGACAAATGAAACG GCCAAGATGGTAAGAAACAAGCCGCACTTTCTCCTGGGGAGACTGATAATTTAAAGG TTTGTGTGTGAGAAACATTCCAGCTTCATCACCAACCTTTCTTCCACCTCTGCC CACTGGAGACCCTTACATCCCGAAGCGGACGCGGAGCTGAAGTCAGGAAACCATGC ATCACATTAGCAGGAGCAACTGCAGACTTTAACTCCGTTCAACATGTGGATGCGGC AGAGAAATGACCTGTCCAGACAAGCCGGGGCAGCTCATAACTGGTTGATCTGCTCCC TGTGCGTCCCGGGTGCCTAAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGAGAAA CCTTCTGCTGGGCACTGCGTGTGCCATCTACTTGGGCTTCTGGTGAGCCAGGTGGGG AGGGCCTCTCTCCAGCATGGACAGCGGGTGAGAAGGGGCCACATCGCAGCCGCGACA CCGCCGAGCCATCCTTCCCTGAGATACCCCTGGATGGTACCTTCCAGAGTC CCAGGGCAATGGTCCACTCTGCAGCCCAATGTGGTGTACATTACCTACGCTCCGAG CGCAGCAAGCCGCGCAATATCCGTGGCACCCTGAAGCCCAAGCGCAGGAAAAGCATG CAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTTGGTGGGACCATCCCTTCAGCCGCA GGAAGCGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAACTG GTTAAGATTGGAGAGCGACCTGGAGGTTGGTGCGGGGTCCGGGAGTGCAGCCGGGG GCCCAGACTTCTGCAGCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAG CGCCCCCTCTGGCTGAGCAAGATGACATCCGAAGAAATGCGACTCTTGGCGGACAGC GCAGTGGCAGGGCTCCGGCTGTGTCTCTAGGAGCGGAGCCGCTTTGCTGGTGTG AGGGGGGCGCACTGGCGCTGTGCTCCGCTGTGGCCCTAGCCCTGTGGGCTTCTCAA GCAGCCCTTGGACATGAGTGAGGTGTTGCTTCCACCTAGACAGGATCCTGGGGCTC AACAGGACCTTCCGTCTGTGAGCAGGAAAGCAGAGTTTATCCAAGATGGCCGCCCAT GCCCCATCATTCTTTGGGATGCATCTTATCTTCCAGCAAGTAATGACACCCATTCTTC TGTTAAGCTCACCTGGGGAATTTATCAGCAGTTGCTGAAACAGAAATGCTGGCAGAAT GGCCGAGTACCAAGCCTGAATCAGGTTGTACTGAAATACATCATGAGTGGTCCA AGATGGCACTCTTTGATTTTGTGTACAGATTATAATCGCTTAGATACAAATGTCTG TGGATTACAGACTCGCAAGGAAGATGCCTGTGTACAGAATGGATTGAGGCCAAAATGT GATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAGCATGACCCAAGGC ATTTGGTTTTTATAGACAACAAGGTTTCTTTGACAGGAGTGAAGATAACTTAACTT CAAATTGTTAGAAAGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTGAAGAGC CAGCACTTACGGCAGAACTTCTTCACTCTCTGTTTCTTGATAAAGTGTATTGGGAAA GTCAAGGAGGTAGACAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAA AATCTTATACCTATATCAATGCACACGGGGTCAAAGTATTACCTATGAATGAATGA CAAAGAATCTTCTGGCTAGGGTGTGTAGATATATTATGCAATTTTGGTTTTGTTTT AAATCAAGCACATCAACCTCAAGCCGTTTAGCAATGAG</p>	
	ORF Start: ATG at 413	ORF Stop: TGA at 1970
	SEQ ID NO: 130	519 aa MW at 57552.4kD
NOV41a, CG57814-01 Protein Sequence	<p>MTCPKPKQLINWFCISLCVPRVRKLWSSRRPRTRNLLLTACAIYGLFLVSQVGRA SLQHGOAEKGPHRSDTAEPSPFPEIPLDGLTAPPESSQNGSTLQPNVVIITLRSERS KPNANIRGTVPKRRKKHAVASAPGQALVGPSPLOPQEAAREADAVAPGYAQAALVK IGERPWRILVRGPGVRAGGPDFLPSSRESNIRIYESAPSWSLKDDIRMRLLADSAV AGLRPVSSRSRGLLLVLEGGAPGAVLRCPSPCGLLKQPLDMSVFAHLDIRLGLNR TLPVSVRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTWGTYYQLLKQKQWQNR VPKPESGCTEIIHHEWSKMAFLDFLLQIYNRLDTNCCGFRPRKEDACVQNGLRPKCDD QGSAAALAHIIQRKHDPRHLVFI DNKGFFDRSEDNLFKLEGIKEFPASAVSVLKSQH LRQKLLQSLFLDKVYWESQGGRGIEKLIDVIEHRAKILITYINAHGVKVLPMNE</p>	
	SEQ ID NO: 131	1740 bp
NOV41b, CG57814-02 DNA Sequence	<p>GGCAGCTGAAGTCAGGAAACCATGCATCACATTAGCAGGAGCCAACTGCAGACTTTAA ACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGTCCAGACAAGCCGGGGCAG CTCATAAAGTGGTTCACTGCTCCTGTGCGTCCCGGGGTGCGTAAGCTCTGGAGCA GCCGGCGTCCAAGGACCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCCATCTACTT GGGCTTCTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACGCGGCTGAG AAGGGGCCACATCGCAGCCCGACACCGCGAGCCATCTCTCCCTGAGATACCCCTGG ATGGTACCTTGGCCCCCTCCAGAGTCCAGGGCAATGGGTCCACTCTGCAGCCCAATGT GGTGATACATTACCTACGCTCCAAGCGCAGCAAGCCGCAATATCCGTGGCACCCTG AAGCCCAAGCGCAGGAAAAAGCATGCAGTGGCATCGGCTGCGCAAGGGCAGAGCCTT TGGTCCGACCATCCCTTCAAGCGCAAGAGCGGCAAGGGAAGCTGATGCTGTAGCACT GGGTACGCTCAGGAGCAAACTGGTTAAGATGGAGAGCGACCCTGAAGGTGGTGCGGGG TCGGGAGTGCGAGCCGGGGGCCAGACTTCTGCGAGCCAGCTCCAGGGAGAGCAACA TTAGGATCTACAGCGAGAGCGCCCCCTCTGCTGAGCAAGATGACATCCGAAGAAT CGGACTCTTGGCGGACAGCGCAGTGGCAGGGCTCCGGCTGTGTCCTTAGGAGCGGA GCCCGTTTGTGCTGGAGGGGGCGCACCTGGCGCTGTGCTCCGCTGTGGCCTTA GCCCTGTGGGCTTCTCAAGCAGCCCTTGGACATGAGTGGGTGTTGCTTCCACCT AGACAGGATCCTGGGGCTCAACAGGACCTTCCGCTCTGTGAGCAGGAAAGCAGAGTTC</p>	

Table 41D. Geneseq Results for NOV41a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV41a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU12276	Human PRO6001 polypeptide sequence - Homo sapiens, 519 aa. [WO200140466-A2, 07-JUN- 2001]	1..519 1..519	518/519 (99%) 519/519 (99%)	0.0
AAM39125	Human polypeptide SEQ ID NO 2270 - Homo sapiens, 519 aa. [WO200153312-A1, 26-JUL- 2001]	1..519 1..519	518/519 (99%) 519/519 (99%)	0.0
AAM40911	Human polypeptide SEQ ID NO 5842 - Homo sapiens, 537 aa. [WO200153312-A1, 26-JUL- 2001]	1..519 19..537	491/527 (93%) 495/527 (93%)	0.0
AAM41373	Human polypeptide SEQ ID NO 6304 - Homo sapiens, 479 aa. [WO200153312-A1, 26-JUL- 2001]	212..512 161..471	130/316 (41%) 180/316 (56%)	1e-64
AAM39587	Human polypeptide SEQ ID NO 2732 - Homo sapiens, 397 aa. [WO200153312-A1, 26-JUL- 2001]	212..512 79..389	130/316 (41%) 180/316 (56%)	1e-64

In a BLAST search of public sequence databases, the NOV41a protein was found to have homology to the proteins shown in the BLASTP data in Table 41E.

Table 41E. Public BLASTP Results for NOV41a				
Protein Accession Number	Protein/Organism/Length	NOV41a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9ET25	HYPOTHETICAL BASIC PROTEIN I-19 - Mus musculus (Mouse), 517 aa.	1..519 1..517	431/519 (83%) 462/519 (88%)	0.0
Q9NYZ0	AD021 PROTEIN - Homo sapiens (Human), 246 aa.	274..519 1..246	246/246 (100%) 246/246 (100%)	e-145
Q9UFP1	HYPOTHETICAL 49.5 KDA PROTEIN - Homo sapiens (Human), 448 aa (fragment).	212..512 130..440	129/316 (40%) 179/316 (55%)	2e-63

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Pfam Domain	NOV41a Match Region	Identities/ Similarities for the Matched Region	Expect Value
SQS_PSY: domain 1 of 1	109..145	8/37 (22%) 29/37 (78%)	9.9

Example 42.

5

Table 42A. NOV42 Sequence Analysis			
	SEQ ID NO: 133	1294 bp	
NOV42a, CG59327-01 DNA Sequence	<p>GATGGCCACCTTGAACGTTGACTGATGTTGATGCCCTTGCCCAGTACATTTTCCAT TGTTTTATACTGTGTCTACTGAAGTACTTGTGTGCAGAGTATGGCTGGAGGAATGCCA TGTTGATCCAAGGCGCGCTTTTCCTTAAACCTGTTTGTTTTTGGGACCCCTCATGAGGCC CCTCCCTCTGGGAAAAACCCAAATGACCCAGAAAGAGAAGATCTGCGCGTCTGCCC CGCACTCCACAGAGTCTGTAATGTCAAATGGACAGCAGGGAAGAATAGAAGAGAAG ATGGCGGGTCTGGGAACGAGGAGACCCTCTGTGACCTGCAAGCCCAGGAGTGCAAGCC CAGGAGTGCCTCGATCAGGCCAGATCATGTGCGCTTTCCGGTCTGTAAGACGGTCAGC TGGCTCATTATGAGAGTCAAGAAGGCTTCGAGGATTGGTACTCAGGCTATTTTGGGA CAGCCAGCCTATTTACAAATCGAATGTTTGTAGCCTTTGTTTTCTGGGCTTCATTGTC ATACAGCAGCTTTGTCATCTCCTTTATTTCATCTCCAGAAATCGTCAATTTGTATAAC TTATTGGAGCAAACGAAGGTTTCCCTCTGACTTCAATTATAGCAATAGTTCACATTG TTGGAAGAGTGATCTCTGGGCGTCATAGCTGACTTACCTTGTCATCAGTGTGGAATGT CTTCCTGTGTGGCAGCTTCGTTCTGTCTCCTCAGTATTTTGTTTTGCTGCCTTTGATG CATATGTACGCTGGCCTGGTGGTCATCTGCACACTGACAGGGTTTCCAGCGGTTATT TCTCCCTAATGCCCATAGTGACTGAAGACTTGGTTGGCATTGAACATTTGGCCAAATGC CTACGGCATCATCATCTGTGCTAATGGCATCTCTGCGTGTGTGGGACCACTTTTGGCA GGTAAACTGTCTGAGGTTTTAAGAGTTTCATAGTGCATATAGATACGGTGTGTTAGCTC TGCGAGGAGACGGATGCAGAGCACTCATCTTCTCTTATACATAGAAGTGAATGGC TTTCTAAAGTTAGATCACTGGCCAGAGTTTTGAGTCACAAGAGCTATTCCACAGATT TCCTTTGAAAAACAATCACCCTGGCAGTCCACTTCAGTGACACGAATGGGTTGCA GAACCTGCTTACTTATGTGACACATTCAACCTGCTCAATGAACCTCAATCTGTCACTTC AGGGGAGAAGGACAACCTGTGTTCAAGTCAGCAAATAAAGTGGCTACATTCAAAACCA ACTGGAATTACGGGGGTG</p>		
	ORF Start: ATG at 2	ORF Stop: TAA at 1049	
	SEQ ID NO: 134	349 aa	MW at 38694.2kD
NOV42a, CG59327-01 Protein Sequence	<p>MATLNVVLMPLAQYIFHCFITVLLKYLCAEYGRNAMLIQGAVSLNLFVFGTLMRP LPFGKPNPDPEEKDLRVLPASTESVMSNGQQGRIEEKDGGSGNETLCDLQAQCKP RSAPIRPDHVRFPVLKTVSWLIMRVKKGFEWDYSGYFTGASLFTNRMFVAFVFWASFA YSSFVISFIHLPEIVNLYNLLLEQTKVFPLTSIIAIVHIVGKVLGVIALDLPICISVNV FLLASFVLVLSIFVLLPLMHMYAGLVVICTLTGFSFGYFSLMPITVEDLVGIEHLANA YGLIICANGISALLGPPFAGKLEVLRVHSAYRYGVLAALRGDGCRLTSSLIHRSEMA F</p>		

Table 42B.

Table 42B. Protein Sequence Properties NOV42a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 32 and 33

A search of the NOV42a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 42C.

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV42a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAO07132	Human polypeptide SEQ ID NO 21024 - Homo sapiens, 107 aa. [WO200164835-A2, 07-SEP-2001]	257..331 5..81	49/77 (63%) 58/77 (74%)	6e-20
AAY31642	Human transport-associated protein-4 (TRANP-4) - Homo sapiens, 465 aa. [WO9941373-A2, 19-AUG-1999]	157..342 221..401	54/197 (27%) 86/197 (43%)	1e-07
AAY02737	Human secreted protein encoded by gene 88 clone HKAFB88 - Homo sapiens, 229 aa. [WO9902546-A1, 21-JAN-1999]	198..342 24..164	41/147 (27%) 65/147 (43%)	9e-06

In a BLAST search of public sequence databases, the NOV42a protein was found to have homology to the proteins shown in the BLASTP data in Table 42D.

Table 42D. Public BLASTP Results for NOV42a				
Protein Accession Number	Protein/Organism/Length	NOV42a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96NI7	CDNA FLJ30794 FIS, CLONE FEBRA2001093, WEAKLY SIMILAR TO MONOCARBOXYLATE	22..331 1..310	250/312 (80%) 266/312 (85%)	e-138

	(Human), 336 aa.			
Q9D1K0	1110004H10RIK PROTEIN - Mus musculus (Mouse), 336 aa.	22..331 1..310	220/312 (70%) 250/312 (79%)	e-119
AAL39716	LD30953P - Drosophila melanogaster (Fruit fly), 894 aa.	142..314 665..843	50/180 (27%) 89/180 (48%)	2e-15
Q9V9B3	CG3409 PROTEIN - Drosophila melanogaster (Fruit fly), 800 aa.	142..314 571..749	50/180 (27%) 89/180 (48%)	2e-15
Q9W0L6	CG13907 PROTEIN - Drosophila melanogaster (Fruit fly), 816 aa.	157..331 565..738	55/178 (30%) 91/178 (50%)	1e-14

Pfam analysis predicts that the NOV42a protein contains the domains shown in the Table 42E.

Table 42E. Domain Analysis of NOV42a			
Pfam Domain	NOV42a Match Region	Identities/ Similarities for the Matched Region	Expect Value
oxidored_q3: domain 1 of 1	197..314	25/177 (14%) 73/177 (41%)	9.1

Example 43.

The NOV43 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 43A.

Table 43A. NOV43 Sequence Analysis			
	SEQ ID NO: 135	455 bp	
NOV43a, CG59494-01 DNA Sequence	TAGAACTGTGTTGAGCTCTCACCCATCAGCATGAGCAACAAATCTTGGGAACCTGGAAGCTGGTCTCCAGTGAAAACCTTGAGGATTACATGAAAGAACTGGGAGTGAATTCGCGAGCCCGGAACATGGCAGGGTTAGTGAAACCGACAGTAACATTAGTGTTGATGGGAAAATGATGACCATAAGAACAGAAAGTTCTTCCAGGACACTAAGATCTCCTTCAAGCTGGGGGAAGAATTTGATGAAACTACAGCAGACAACCGGAAAGTAAAGAGCACCATAACATTAGAGAATGGCTCAATGATTCACGTCCAAAAATGGCTTGGCAAAGAGACAACAATCAAAAGAAAAATTGTGGATGAAAAAATGGTAGTGAATGTAAATGAATAATATTGTCAGCACCGAATCTACGAAAAGGTCTGAAAAATCATTCTTCATTGAAGTGGCT		
	ORF Start: ATG at 31	ORF Stop: TGA at 427	
	SEQ ID NO: 136	132 aa	MW at 15096.4kD
NOV43a, CG59494-01 Protein Sequence	MSNKFLGTWKLVSSENFEDYMKELGVNFAARNMAGLVKPTVTISVDGKMMTIRTESSFQDTKISFKLGEEDFETADNRKVKSTITLENGSMIHVQKWLGETTIKRKIVDEKMOVVECKMNNIVSTRIYEKV		

Further analysis of the NOV43a protein yielded the following properties shown in Table 43B.

Table 43B. Protein Sequence Properties NOV43a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0053 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV43a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 43C.

Table 43C. Geneseq Results for NOV43a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV43a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW40227	Human myelin P2 protein - Homo sapiens, 136 aa. [WO9803647-A2, 29-JAN-1998]	1..130 1..130	89/130 (68%) 107/130 (81%)	2e-47
AAW40228	Bovine myelin P2 protein - Bos taurus, 136 aa. [WO9803647-A2, 29-JAN-1998]	1..130 1..130	89/130 (68%) 106/130 (81%)	9e-47
AAY90320	Human AFABP protein sequence - Homo sapiens, 132 aa. [WO200047734-A1, 17-AUG-2000]	1..131 1..131	84/131 (64%) 110/131 (83%)	3e-46
AAY90319	Mouse AFABP protein sequence - Mus sp, 132 aa. [WO200047734-A1, 17-AUG-2000]	1..131 1..131	83/131 (63%) 108/131 (82%)	7e-45
AAG66576	Mouse MDGI polypeptide - Mus sp, 133 aa. [US6232291-B1, 15-MAY-2001]	1..131 1..131	73/131 (55%) 103/131 (77%)	6e-40

- 5 In a BLAST search of public sequence databases, the NOV43a protein was found to have homology to the proteins shown in the BLASTP data in Table 43D.

Table 43D. Public BLASTP Results for NOV43a

Protein Accession Number	Protein/Organism/Length	NOV43a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
MPRB2	myelin P2 protein - rabbit, 132 aa.	1..132 1..132	95/132 (71%) 109/132 (81%)	3e-49
P02691	Myelin P2 protein - Oryctolagus cuniculus (Rabbit), 131 aa.	2..132 1..131	94/131 (71%) 108/131 (81%)	1e-48
MPHU2	myelin P2 protein [validated] - human, 132 aa.	1..132 1..132	92/132 (69%) 109/132 (81%)	3e-48
Q90X56	ADIPOCYTE FATTY ACID BINDING PROTEIN - Gallus gallus (Chicken), 132 aa.	1..131 1..131	86/131 (65%) 113/131 (85%)	1e-47
P02689	Myelin P2 protein - Homo sapiens (Human), 131 aa.	2..132 1..131	91/131 (69%) 108/131 (81%)	1e-47

PFam analysis predicts that the NOV43a protein contains the domains shown in the Table 43E.

Table 43E. Domain Analysis of NOV43a

Pfam Domain	NOV43a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lipocalin: domain 1 of 1	4..132	45/157 (29%) 113/157 (72%)	3.2e-36

Example 44.

- 5 The NOV44 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 44A.

Table 44A. NOV44 Sequence Analysis

Table 44A. NOV44 Sequence Analysis		
	SEQ ID NO: 137	1561 bp
NOV44a, CG59432-01 DNA Sequence	AAGAATTGTAGCTCTCCACTGAATTGCAGGGGTTCTTGAATGTTGTCAACATTGGAG GCAGTTGGAGGAGGGAGCTCTATTGATGAAAAATGGCTACATATTCAAATTTTCAGTG TATACCAGGAAGATAATTCAATTCAATCTCTGGCTTACCCAAAGAATCTTGGAGTTAC TGCCAATGAGGAAATCCCGAGGTCTAATAAAAATATCTTAGGAGTGAAGGAGTTAA CTGAGTGTGTAAGCTTTATCTTCTGTCCAAATGGACTTGTGGTTTGCTTATAAACTCT CCAGTAAATAATTGTTAGAGACCTGTCAATTGATAGCAGTTGCTAGTTGCTGCCTTTTA AGAGCTCGTTGATTCCTCTGCAAGGTGGTGCAGCATCCTCTGTCCCTTCATTCAATTC AGATCTACTCAGGTCTCCCTGTAAACAGATCTCTCGGATCAATAAGCATGAATGACGA AGACTACAGCACCATCTATGACACAATCCAAATGAGAGGACGTATGAGGTTCCAGAC CAGCCAGAAGAAATGAAAGTCCCCATTATGATGATGTCCATGAGTACTTAAGGCCAG AAAATGATTATATGCCACTCAGCTGAATACCCATGAGTATGATTTGTGTCACTCTA	

	TACCATTAAAGGGTGAAGAGACCAGCTTGGCCTCTGTCCAGTCAGAAGACAGAGGCTAC CTCCTGCCTGATGAGATATACTCTGAACTCCAGGAGGCTCATCCAGGTGAGCCCAGG AGGACAGGGGCATCTCAATGGAAGGGTTATATTCATCAACCCAGGACCAGCAACTCTG CGCAGCAGAACTCCAGGAGAATGGGAGTGTGATGAAGGAAGATCTGCCTTCTCCTTCA AGCTTCACCAATTACAGCACAGTAAGGCCTTCTCTACCACCAAGTATTCCTGCTATTCTG ATGCTGAAGGTTTGGAAAGAAAAGGAGGGAGCTCACATGAACCTGAGATTTACCTCTT TGTGAAGGTAAAGTCTGCCTCTGACAGGCATACCCCTGTTTCATGCAGATATTATGGCTG GTGTTTTATTTTGTCTCTGAATGACCAGGGAAGATTCTAATGCCATGGTCTTGGAT CTCAATACATATTACAGGAGTCGGAGGGACTAAATCAGTCATTAGAGTGTACTCAGCTC TTCACAAAATTAGAGGAATTGGAAGGTGCATTTAAAGCAGCTATTTAATCACTGACTT TTACATACCATGGGCAAAGTATTTTTCAAACCGGTTTCACATAAGTGAGGCATAACTGC TGCCCAAATCCTTGCCATTGTGGCTGACATTAAGTACATTTTTCTGCTCTGGTTAAATT TCCTTTGTGCGACATGTTTAAAGTGAACCAAAGCTTGTGAAAGAAAGACCTTCTTGT GCTTCTAAGGTACAGATTTGTCTAGATAGGTGGTCAATAAAGGCTATCTCTGTCTACTA GCTTGCCCTTTTGGCACCAATATACTAAAAATTTGATGAAGTCAAATGATTTTCAGTA GTAGTAAGACACTACCAGTGTTAATGTTTAACTACTACGATATCTAAACAGAA		
	ORF Start: ATG at 454		ORF Stop: TAA at 1132
	SEQ ID NO: 138	226 aa	MW at 26132.2kD
NOV44a, CG59432-01 Protein Sequence	MNDEDYSTIYDTIQNERTYEVDPQPEENESPHYDDVHEYLRPENDLYATQLNTHEYDF VSVYTIKGEETSLASVQSEDRGYLLPDEIYSELQEAHPGEPOEDRGISMEGLYSSTQD QQLCAAELQENGSMKEDLPSPSSFTIQHSAFSTTKYSCYSDAEGLEEKEGAHMNPE IYLFVKVRSASDRHTLFMQILWLVFYFALNDQGKIHNAMVLGSQYIFRSRRD		
	SEQ ID NO: 139	809 bp	
NOV44b, CG59432-02 DNA Sequence	ATCCTCTGTCCTTCATTTCATTTCAGATCTACTCAGGTCTCCCTGTAAACAGATCTCT CGGATCAATAAGCATGAATGACGAAGACTACGGCACCATCTATGACACAATCCAAAAT GAGAGGACGTATGAGGTTCCAGACCAGCCAGAAGAAAATGAAAGTCCCATTTATGATG ATGTCCATGAGTACTTAAGGCCAGAAAATGATTTATATGCCACTCAGCTGAATACCCA TGAGTATGATTTTGTGTCTAGTCTATACCATTAAAGGTGAAGAGACCAGCTTGGCCTCT GTCCAGTCAGAAGACAGAGGCTACCTCCTGCCTGATGAGATATACTCTGAACCTCAGG AGGCTCATCCAGGTGAGCCCCAGGAGGACAGGGGCATCTCAATGGAAGGGTTATATTC ATCAACCCAGGACCAGCAACTCTGCGCAGCAGAACTCCAGGAGAAATGGGAGTGTGATG AAGGAAGATCTGCCTTCTCCTTCAAGCTTCACCATTCAGCAGCAGTAAGGCCCTTCTCTA CCACCAAGTATTCTGCTATTCTGATGCTGAAGGTTTGAAGAAAAGGAGGAGCTCA CATGAACCTGAGATTTTACCTCTTTGTGAAGGTAAGGTCTGCCTCTGACAGGCATACC CTGTTTCATGAGATATTATGGCTGGTGTGTTTTATTTGTCTCTGAATGACAGGGAAGA TTCATAATGCCATGGTCTTGGATCTCAATACATATTCAGGAGTCGGAGGGACTAAAT CAGTCATTAGAGTGACTCAGCTCTTCAAAAATTAGAGGAATTGGAAGGTGCAT		
	ORF Start: ATG at 72		ORF Stop: TAA at 750
	SEQ ID NO: 140	226 aa	MW at 26102.2kD
NOV44b, CG59432-02 Protein Sequence	MNDEDYGTIYDTIQNERTYEVDPQPEENESPHYDDVHEYLRPENDLYATQLNTHEYDF VSVYTIKGEETSLASVQSEDRGYLLPDEIYSELQEAHPGEPOEDRGISMEGLYSSTQD QQLCAAELQENGSMKEDLPSPSSFTIQHSAFSTTKYSCYSDAEGLEEKEGAHMNPE IYLFVKVRSASDRHTLFMQILWLVFYFALNDQGKIHNAMVLGSQYIFRSRRD		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 44B.

Table 44B. Comparison of NOV44a against NOV44b.		
Protein Sequence	NOV44a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV44b	1..226	225/226 (99%)
	1..226	225/226 (99%)

Further analysis of the NOV44a protein yielded the following properties shown in Table 44C.

Table 44C. Protein Sequence Properties NOV44a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV44a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 44D.

Table 44D. Geneseq Results for NOV44a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV44a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found				

In a BLAST search of public sequence databases, the NOV44a protein was found to have homology to the proteins shown in the BLASTP data in Table 44E.

Table 44E. Public BLASTP Results for NOV44a				
Protein Accession Number	Protein/Organism/Length	NOV44a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96JT5	CLIC5B - Homo sapiens (Human), 410 aa.	1..200 1..202	185/202 (91%) 191/202 (93%)	e-104
Q9NPY9	DJ447E21.4 (SIMILAR TO BOVINE CHLORIDE CHANNEL PROTEIN (P64)) - Homo sapiens (Human), 180 aa (fragment).	1..180 1..180	180/180 (100%) 180/180 (100%)	e-103
A47104	chloride channel 64K chain - bovine, 437 aa.	1..197 1..229	104/231 (45%) 133/231 (57%)	1e-39
P35526	Chlorine channel protein p64 - Bos taurus (Bovine), 437 aa.	1..197 1..229	103/231 (44%) 131/231 (56%)	1e-38

PFam analysis predicts that the NOV44a protein contains the domains shown in the Table 44F.

Table 44F. Domain Analysis of NOV44a			
Pfam Domain	NOV44a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 45.

The NOV45 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 45A.

Table 45A. NOV45 Sequence Analysis			
	SEQ ID NO: 141	877 bp	
NOV45a, CG59394-01 DNA Sequence	ACTTTGTCTCTTGGGCTTCACACAGAATCCAAAGGAGCAGAAAGTACTTTTGTATT GTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCTGCTCATTGTAGTGACCGTA ACTGTCAGTGAGACCTGGGCTCACC AATGTA CTCTTTCTTGCTGGCTTATCATTTA TAGATATCATTTATTCTTCATCCATTTC C C C CAGATTGATTTCAGGCTTGTTCTTTGG GAATAATTCCATATCCTTCCAATCTTGCATGGCCAGCTCTTTATCGAGCACATTTTC GGTGGGT CAGAGGTCTTCTCTGTTGGTGATGGCCTATGACTGCTATGTGGCCATCT GTAAGCCCTTGCATTATTGGTTATCATGAGACAATGGGTGTGTGTTGTGCTGCTGGT AGTGTCTGGGTTGGAGGATTCTGCACTCAGTATTTCAACTTAGCATTATTTATGGG CTCCCATCTGTGGCCCAATGTCA TTGATCATTTTCTGTGACATGTATCCCTTAT TGAAACTGGTCTGCACTGACACCCATGCTATTGGCCTCTTAGTGGTGGCCAATGGAGG ACTGGCTTGCATATTGTGTTTCTGCTCTTACTCATCTCTTATGGTGTCACTTTGCAC TCTTTAAAGAACCTTAGTCAGAAAGGAGGCAAAAGCCCTCTCAACCTGCAGTTCCC ACATGACTGTGGTTGTCTTCTTCTTTGTTCTCTTGTATTTTATGTATGCTAGACCTGC TAGGACCTTCCCCATTGACAAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATG CTGAACCCCTTAATCTACACTCTGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGC TTTAGAG		
	ORF Start: TTT at 3	ORF Stop: TAG at 873	
	SEQ ID NO: 142	290 aa	MW at 32485.7kD
NOV45a, CG59394-01 Protein Sequence	FVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMYFFLAGLSFI DIIYSSSISPRLISGLFFGNNSISFQSCMAQLFIEHIFGGSEVFLLVMAYDCYVAIC KPLHYLVIMRQWVCVLLVSVWVGFLHSVFQLSIIYGLPFCGPNVIDHFFCDMYPLL KLVCTDTHAIGLLVVANGGLACTIVFLLLLISYGVILHSLKNLSQKGRQKALSTCSSH MTVVVFFVPCIFMYARPARTFPIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL		

Further analysis of the NOV45a protein yielded the following properties shown in
5 Table 45B.

Table 45B. Protein Sequence Properties NOV45a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 42 and 43

A search of the NOV45a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 45C.

Table 45C. Geneseq Results for NOV45a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV45a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU24536	Human olfactory receptor AOLFR21 - Homo sapiens, 299 aa. [WO200168805-A2, 20-SEP-2001]	1..290 10..299	273/290 (94%) 278/290 (95%)	e-155
AAG71950	Human olfactory receptor polypeptide, SEQ ID NO: 1631 - Homo sapiens, 299 aa. [WO200127158-A2, 19-APR-2001]	1..290 10..299	273/290 (94%) 278/290 (95%)	e-155
AAG72258	Human olfactory receptor polypeptide, SEQ ID NO: 1939 - Homo sapiens, 262 aa. [WO200127158-A2, 19-APR-2001]	33..290 1..250	234/258 (90%) 240/258 (92%)	e-131
AAG72553	Human OR-like polypeptide query sequence, SEQ ID NO: 2234 - Homo sapiens, 327 aa. [WO200127158-A2, 19-APR-2001]	1..290 10..299	198/290 (68%) 242/290 (83%)	e-121
AAG71909	Human olfactory receptor polypeptide, SEQ ID NO: 1590 - Homo sapiens, 327 aa. [WO200127158-A2, 19-APR-2001]	1..290 10..299	198/290 (68%) 242/290 (83%)	e-121

In a BLAST search of public sequence databases, the NOV45a protein was found to have homology to the proteins shown in the BLASTP data in Table 45D.

Table 45D. Public BLASTP Results for NOV45a

Protein Accession Number	Protein/Organism/Length	NOV45a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9QW37	OR18=ODORANT RECEPTOR - Rattus sp, 307 aa.	1..290 10..299	192/290 (66%) 237/290 (81%)	e-115
Q96R66	OLFACTORY RECEPTOR - Homo sapiens (Human), 213 aa (fragment).	57..269 1..213	198/213 (92%) 202/213 (93%)	e-111
Q9R0K2	ODORANT RECEPTOR MOR18 - Mus musculus (Mouse), 308 aa.	1..290 10..299	177/290 (61%) 229/290 (78%)	e-105

Q9R0K1	ODORANT RECEPTOR A16 - Mus musculus (Mouse), 302 aa.	1..290 10..299	171/290 (58%) 226/290 (76%)	e-102
CAC88333	SEQUENCE 34 FROM PATENT WO0164879 - Homo sapiens (Human), 309 aa.	1..290 10..299	167/290 (57%) 221/290 (75%)	5e-99

Pfam analysis predicts that the NOV45a protein contains the domains shown in the Table 45E.

Table 45E. Domain Analysis of NOV45a			
Pfam Domain	NOV45a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	30..276	50/268 (19%) 174/268 (65%)	4.4e-23

Example 46.

- 5 The NOV46 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 46A.

Table 46A. NOV46 Sequence Analysis			
	SEQ ID NO: 143	1746 bp	
NOV46a, CG59383-01 DNA Sequence	<u>ATAATTCAAGTTTGAAGCAAGTGGTTCCTCTTTCCCTTCCCTATAGGTGTAAGAATAT</u> <u>CCAGCTGGTGGCTACAGTTCCTCTGGTTTGGCTGCCATGCATCCTGGGCGAACTA</u> <u>CTGGTAAAGGGCCCTCTACTCACACTCAGATTGACCAGCAACCTCCACGGCTTCTCAT</u> <u>TGTGCACATTGCTCTACCGTCTGGGCTGACATCTGCACCAACCTCTGTGAGGCTCTG</u> <u>CAGAACTTCTTCTCTAGCCTGCAGCTTGTATGGGCCCCAGCCGATGTCCTGTTC</u> <u>GTTTATACATGGTACAAGATCAGCATGAGTGCATCCTCCCTTTTGTGCAAGTGAAAGG</u> <u>GAACCTTTGTAGTTGCAGACCTGCATCTCAGAACTCCGCTATGTTACAGAGAGAAGGG</u> <u>TGTTTCAGATCACAAGGTGCTTCTCTGCGGCTGGCAGTAGAGGATGGGCTCCAGCAAT</u> <u>TCAAACAATACAGCAGACATGTGACCACAAGGGCAGCTCTGACCTATACCTCCCTGGA</u> <u>GATTACTATTCTGACTTCTCAGCCTGGAAAAGAGGTGGTCAAACAGTTGGAGGAAGGG</u> <u>TTGAAAGATACAGACCTAGCCAGAGTCAGGAGGTTTCAGGTCTGTGAGGTCAAAAAGG</u> <u>GAATCCTAGAGCACGTGGACTCAGCGTCTCCTGTTGAGGATACCAGCAATGATGAGAG</u> <u>TTCTATTCTGGGAAGTACATTGACCTTCAGACTATAGACAATGATATCGTCAGCATG</u> <u>GAGATTTTCTTCAAAGCCTGGCTACATAACAGTGGAAACAGCAAGCAAAACCAATC</u> <u>TTCTTCTTCTTTCACAGTGTTCAGCAACATTTCCAGACCCAGAGATAATCCAATGTG</u> <u>TCTGAAATGTGATCTCCAAGAGCGACTGCTCTGCCATCCCTACTCGCTGGCACAGCT</u> <u>GACGGCTCCTTGAGAATGGATGACCCTAAAGGAGACTTCATCACACTTACCAGATGG</u> <u>CTTCCCAGTCATCGGCTCTCATTACAAGCTCCAAGTGATCAAGGCTTTAAATCTAG</u> <u>CGGCTCTGCGAGTCATTGACATATGGACTCCCGTTTCATCTCAGACCTACAAGCTGT</u> <u>TGGCAGCTGGACTGGGATGAGCTGGAGACAAATCAGCAACATTTTCATGCTTTGTGTC</u> <u>ACAGCTGCTGAAAAGGGAATGGCTGCTGTTAGCCAAGGGGGAACCAACGGGCCAGG</u> <u>ACACAGCCAGAGAATTCCTGCCAGACCTTCTATGTGATCATGCCGTCACTCCCTC</u> <u>ACACTGCTGGTAAAGGCGGTGGCCACGCGGGAAGTATGCTGCCAGCACCTTCCCC</u> <u>TGCTACCTGAGGACCCACATGATGATAGCCTTAAGAAATAGCATGCTGGACAGCCTGGA</u> <u>GCTGGAGCCCACTACAACCCCTTGCATGTTCAAAGCCACCTGTACTCACACCTGAGC</u> <u>AGCATCTATGCCAAGCCTCAGGGGCGGCTCCACCCCACTGGGAGAGCCGAGCTCCGA</u> <u>GAAAGACTGGGCAGTTGCAGACCAACCGAGCTCGAGTACTGTGGCCCCCTGCCTAT</u> <u>GACTCCTGTCCAGGCGAGCGCTCCAAGATGCCAGCAGCCAGCAATCTTCTCAGAT</u> <u>GCCTTCTTCTCGCCTTCAGAGTGGGAGAAGGATCCCTCAAGGCCCTAAGTCACAGCA</u> <u>CCAGAGCCAGCTGCCAGCTTAACCATATCCATGCTCAGGTTACATAATGGCTATC</u> <u>TGTGGT</u>		
	ORF Start: ATG at 98	ORF Stop: TAA at 1670	
	SEQ ID NO: 144	524 aa	MW at 58691.3kD

NOV46a, CG59383-01 Protein Sequence	MHPGRTTGKGPSTHTQIDQPPRLLIVHIALPSWADICTNLCEALQNFFSLACSLMGP SRMSLFSLYMVQDQHECILPFVQVKNFARLQTCISELRMLQREGCFRSGQASLRLAV EDGLQFKQKQYSRHVTTRAALTYTSLEITILTSQPGKEVVKQLEEGLKDDTLARVRRFQ VVEVTGKILEHVDASPVEDTSNDESSILGTDIDLQTDNDIVSMEIFFKAWLHNSGT DQEQIHLLSSQCFNSISRPRDNPMCLKCDLQERLLCPSELLAGTADGSLRMDDPKGDF ITLYQMASQSSASHYKLQVIKALKSSGLCESLTYGLPFI LRPTSCWQLDWDELETNQ HFHALCHSLLKREWLLAKGEPGPGHSQRI PASTFYVIMPSHSLTLLVKAVATRELM LPSTFPLL PEDPHDDSLKNSMLDSLELEPTYNPLHVQSHLYSHLSSIYAKPQGRHLPH WESRAPRKTGQLQTNRRATVAPLPMTVPVGRASKMPAASKSSSDAFLPSEWEKDPS RP		
	SEQ ID NO: 145	1647 bp	
NOV46b, CG59383-02 DNA Sequence	AAAGAATATCCAGCTGGTGGCTACAGTTCCTCCCTCTGGTTTGTGCGCATGCATCCTG GGCGAACTACTGGTAAAGGGCCCTCTACTCACACTCAGATTGACCAGCAACCTCCACG GCTTCTCATTGTGCACATTGCTCTACCGTCTCTGGGCTGCACATCTGCACCAACCTCTGT GAGGCTCTGCAGAACTTCTTCTCTCTAGCCTGCAGCTTGATGGGCCCGACGCGCATGT CCCTGTTCAAGTTTATACATGGTACAAGATCAGCATGAGTGCATCTCTCCCTTTTGTGCA AGTGAAAGGGAACCTTTGCTAGGTTGCAGACCTGCATCTCAGAACTCCGCATGTTACAG AGAGAAGGGTGTTCAGATCACAAAGGTGCTTCTCTGCGGCTGGCAGTAGGAGTGGGC TCCAGCAATTCAAACAATACAGCAGACATGTGACCACAAGGGCAGCTCTGACCTATACT CTCCCTGGAGATTACTATTCTGACTTCTCAGCCTGGAAAAGAGGTGGTCAAACAGTTG GAGGAAGGGTTGAAAGATACAGACCTAGCCAGAGTCAGGAGGTTTCAGGTCGTTGAGG TCACAAAGGGAATCCTAGAGCACGTGGACTCAGCGTCTCTGTTGAGGATACCAGCAA TGATGAGAGTTCTATTCTGGGAACTGACATTGACCTTCAGACTATAGACAATGATATC GTCAGCATGGAGATTTTCTTCAAAGCCTGGCTACATAACAGTGGAAACAGACCGAGGAA CAATCCATCTTCTTCTTCTTCAAGTGTTCAGCAACATTTCCAGACCCAGAGATAA TCCAATGTGTCTGAAATGTGATCTCCAAGAGCGACTGCTCTGCCATCCCTACTCGCT GGCACAGCTGACGGCTCCTTGAGAATGGATGACCTTAAAGGAGACTTCATCACACTCC ACCAGATGGCTTCCAGTCATCGGCCTCTCATTACAAGCTCCAAGTGATCAAGGCTTT AAAATCTAGCGGCTCTGCGAGTCATTGACATATGGACTCCCGTTTATCTCTCAGACCT ACAAGCTGTTGGCAGCTGGACTGGGATGAGCTGGAGACAAATCAGCAACATTTCCATG CTTTGTGTACAGCCTGCTGAAAAGGGAATGGCTGCTGTTAGCCAAAGGGGGAACCA GGGCCCAGGACACAGCCAGAGAATTCTGCCAGCACCTTCTATGTGATCATGCCGTCA CACTCCCTCACACTGCTGGTAAAGGCGGTGGCCACGCGGGAACATGATGCTGCCAGCA CCTTCCCCCTGCTGCTGAGGACCCACATGATGATAGCCTTAAGAAATGTGGAGAGCAT GCTGGACAGCCTGGAGCTGGAGCCCACCTACAACCCCTTGATGTTCAAAGCCACCTG TACTCACACCTGAGCAGCATCTATGCCAAGCCTCAGGGGCGGCTCCACCCACACTGGG AGAGCCGAGCTCCGAGAAAGCATCCCTGCAAGACTGGGCAGTTGAGACCAACCGAGC TCGAGCTACTGTGGCCCCCTGCCTATGACTCCTGTCCAGGCAGAGCCTCCAAGATG CCAGCAGCCAGCAAATCTTCTCAGATGCCTTCTTCTGCTTCAGAGTGGGAGAAGG ATCCCTCAAGGCCCTAAGTCACC		
	ORF Start: ATG at 49		ORF Stop: TAA at 1639
	SEQ ID NO: 146	530 aa	MW at 59359.1kD
NOV46b, CG59383-02 Protein Sequence	MHPGRTTGKGPSTHTQIDQPPRLLIVHIALPSWADICTNLCEALQNFFSLACSLMGP SRMSLFSLYMVQDQHECILPFVQVKNFARLQTCISELRMLQREGCFRSGQASLRLAV EDGLQFKQKQYSRHVTTRAALTYTSLEITILTSQPGKEVVKQLEEGLKDDTLARVRRFQ VVEVTGKILEHVDASPVEDTSNDESSILGTDIDLQTDNDIVSMEIFFKAWLHNSGT DQEQIHLLSSQCFNSISRPRDNPMCLKCDLQERLLCPSELLAGTADGSLRMDDPKGDF ITLHMASQSSASHYKLQVIKALKSSGLCESLTYGLPFI LRPTSCWQLDWDELETNQ HFHALCHSLLKREWLLAKGEPGPGHSQRI PASTFYVIMPSHSLTLLVKAVATRELM LPSTFPLL PEDPHDDSLKNVESMLDSLELEPTYNPLHVQSHLYSHLSSIYAKPQGRHL PHWESRAPRKHPCKTGQLQTNRRATVAPLPMTVPVGRASKMPAASKSSSDAFLPSE WEKDPSRP		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 46B.

Table 46B. Comparison of NOV46a against NOV46b.		
Protein Sequence	NOV46a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV46b	1..524	509/530 (96%)
	1..530	510/530 (96%)

Further analysis of the NOV46a protein yielded the following properties shown in Table 46C.

Table 46C. Protein Sequence Properties NOV46a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV46a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 46D.

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV46a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM34317	Peptide #8354 encoded by probe for measuring placental gene expression - Homo sapiens, 52 aa. [WO200157272-A2, 09-AUG-2001]	259..310 1..52	52/52 (100%) 52/52 (100%)	7e-23
ABB18624	Protein #623 encoded by probe for measuring heart cell gene expression - Homo sapiens, 42 aa. [WO200157274-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16
AAM66343	Human bone marrow expressed probe encoded protein SEQ ID NO: 26649 - Homo sapiens, 42 aa. [WO200157276-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16
AAM53955	Human brain expressed single exon probe encoded protein SEQ ID NO: 26060 - Homo sapiens, 42 aa. [WO200157275-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16
AAM26622	Peptide #659 encoded by probe for measuring placental gene expression - Homo sapiens, 42 aa. [WO200157272-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16

In a BLAST search of public sequence databases, the NOV46a protein was found to have homology to the proteins shown in the BLASTP data in Table 46E.

Table 46E. Public BLASTP Results for NOV46a				
Protein Accession Number	Protein/Organism/Length	NOV46a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z0E1	D6MM5E PROTEIN - Mus musculus (Mouse), 529 aa.	1..524 1..526	380/526 (72%) 423/526 (80%)	0.0
Q96L07	SIMILAR TO DNA SEGMENT, CHR 6, MIRIAM MEISLER 5, EXPRESSED - Homo sapiens (Human), 365 aa.	1..358 1..358	358/358 (100%) 358/358 (100%)	0.0

- 5 PFam analysis predicts that the NOV46a protein contains the domains shown in the Table 46F.

Table 46F. Domain Analysis of NOV46a			
Pfam Domain	NOV46a Match Region	Identities/ Similarities for the Matched Region	Expect Value
RA: domain 1 of 1	124..214	18/115 (16%) 65/115 (57%)	8.4

Example 47.

The NOV47 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 47A.

Table 47A. NOV47 Sequence Analysis		
	SEQ ID NO: 147	960 bp
NOV47a, CG58526-01 DNA Sequence	AGGACTAAATAAAATGGCCTAAATTTAAATATGGATTGGGATTTCATTCTCTGCAG ATGCCAGAACCAAGAAGAGGTCTGCCTGGTTTTCTTCTGGAGCTCCAGACCCAGA CCAAAGCCTTCTGCCTCTTCCAATCCAGGGAACCAAGCATGGCAGCTGAGTCTCCCT CTGCCAAGCAGTTTCTGCCAACAGTCAGTCTCCCTCCTGGTCTAGAATATTTAAGCC AGTTAGACCTGATAATTATACACCAGCAGGTGGAGCTGCTTGTGATACTTGGTACTGA GACCTCCAACAATATGAGATTAAAAACAGCTTGGGACAAGAATTTACTTTGCAGTG GAGGAAAGCATCTGCTTCAATCGTACTTTCTGTTCCACTCTGCATCTTGCACCCCTGA GGATCACAGATAACTCAGGTCGAGAGGTCATTACAGTGAACAGGCCCTTGAGATGTAA CAGCTGCTGGTGCCTTGCTACCTACAAGAGTTAGAAATCCAAGCCCCTCCTGGTACT ATAGTTGGTTACGTTACGCAGAAGTGGGACCCCTTCTGCCTAAATTCACAATCCAAA ATGCAACAAAGAAGATATTTGAAAATTGTTGGTCTTGTGTGACATGTGGCTGTTT TGGCGATGTGGATTTTGAGAAGGTGAAAACCATTAATGAAAAGCTTACAATTGGGAAG ATTTCAAAGTACTGGTCAGGATTTGTAAATGATGTCTTCACAAATGCTGACAATTTG GAATTCATGTTCTGCAGATCTAGATGTAAACAGTCAAAGCAGCAATGATCGTGCCCTG TTTCTCTTTGTAAGTATGGGCTTGAGAGCCCAGCCCTCCAAGATGAGAAAGAGTCA GTGTGGCAATTCAAAAATCAGAGTGCCCTCTCACCTCCAAACAAGCCCACTTGTTCC	

AA09309	Human phospholipid scramblase - Homo sapiens, 318 aa. [WO9919352-A2, 22-APR-1999]	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84
AA029323	Human PL scramblase - Homo sapiens, 318 aa. [WO9936536-A2, 22-JUL-1999]	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84

In a BLAST search of public sequence databases, the NOV47a protein was found to have homology to the proteins shown in the BLASTP data in Table 47D.

Table 47D. Public BLASTP Results for NOV47a				
Protein Accession Number	Protein/Organism/Length	NOV47a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JJ00	Phospholipid scramblase 1 (PL scramblase 1) (Transplantability associated protein 1) (TRA1) (NOR1) - Mus musculus (Mouse), 328 aa.	20..283 66..328	150/267 (56%) 191/267 (71%)	4e-84
Q99M50	PHOSPHOLIPID SCRAMBLASE 1 - Mus musculus (Mouse), 327 aa.	20..282 66..327	150/266 (56%) 191/266 (71%)	6e-84
O15162	Phospholipid scramblase 1 (PL scramblase 1) (Erythrocyte phospholipid scramblase) (Ca ²⁺ dependent phospholipid scramblase 1) (MmTRA1b) - Homo sapiens (Human), 318 aa.	24..282 60..318	152/263 (57%) 187/263 (70%)	2e-83
P58195	Phospholipid scramblase 1 (PL scramblase 1) (Ca ²⁺ dependent phospholipid scramblase 1) - Rattus norvegicus (Rat), 335 aa.	28..282 84..335	145/256 (56%) 183/256 (70%)	3e-81
Q9NRY7	Phospholipid scramblase 2 (PL scramblase 2) (Ca ²⁺ dependent phospholipid scramblase 2) - Homo sapiens (Human), 224 aa.	55..270 6..221	135/217 (62%) 164/217 (75%)	1e-75

PFam analysis predicts that the NOV47a protein contains the domains shown in the

5 Table 47E.

Table 47E. Domain Analysis of NOV47a			
Pfam Domain	NOV47a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 48.

The NOV48 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 48A.

Table 48A. NOV48 Sequence Analysis			
	SEQ ID NO: 149	957 bp	
NOV48a, CG57851-01 DNA Sequence	<p>CCCCCTGCTGGTGCCCAAGACCACCGTGGGAAGGAATGGCTAAAGAGGAGACAAGTGAGT TAGAATGGGGCTTGTTACCCCCAGAGAATTTTCCCAAGTGAATGGAATCATTCTTCA AAAGAAAATGTGCGATTCTCTGGGATAAGATCTGGAACCTTCCAAGCCAAGCCTGATGAC CTGCTCATGTGCTTCTTACCCCAAAGCAGGTACCCTTGGACACAGGAAATTTGATAGATC TGATACAAAATGATGGCGATATTGAGAAAAGCAGGCGCGCTTCCATTCAACTTCAACA CCCTTTCCTGGAGTGGATAAGAATGACACACGCCAGGAAAATTTTGCAGGGATTGAC CAGGCTAACACAATGCCTTCCCAAGGACCTGAAAACCTCATCTTCTGTACAACACTAC TGCTCCATCCTTCTGGGAGGAAAACCTGTAAGATAATCTATGTGGCAAGAAATGCCAA GGATAACCTGGTGTCTACTACCATTTCCTCAAGGATGAGCAAAGCACTCCCTGACGTT TTGACAGTGGGAGAATACATTATGTGTGGGAAGTGTGTGGGGAATATGGGAAGAGA TTCGGACTTGGCAACTGCATAGGTTGTTCTGCTGGTCTTTGATCATGCTTCTGAGAA TCCTAGAAAAGTTCAAAGGATAATGGAATTTATGGGGAATAAACTAGATGAAGATCCT GTCAAAAAGATTGTTTACGACACATCTTTTGAAGTAAGAAGAAAACCATGACCA ACTATGTAATGATAACCTGTGACATCATGGACCACTCCATCTCCCCATTATGAGGAA AGGGACCGTTGGAGAGTGAAGGATTACTTCTCAGCAGCACAGAATAAGAGATTTGAT GAAGACAGGAAAATGGCTGACTCTTCTCTGACCTTCCACACGGAGCTCTAAAGAGAGA GAGACAAAGTCTATACTACACAGGGGCAC</p>		
	ORF Start: ATG at 34	ORF Stop: TAA at 919	
	SEQ ID NO: 150	295 aa	MW at 34853.7kD
NOV48a, CG57851-01 Protein Sequence	<p>MAKEETSELEWGLLPPEEFSQVNGIILQKKMCDFWDKIWNFQAKPDDLIIASYPKAGT TWTQEIVDLIQNDGDIKSRRAISQLQHPFLEWIRMTARKIFAGIDQANTMPSRTL KTHLPVQLLPSPFWEENCKIIYVARNAKDNLSYVHFQRMKALPDVLTVGEYIMCGE VLWGIWEEIIRTWQLHRLFCWFFDHAENPRKFKRIMEFMGNKLDEDPVKRIVQHTSFE SKKNQMTNYVMITCDIMDSISPFMRKGTVGEWKDYFSAQNRKFDDEDRKMADSSLT FHTEL</p>		

Further analysis of the NOV48a protein yielded the following properties shown in

5 Table 48B.

Table 48B. Protein Sequence Properties NOV48a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV48a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 48C.

Table 48C. Geneseq Results for NOV48a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV48a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE12209	Human ST drug-metabolising protein 2 encoded by DNA transcript 2 - Homo sapiens, 304 aa. [WO200172977-A2, 04-OCT-2001]	16..295 15..304	137/293 (46%) 200/293 (67%)	9e-74
AAE12210	Human ST drug-metabolising protein 3 encoded by cDNA - Homo sapiens, 304 aa. [WO200172977-A2, 04-OCT-2001]	16..295 15..304	129/293 (44%) 190/293 (64%)	1e-67
AAE12208	Human ST drug-metabolising protein 1 encoded by DNA transcript 1 - Homo sapiens, 304 aa. [WO200172977-A2, 04-OCT-2001]	16..295 15..304	128/293 (43%) 190/293 (64%)	6e-67
AAE05178	Human drug metabolising enzyme (DME-9) protein - Homo sapiens, 304 aa. [WO200151638-A2, 19-JUL-2001]	16..295 15..304	128/293 (43%) 189/293 (63%)	1e-66
AAY67294	Human STP2 (phenol sulphotransferase 2) amino acid sequence - Homo sapiens, 295 aa. [WO9964630-A1, 16-DEC-1999]	15..295 10..295	133/292 (45%) 186/292 (63%)	5e-66

- 5 In a BLAST search of public sequence databases, the NOV48a protein was found to have homology to the proteins shown in the BLASTP data in Table 48D.

Table 48D. Public BLASTP Results for NOV48a				
Protein Accession Number	Protein/Organism/Length	NOV48a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q90WR6	SULFOTRANSFERASE 1C - Gallus gallus (Chicken), 307 aa.	3..295 5..307	170/304 (55%) 218/304 (70%)	3e-94

P50237	N-hydroxyarylamine sulfotransferase (EC 2.8.2.-) (HAST-I) - Rattus norvegicus (Rat), 304 aa.	1..295 1..304	172/308 (55%) 222/308 (71%)	3e-92
O70262	PHENOL SULFOTRANSFERASE - Mus musculus (Mouse), 304 aa.	18..295 19..304	164/289 (56%) 215/289 (73%)	1e-91
O75897	Sulfotransferase 1C2 (EC 2.8.2.-) (SULT1C) (SULT1C#2) - Homo sapiens (Human), 302 aa.	22..292 22..299	160/282 (56%) 203/282 (71%)	1e-87
O00338	Sulfotransferase 1C1 (EC 2.8.2.-) (SULT1C#1) (ST1C2) (humSULTC2) - Homo sapiens (Human), 296 aa.	18..295 12..296	149/289 (51%) 201/289 (68%)	1e-80

PFam analysis predicts that the NOV48a protein contains the domains shown in the Table 48E.

Table 48E. Domain Analysis of NOV48a			
Pfam Domain	NOV48a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Sulfotransfer: domain 1 of 1	23..285	116/298 (39%) 207/298 (69%)	6.2e-82

Example 49.

The NOV49 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 49A.

Table 49A. NOV49 Sequence Analysis		
	SEQ ID NO: 151	1934 bp
NOV49a, CG59377-01 DNA Sequence	<p>CTTGATTACGGAGACTGAACCTTCATAGGGTGCGCACTTACCAAGGACAGGAAGGTTTCTCTGTTTGAAGGGCTTTAAACTTATAACAAAGAAAATAAAATGACGACTTCGTCTATCAGACGGCAGATGAAAAACATCGTGAACAATTACTCAGAGGCAGAAATCAAAGTCCGGGAAGCCACCTCCAATGACCCGTGGGCCCCGTCCAGTTCTCTGATGACCGAGATTGCCGACCTGACCTACAACGTGGTGGCCTTCTCGGAGATCATGAGCATGGTGTGGAAGCGGCTGAATGACCATGGCAAGAACTGGCGGCATGTGTACAAGGCGCTGACCTGCTGGACTACCTCATCAAGACAGGCTCCGAACGTGTGGCCAGCAGTGCCGGGAGAACATCTTCGCCATCCAGACCCTGAAGGACTTCCAGTACATTGACCGAGATGGCAAGGACCAGGGCATCAATGTGCGTGAGAAGTCAAAGCAACTGGTGGCTCTCCTCAAGGACGAGGAACGGTTGAAAGGCTGAGAGGGGCCAGGCTCTCAAAACCAAGAGCGCATGGCCAGGTTGCCACTGGCATGGGAGCAACAGATCACCTTTGGGCGAGGCTCCAGCCAGCCCAACCTCTCCACCAGCCACTCGGAGCAGGAGTATGGCAAGGCCGGGGCTCCCGGCCCTCCTACCATGGCTCACCTCCCGCGAGTGTCTCCGAGCTGGAGCAAGCCCGCCAGACTAGTGGAGAAAGGAGCTTCAGCTGCAGCTGGCACTTGCCATGAGCAGAGAAGTGGCTGAGCAGGAAGAACGCCTCAGGCGGGGTGATGACCTCAGATTACAGATGGCCCTGGAAGAAAGCCGAAGGACACAGTTAAATTCAAAAAAGAAAGACAGACTACGCTGTGGATTAAATGGATGCTCTCCCGAGCTCGGGCCCCGCGGCCAGAAAGCAGAGCCCTGGGGCCCGTCAGCCTCCACTAACCAGACCAACCCCTGGGGCGGGCCAGCGGCTCCTGCGAGTACTTCAGACCCCTGGCCATCGTTTGGTACCAAGCCAGCTGCCTCCATTGACCCATGGGGGGTGCCCACT</p>	

	GGAGCCACCGCACAAATCTGTCCCAAGAACTCGGACCCCTGGGCAGCTTCACAGCAGC CTGCCTCCAGTGCTGGGAAAAGAGCTTCTGACGCGTGGGGCGCAGTCTCCACCACCAA GCCCCTGTCTGTCTCTGGGTCTTTGAGCTCTTCAGTAATCTGAATGGTACAATTAA GATGACTTTTCTGAATTGACAACCTTCGGACTTCAAAAAAACAGCCGAATCTGTGA CCTCTCTGCCATCCAAAAACAATGGAACCTACCAGCCCTGACCCCTTTGAGTCTCAACC CCTGACTGTGCCTCAAGCAAGCCAGCAGTGCCCGGAAAAACCTGAGTCTCTTCTCTG GGCCCAACGCGGCCCTGGTGAACCTGGACTCACTGGTGACCAGGCCTGCCCCACCAG CCCAGTCCCTCAACCTTTCTGGCACCAGGTGCTCCCGCCACCTCGGCCCTGTAA CCCTTTCAGGTGAACCAGCCCGCTGACACTGAACAGCTTCGGGGGAGCCCA GTCTGGGGACCAGCACATCCTTTGGGCTGGCCAGGAGTGGAGTCCATGGCTGTGG CCTCGATGACCTCCGCGGCCACAGCCAGCTCTGGGGGCCACTGGTTCCTCTCTGAC ACCCTGGGCCCTGCAATGATGAACATGGTGGGCAGTGTGGGTATACCCCATCAGCA GCCAGGCCACTGGCACAACCAACCTTTCTTCTCTAGTGCCTGGGCTGGGACCCA CCCAGAGCACCTGTGCTGGAGGATGCCGAGCAGGACTCTCGTCTGTGGGACGGGATC CAAGAGTTTGGGGATTAGGG		
	ORF Start: ATG at 101	ORF Stop: TAG at 1835	
	SEQ ID NO: 152	578 aa	MW at 61651.2kD
NOV49a, CG59377-01 Protein Sequence	MTTSSIRQMKNIVNNYSEAEIKVREATSNDPWPSSSLMTEIADLTYNVVFSEIMS MVWKRLNDHGKNRHVYKALTLDDYLIKTSERVAQQCRENIFAIQTLKDFQYIDRDG KDQGINVREKSKQLVALLKDEERLKAERAQALKTKERMAQVATMGMSNQITFGRSSQ PNLSTSHSEQEYKAGGSPASVHGSTSPRVSELEQARPQTSGEELQLQLALAMSRE VAEQEERLRRGDDLRLQMALEESRRDVKIPKKKEQTTLDDLMDALPSSGPAQKAEP WGPSASTNQTNPWGGPAAPASTSDPWPSFGTKPAASIDPWGPTGATAQSVPKNSDPW AASQQPASSAGKRASDAWAVSTTKPVSVSGSFELFSNLNGTIKDDFSEFDNLRTSKK TAESVTSLSQNGTSTSPDPFESQPLTVASSKPSSARKTPESFLGPNAALVNLDLSLT RPAPPAQSLNPFLLAPGAPATSAPVNPFPQVNPQPLTLNQLRGSFVLGTSTSFPGPGV ESMAVASMTSAAPQALGATGSSLTPLGPAMNMVGSVGI PPSAAQATGTTNPFLL		

Further analysis of the NOV49a protein yielded the following properties shown in Table 49B.

Table 49B. Protein Sequence Properties NOV49a	
PSort analysis:	0.4936 probability located in mitochondrial matrix space; 0.3000 probability located in nucleus; 0.2087 probability located in mitochondrial inner membrane; 0.2087 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV49a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded 5 several homologous proteins shown in Table 49C.

Table 49C. Geneseq Results for NOV49a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV49a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB93525	Human protein sequence SEQ ID NO:12872 - Homo sapiens, 584 aa. [EP1074617-A2, 07-FEB-2001]	1..578 1..584	578/584 (98%) 578/584 (98%)	0.0

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Table 49E. Domain Analysis of NOV49a

Pfam Domain	NOV49a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ENTH: domain 1 of 1	17..140	70/131 (53%) 117/131 (89%)	7.9e-68
VHS: domain 1 of 1	14..158	33/160 (21%) 90/160 (56%)	3.3
UIM: domain 1 of 2	217..234	11/18 (61%) 16/18 (89%)	0.043
UIM: domain 2 of 2	242..259	5/18 (28%) 12/18 (67%)	80

Example 50.

The NOV50 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 50A.

Table 50A. NOV50 Sequence Analysis

	SEQ ID NO: 153	2580 bp
NOV50a, CG59258-01 DNA Sequence	ATGCTGCTGGCCCCCTTTATTGCTGGGTGTGTGCCCATGCTGCTGGCCCCCTTTAT TGCTGGGCAGTGACAACTGTACCATCAGTGGCTCTCCACTGTCCGGAAGGAAGTGG AGCAATCTGAATACTGTAAAGACCAAGCAAATCCGGCCATGAAGACTGTCTACAAG TTCGACATTGCCGAGAATGGCTGCGCCCCACCCAGAAAGAGCAGCTGCCAAAGACTG CACCGTCCCCACTGGTGGAGGCCAAGGACCCCAAGCTCCGAGAAGACGGCGGCCAAT CACAGTCCACTTTGGACAGGACCACTGTAGATGTCTTCAGCTCAGCACTCACTCAC GGCAAGAGAGTGTCCCGACCCAGCCGAGAGAGTCTGTGACAGACTGGCGAGCCCC TGAATCCTGAGCGCTCTCTCCGAGATCATCTCTGGCCTGTTACGCACTTGTCTG GGCAACCTGGGCAAGTCTTGTCTGCTCATCTGTGAATGGGTAGCAGCCCTCGT TCCCTGCAGAGGAGCCTTGCCTGCTGCTGGGACACCCAGCTTATTGGGAACTGCAA CCACCATGGCCGATGGCCCCACCAAGCCCTGTCTAGGAAGCAGAGGCCTCCCCAGCAG CGTGTCCACTGTGCCCCCTGGCCCTGCGTGAAGTGCCATCAGATGCCCCGATCCTGTC AGCAGGGCCCTCGTACTGGCCTCACAGATGAGGACACAGAGGCCAGGGAAGTCACT TGCTTGCCAAAGTCACTCAGCAAACCATGTCTGTCTGGCTCTCAGAAAATGGGAAAGA AGCCTGGGCATTAGCCATGAGGGAGCCACGGCTGTAGCCAGTGAATGACGTACCTC CAGTCCAGGATGTGCACCGGGCAGCCAGGTCCACAGCCACTACTTTCTTGCCCCCA CCACTGCTCCACAGTTCACAGAACTCAGTCTCAGATCTGGGCTCCAGGATGCAGAG GCTGTCTCAGGCCTGGTAAAGCCCTTGCACACTATGCGGTCTTCTCTCCGAAGAC TCCTCTGATGATGAATGCCAGCGGGAAGAGGGCCCGAGCTCTGGCTTCCCGAGAGCT TTTTCTTCTCCGCTCCCTTTGAATGGCCGAGCCGTATCGGACACTCAGGGAGTCAGA CAGCGCGGAAGGCGACGAGGCAGAGAGTCCAGAGCAGCAAGTGCAGGAAGTCCACAGGC CCTGTCCAGCTCCCCCTGACCGGGCTGCCAGCATCGACCTTCTGGAAGACGTTTCA GCAACCTGGACATGGAGCCGCACTGCAGCCACTGGGCCAGGCCAAGAGCTTAGAGGA CCTTCGTGCCCCAAAGACCTGAGGGAGCAGCCAGGGACCTTTGACTATCAGAGGCTG GATCTGGGCGGGAGTGAGAGGAGCCGCGGGGTGACAGTGGCCTTGAAGCTTACCCACC CGTACAACAAGCTCTGGAGCCTGGGCCAGGACGACATGGCCATCCCCAGCAAGCCCC AGCTGCCTCCCCCTGAGAAGCCCTCAGCCCTGCTCGGAACTCCCTGGCCCTGCCTCGA AGGCCCCAGAACCGGGACAGCATCTTGAACCCAGTGACAGGAGGAGGTGCCACCC CTACTCTGGGCAGCATCACCATCCCCCGCCCCAAGGCAGGAAGACCCAGAGCTGGG CATCGTGCCTCCACCGCCATTTCCCGCCCCGCCCCAAGCTCCAGGCTGCCGGCGCGCA CTTTGTGAGCTCTCAGAGCGGCTGCAGACGGATCGGGACAGGCGAGTGCCTTGAGTC CAGGGCTCCTGCTGGTGTGTCCCCAAGGCCCACTGAACTGCTCCAGCCGCTCAG CCCTGGCCCCGGGGCTGCAGGCACGAGCAGTGAAGCCCTGCTCGCCCTCTGGACCCG CTCAGCACAGCCTGGTCAAGGCAGCACCTTCCGTCAGCGCCCGCCGCAATGTAG CCACCCATTACCCCCCAATTACAGCTTCCCCCTGCAGGGACACCCACCCATTCCC ACAGCCCACTCAACCCCTTTGTCCCATCCATGCCAGCAGCCCCACCCACCTGCCC CTGGTCTCCACAGCCGGGCTTTTCGGGGCCCTCCAGCTTCCCTGGGGCCGCTT TTGGCTCCGGCTCTGCTGTCCAGTGTGGCTTGTGTGCCCTCACAGGTCTCAGCC CAACCTCTCCGCTCTCCATGCCCAACCTTTTGGCCAGATGCCATGGGCACCCAC ACGAGCCCCCTACAGCCGCTGGGTCCCCAGCAGTTGCCCGTCCAGGATCCGAACGT	

	TGCCCTGGCCCGCTCAAGTGCCAGGGCTGCTGAGACCAAGCAGGGGCTGGCCCTGAG GCCTGGAGACCCCGCTTCTGCCTCCAGGCCCTCAAGGCCTGGAGCCAACACTG CAGCCCTCTGCTCCTCAACAGGCCAGAGACCCCTTGAGGATTGTTACAGAAAACCA AGCAAGACGTGAGCCCGAGTCCGGCCCTGGCCCGGCCCCAGACTCGTGAGCAGCT CAGGAAGCAGTGGGAGACCTTCGAGTGA		
	ORF Start: ATG at 1		ORF Stop: TGA at 2578
	SEQ ID NO: 154	859 aa	MW at 91746.7kD
NOV50a, CG59258-01 Protein Sequence	MLLAPFYCWCAHAAGPLLLGSDKLYHQWLSTVRKSGAILNTVKTKANPAMKTVYK FDIAENGCAPTPEEQPKTAPSPLEAKDPKLRDRRPIIVHFGQDQSEMSFSSALTH GKESARTQPERVVDRTGEPLNPERALSGDHLWPVTHLLWATIGKSLALI CEMGSSPR SLQRLALLGTPQLIWETATTMADGPTTCLGSRGLPSSVSTVPLALREVPSDAPHPC SRALVTGLTDEDTEAQGSHLLAKVTQQTMSVWLSENGKEAWAFSHEGATAVASGMTYP QSRMCTRAARSHSHYFLAPTPTAPTVPRTQSPDLGSRMQRLLSSGLVKPLRHYAVFLSED SSDDECQREEGPSSGFTESSFFSAPFEWPQPYRTLRESDSAEGDEAESPEQQVRKSTG PVPAPPDRAASIDLLEDVFSNLDMEALQLGQAKSLEDLRAPKDLREQPTFDYQRL DLGGSESRGVTVALKLTHPYNKLWSLGQDDMAIPSKPPAASPEKPSALLGNSLALPR RPQNRDSILNPSDKKEEVPPTLGSITIPRPQGRKTPELGIVPPPIIPRAKLQAAGAA LGDVSERLQTDRRRAALSPGLPGVVPQGPTTELLQPLSPGPGAAGTSSDALLALLDP LSTAWSGSTLPSRPATPNVATPFTPPQFSFPPAGTPTFPQPPLNPFVPSMPAAPPTLP LVSTPAGPFGAPPASLGPAPASGLLLSSAGFCAPHRSQPNLSALSMPLNFGQMPMGTH TSPLQPLGPPAVAPSRIRTLPLARSSARAETKQGLALRPGDPLLPRPPQGLEPTL QPSAPQQARDPFEDLLQKTKQDVSPSPALAPADSVEQLRKQWETFE		

Further analysis of the NOV50a protein yielded the following properties shown in Table 50B.

Table 50B. Protein Sequence Properties NOV50a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1940 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	Likely cleavage site between residues 15 and 16

A search of the NOV50a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 50C.

Table 50C. Geneseq Results for NOV50a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV50a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41501	Human polypeptide SEQ ID NO 6432 - Homo sapiens, 545 aa. [WO200153312-A1, 26-JUL-2001]	22..103 401..482	82/82 (100%) 82/82 (100%)	2e-42
AAM39715	Human polypeptide SEQ ID NO 2860 - Homo sapiens, 559 aa. [WO200153312-A1, 26-JUL-2001]	22..103 396..496	82/101 (81%) 82/101 (81%)	6e-39

AAW31855	Mycobacterium tuberculosis 55 kDa protein - Mycobacterium tuberculosis, 572 aa. [WO9741252-A2, 06-NOV-1997]	498..845 71..389	96/358 (26%) 125/358 (34%)	8e-12
AAW31852	Mycobacterium tuberculosis 74 kDa protein - Mycobacterium tuberculosis, 763 aa. [WO9741252-A2, 06-NOV-1997]	498..845 262..580	96/358 (26%) 125/358 (34%)	8e-12
AAB50363	Human SRCAP - Homo sapiens, 2972 aa. [WO200073467-A1, 07-DEC-2000]	501..845 1235..1575	112/369 (30%) 141/369 (37%)	1e-11

In a BLAST search of public sequence databases, the NOV50a protein was found to have homology to the proteins shown in the BLASTP data in Table 50D.

Table 50D. Public BLASTP Results for NOV50a				
Protein Accession Number	Protein/Organism/Length	NOV50a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9HCG4	KIAA1608 PROTEIN - Homo sapiens (Human), 603 aa (fragment).	309..859 62..603	501/555 (90%) 510/555 (91%)	0.0
Q9H796	CDNA: FLJ21129 FIS, CLONE CAS06266 - Homo sapiens (Human), 559 aa.	22..103 396..496	81/101 (80%) 81/101 (80%)	2e-37
AAK44515	HYPOTHETICAL 58.5 KDA PROTEIN - Mycobacterium tuberculosis CDC1551, 598 aa.	499..845 299..562	104/354 (29%) 121/354 (33%)	8e-14
Q9SN46	EXTENSIN-LIKE PROTEIN - Arabidopsis thaliana (Mouse-ear cress), 839 aa.	604..848 407..626	73/249 (29%) 100/249 (39%)	3e-12
Q41805	EXTENSIN-LIKE PROTEIN PRECURSOR - Zea mays (Maize), 1188 aa.	492..848 415..749	88/361 (24%) 124/361 (33%)	5e-12

PFam analysis predicts that the NOV50a protein contains the domains shown in the Table 50E.

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Table 50E. Domain Analysis of NOV50a			
Pfam Domain	NOV50a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 51.

The NOV51 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 51A.

Table 51A. NOV51 Sequence Analysis			
	SEQ ID NO: 155	1394 bp	
NOV51a, CG59492-01 DNA Sequence	GTGGCCTGCTCCTGCAGCAATCCCAGGACCCCTGCTCATGGGGCTGTTTCTCTACTAA CCCCAAAGAGAAGACCAGGAGGAACCCCTGGCCAGAGCAGGGCCCCCTGTGTTGACC GTGGTGTCCAAGTTCAAGGCCTCACTGGAGCAGCTTCTGCAGGCTCTACACAGCACCA CGCCCCACTACATTGCTGCATCAAGCCCCAACAGCCAGGGCCAGGCGCAGACCTTTCT CCAAGAGGAGGTCTCTGAGCCAGCTGGAGGCCTGTGGCCCTCGTGAGACCATCCATATC AGTGCTGTGGCTTCCCCATCCGGGTCTCTCACCGAAACTTTGTAGAACGATACAAGT TACTAAGAAGGCTTCATCCTTGCACATCCTCTGGCCCCGACAGCCCATATCCTGCCAA AGGGCTCCCTGAATGGTGTCCACACAGCGAGGAAGCCACGCTTGAACCTCTCATCCAG GACATTCTCCACACTCTGCCGGTCTTAACTCAGGCAGCAGCCATAACTGGTGACTCGG CTGAGGCCATGCCAGCCCCCATGCACTGTGGCAGGACCAAGGTGTTCTATGACTGACTC TATGCTGGAGCTTCTGGAATGTGGGCGTGCCCGGTGCTGGAGCAGTGTGCCCGCTGC ATCCAGGGTGGCTGGAGGCGACACCGGCACCGAGAGCAGGAGCGGCAGTGGCGGGCCG TCATGCTCATCCAGGCAGCCATTCTGTTCTGGTTAACTCGGAAACACATCCAGAGGCT GCATGCAGCTGCCACAGTCATCAAGCGTGCATGGCAGAAGTGGAGAATCAGAATGGCC TGCCTTGCTGCTAAAGAGCTGGATGGTGTGGAAGAAAAACACTTCTCTAAGCTCCCT GTTCCCTGAGCACCTCGCCGCTGCAGACCAGGCTCCTGGAGGCAATAATCCGCTTCTG GCCCTGGGACTGGTCTTGCCCAATACGGCTATGGGTGTAGGCAGCTTTCAGAGGAAA TTAGTGGTCTGGGCTTGCTCCAGCTCCCCAGGGGCAGCCCCAGTAGCTACACTGTCC AGACAGCACACAAGACCAGGCTGGTGTACGTCCATCCGAGCGCTGCCTCAGGGATCGAT AAAGTTTCACTGCAGAAAGTCTCCACTGCGGTATGCTGACATCTGCCCTGAACCTTCA CCCTACAGCATTGCAGGCTTTAATCAGATTCTGCTGGAAGACACAGGCTGATCCACG TGACCTCTTCTGCCTTCACTGGGCTGGGGTGAATCCTTGGTGCCTTTGTTTCCACAAGG CCTTTTCTGCCCCCTGCCTTGCCAAAGACATTTAATCAGACACAGTCCAGCACTA TTCCACAGTGCTCAAATGCACATGAACAACAGTGACGGCTCCAGCCTTCGACCCAG AG		
	ORF Start: ATG at 39	ORF Stop: TGA at 1248	
	SEQ ID NO: 156	403 aa	MW at 45142.8kD
NOV51a, CG59492-01 Protein Sequence	MGLFPTNPKEKTQEEPPGQSRAPVLTVVSXFKASLEQLLQVLHSTTPHYIRCIKPN SQ GQAQTFLEQEVLSQLEACGLVETIHSAGFPPIRVSHRNVERYKLLRRLHPMTSSGP DSPYPAGKLPWCPEHSEATELEPLIQDILHTLPVLTQAAAITGDSAEAMPAPMHCGR KVFMTDSMLELLECGRRARVLEQCARCIQGGWRRHRHREQERQWRVMLIQAAIRSWLT RKHIQRLHAAATVIKRAWQKWRIRMACLAAKELDGVEEKHFSQAPCSLSTSPLOTRLL EAIIRFWPLGLVLANTAMGVGSFQRKLVVWACLQPRGSPSSYTVQTAQDQAGVTSIR ALPQGSIKFHCRRKSPRYADICPEPSPYSIAGFNQILLERHRLIHVTSSTFTGLG		

Further analysis of the NOV51a protein yielded the following properties shown in

5 Table 51B.

Table 51B. Protein Sequence Properties NOV51a	
PSort analysis:	0.3000 probability located in nucleus; 0.2029 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0320 probability located in microbody (peroxisome)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV51a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 51C.

Table 51C. Geneseq Results for NOV51a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV51a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAV94290	Human myosin heavy chain homologue - Homo sapiens, 612 aa. [WO200026372-A1, 11-MAY- 2000]	1..403 210..612	401/403 (99%) 401/403 (99%)	0.0
AAU23676	Novel human enzyme polypeptide #762 - Homo sapiens, 387 aa. [WO200155301-A2, 02-AUG- 2001]	17..403 1..387	384/387 (99%) 384/387 (99%)	0.0
ABB10243	Human cDNA SEQ ID NO: 551 - Homo sapiens, 570 aa. [WO200154474-A2, 02-AUG- 2001]	1..365 206..570	365/365 (100%) 365/365 (100%)	0.0
AAU23123	Novel human enzyme polypeptide #209 - Homo sapiens, 567 aa. [WO200155301-A2, 02-AUG- 2001]	1..365 203..567	364/365 (99%) 364/365 (99%)	0.0
AAM23563	Human EST encoded protein SEQ ID NO: 1088 - Homo sapiens, 477 aa. [WO200154477-A2, 02-AUG- 2001]	1..189 288..476	188/189 (99%) 188/189 (99%)	e-108

- 5 In a BLAST search of public sequence databases, the NOV51a protein was found to have homology to the proteins shown in the BLASTP data in Table 51D.

Table 51D. Public BLASTP Results for NOV51a				
Protein Accession Number	Protein/Organism/Length	NOV51a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96H55	HYPOTHETICAL 86.7 KDA PROTEIN - Homo sapiens (Human), 770 aa.	72..403 439..770	330/332 (99%) 330/332 (99%)	0.0
Q9D2Z3	1110055A02RIK PROTEIN (RIKEN CDNA 1110055A02 GENE) - Mus musculus (Mouse), 395 aa.	3..394 2..395	288/394 (73%) 320/394 (81%)	e-162
Q948A2	PUTATIVE MYOSIN HEAVY CHAIN - Oryza sativa (Rice), 1601 aa.	2..255 663..876	84/258 (32%) 125/258 (47%)	1e-23
O74805	HYPOTHETICAL MYOSIN-LIKE PROTEIN C2D10.14C IN CHROMOSOME II - Schizosaccharomyces pombe (Fission yeast), 1471 aa.	20..347 615..903	96/340 (28%) 152/340 (44%)	1e-21
T30148	hypothetical protein E02C12.1 - Caenorhabditis elegans, 1019 aa.	5..249 619..830	74/248 (29%) 119/248 (47%)	6e-21

PFam analysis predicts that the NOV51a protein contains the domains shown in the Table 51E.

Table 51E. Domain Analysis of NOV51a			
Pfam Domain	NOV51a Match Region	Identities/ Similarities for the Matched Region	Expect Value
myosin_head: domain 1 of 1	26..105	37/81 (46%) 60/81 (74%)	5.1e-25

5

Example 52.

The NOV52 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 52A.

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Table 52A. NOV52 Sequence Analysis			
	SEQ ID NO: 157	1380 bp	
NOV52a, CG59564-01 DNA Sequence	<u>TAGAATTCCAGCGGCCGCTGAAATCCTCACTCGGTCAAGTTCTCTCGGGCAGGTTACGGG</u> <u>GACGACCTGCGGGAGCACGCGGGCAGTGGCCGGACGCTGAAGCCAGGAGACGATGG</u> <u>AGACGTATGCGGAGGTTGGGAAGGAGGGCAAGCCTTCTGTGCATCGGTGGATCTGCA</u> <u>GGGAGACAGCTCCTTACAGGTGGAGATTCTGACGCACTGAGTGAGCGGGACAAGGTG</u> <u>AAATTCACCTGTTCAAACAAGAGCTGCCTCCCTCACTTCGCCACGACCGAGTTCTCAG</u> <u>TCGTGCGGCAGCACGAGGAGTTTCATCTGGCTGCATGATGCCTACGTGGAGAATGAGGA</u> <u>GTACGCGCGCCTCATCATCCCCCAGCCCCCTCCGAGGCCAGACTTTGAGGCTTCGAGG</u> <u>GAAAAGCTACAGAAATTGGGCGAGGGGGACAGCTCTGTCACTCGGGAAAGAGTTTGCCA</u> <u>AGATGAAGCAGGAGCTGGAAGCGGAGTACCTGGCCATCTTTAAGAAGACAGTTGCGAT</u> <u>GCACGAAGTCTTTCTGCAGCGCCTGGCGGGCCACCCACCCTGCGTCGAGACCACAAC</u> <u>TTCTTTTGTGTTTTTGGAAATATGGACAGGATCTGAGTGTCCGGGGGAAGAACAGGAAGG</u> <u>AGCTCCTCGGAGGGTTTCTGAGGAATATTGTGAAGTCCGCGGATGAAGCCCTCATCAC</u> <u>GGGCATGTGAGGGCTCAAGGAGGTGGATGACTTCTTTGAGCATGAGAGGACCTTCTCTG</u> <u>TTGGAGTATCACACCCGTATCCGAGATGCCTGCCTGCGGGCCGACCCGCTCATGCGCG</u> <u>CCCACAAGTGCCCTGGCAGACGATTATATCCCTATCTCAGCTGCGCTGAGCAGTCTGGG</u> <u>AACACAGGAAGTCAACCAGCTAAGGACGAGCTTCTCAAATTGGCAGAGCTCTTTGAC</u> <u>CGGCTGAGGAAGCTGGAGGGCCGGGTGGCTTCCGATGAGGACCTGAAGCTGTGACAGA</u> <u>TGCTGAGGTACTACATGCGTGACTCACAGGCAGCCAAGGACCTGCTGTACCGGCGGCT</u> <u>GCGGGCACTGCGCGACTACGAGAATGCCAACAAGGCGCTGGACAAGGCGCGCACCCAGG</u> <u>AACCGGGAGGTGCGGCCCCGCCGAGAGCCACCAGCAGCTGTGCTGCCAACGCTTCGAGC</u> <u>GCCTCTCCGACTCCGCCAAGCAAGAGCTCATGGACTTCAAGTCCCGCCGGGTCTCCTC</u> <u>TTTTCGAAAGAATCTATTGAGCTGGCAGAGCTGGAGCTCAAACACGCCCAAGGCCAGC</u> <u>ACCCTGATTCTCCGGAACACCCTTGTGCCCTAAGGGGGAGCCTTAGAGTAGCCAGA</u> <u>GCTCAGCCAGACCCTAATCTGGGATCTCCAGTGACCAGGGTATCCC</u>		
	ORF Start: ATG at 113	ORF Stop: TAG at 1322	
	SEQ ID NO: 158	403 aa	MW at 46384.2kD
NOV52a, CG59564-01 Protein Sequence	METYAEVVGKEGKPCASVDLQGDSSSLQVEISDAVSRDKVKFTVQTKSLPHFAQTEF SVVRQHEEFIWLHDAVENEYAGLIIPPAPPRPDFEASREKLQKLEGDDSSVTREEF AKMKQELEAEYLAIFFKKTVMHEVFLQRLAAHPTLRDHNFFVFLYGGDLSVRGKNR KELGGFLRNIVKSADEALITGMSGLKEVDFFEHERTFLLEYHTRIRDACLRAADRVM RAHKCLADDYIPISAALSSSLGTQEVNQLRTSFLKLAELFDRLRLKLEGRVASDEDLKLS DMLRYMYRDSQAADLLYRRLRALADYENANKALDKARTNRNREVRPAESHQQLCCQRF ERLSDSAKQELMDFKSRVSSFRKNLIELAELELKHAKASTLILRNTLVALKGEP		

Further analysis of the NOV52a protein yielded the following properties shown in Table 52B.

Table 52B. Protein Sequence Properties NOV52a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV52a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 52C.

Table 52C. Geneseq Results for NOV52a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV52a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY94209	Human TRAF four associated factor TFAF2 - Homo sapiens, 406 aa. [CA2245340-A1, 19-FEB-2000]	17..402 23..405	273/386 (70%) 333/386 (85%)	e-160
AAB07856	Amino acid sequence of Smad1 interactor protein clone S1+12-2 - Homo sapiens, 414 aa. [WO200047102-A2, 17-AUG-2000]	17..402 31..413	273/386 (70%) 333/386 (85%)	e-160
AAB43157	Human ORFX ORF2921 polypeptide sequence SEQ ID NO:5842 - Homo sapiens, 460 aa. [WO200058473-A2, 05-OCT-2000]	17..402 77..459	273/386 (70%) 333/386 (85%)	e-160
AAB58368	Lung cancer associated polypeptide sequence SEQ ID 706 - Homo sapiens, 414 aa. [WO200055180-A2, 21-SEP-2000]	17..402 31..413	273/386 (70%) 333/386 (85%)	e-160
AAO13507	Human polypeptide SEQ ID NO 27399 - Homo sapiens, 443 aa. [WO200164835-A2, 07-SEP-2001]	17..400 61..441	242/384 (63%) 317/384 (82%)	e-144

In a BLAST search of public sequence databases, the NOV52a protein was found to have homology to the proteins shown in the BLASTP data in Table 52D.

Table 52D. Public BLASTP Results for NOV52a				
Protein Accession Number	Protein/Organism/Length	NOV52a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UNH7	Sorting nexin 6 (TRAF4-associated factor 2) - Homo sapiens (Human), 406 aa.	17..402 23..405	273/386 (70%) 333/386 (85%)	e-159
Q9CZ03	2810425K19RIK PROTEIN - Mus musculus (Mouse), 406 aa.	17..402 23..405	271/386 (70%) 333/386 (86%)	e-159
Q9Y5X3	Sorting nexin 5 - Homo sapiens (Human), 404 aa.	17..400 22..402	242/384 (63%) 317/384 (82%)	e-143

Q9D8U8	Sorting nexin 5 - Mus musculus (Mouse), 404 aa.	17..400 22..402	241/384 (62%) 314/384 (81%)	e-142
Q96NG4	CDNA FLJ30934 FIS, CLONE FEBRA2007017, MODERATELY SIMILAR TO HOMO SAPIENS TRAF4-ASSOCIATED FACTOR 2 MRNA - Homo sapiens (Human), 277 aa.	1..237 1..237	236/237 (99%) 236/237 (99%)	e-134

PFam analysis predicts that the NOV52a protein contains the domains shown in the Table 52E.

Table 52E. Domain Analysis of NOV52a			
Pfam Domain	NOV52a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PX: domain 1 of 1	23..164	39/160 (24%) 103/160 (64%)	1.6e-15

Example 53.

The NOV53 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 53A.

Table 53A. NOV53 Sequence Analysis		
	SEQ ID NO: 159	3056 bp
NOV53a, CG59553-01 DNA Sequence	CTCCTGCGGGGTCAAATACAGAAATTTACGCACCCTTGGCTTCCTTGGAGCCTAGCGGC TCTCCCCGCGTCCAAGATGGCGGCAGAACGAGCTGGTGGGAAATACAGAACACAGTC AGCAAAAGCAAAGACCCTCGGGGCTGCTCATCTCTGTGATCAGGACTCTGTCTACTA GTGACGATGTGGAAGACAGGGAATGAAAGGGTTCGCTTGAAGAAGCCTACGAGAA ATGTGACCGTGACCTGGATGAATTGATTGTACAGCACTACACAGAATTGACGACAGCC ATTGCGACATACCAGAGCATCACAGAGCGCATCACTAACTCCCGAAATAAAATAAAGC AGGTAAAGAGAACTGCTTTTCATGCAAGATGCTGCTGCACTGCAACGGGATGAGCT TCGGAACCTGTGGATTGAAGGAATTGAGCATAAGCATGCTCTGAACCTGTTGGATGAA ATTGAGAATATCAAGCAAGTGCTCAAAAGCTGGAACAGTGCATGGCCAGCAAGCACT ATCTCAGTGCCACTGACATGTTGGTGTGAGCAGTTGAGTCTTTGGAGGGCCCCCTGCT CCAGGTGGAAGGACTGAGTGACCTTCGACTAGAGCTTCACAGCAAGAAGATGAACCTT CACTTGGTTCTCATAGATGAACACACCGGCACCTGTACATCAAATCGACTAGCCGAG TTGTGCAGCGTAACAAGGAAAAGGGAAATCAGCTCCCTCGTGAAAGATGCTTCTGT TCCTCTGATTGATGTTACAAACCTCCCTACTCCTCGAAAATTCCTTGATACCTCTCAC TATTCTACTGCTGGAAGCTCAAGTGTGAGGGAGATAAATCTGCAGGACATCAAGGAAG ATTTAGAAATTGGATCCAGAGGAAAACAGCACCCCTGTTATGGGTATCCTCATTAAGGG CTTGGCGAACTGAAGAAGATCCAGAAACAGTTAAGGCAATCATAGAGCGCTTGGAG CAGGAGTTGAAGCAAATTTGTGAAGAGGTCTACAACCCAGGTGGCAGACAGTGGCTATC AGCGGGGGAGAACGTTACTGTGGAGAACCAACCAAGGTGCTTCTAGAACTGCTGCGAGA GTTACTGTTTGACAAGTTAATGCTGTAGCCGCTGCACACTCTGTGGTCTCTGGGATAC CTGCAGGACACTGTAGTGACTCCACTGACTCAGCAGGAAGATATCAAACCTGTATGATA TGGCAGATGTATGGGTGAAGATCCAGATGTTCTACAGATGCTATTAACCTGAGTACTT GGATATGAAAATACTCGTACGGCCTCTGAACCATCAGTCAACTAAGCTATGCCAGC ACTGGACGAGAGTTTGCAGCCTTTTGTGCAAGAAAGAACTCAAAGGCCAAAAAATT CTCTTTTCAAGTTCGAATCGTCCCTCCATGCCATCAGTATGAGCGCCTATCTGCGAGA ACAGAGAAGGGAGCTCTATAGTCGGAGTGGAGAAGTGAAGGGGGTCTGTATGACAAC TTAATTGAAGGTGGAGGAACAAATTTGTCTGCAACCTGGAGCCAGAAACATTACCG TCATATTCCACCATTACTAAGATTATTAGGAGATTGAGCATGCTCTGGGCTCTGG CCCAGCCAAACAGTGTCTCTCGAGAGTTTCTACCGTGTACATCAAAACATCTTT CTCAATCAAGTCTGGCTGAGATCAACAAGGAGATTGAAGGAGTCACTAAACATCTG	

	ACCCTTTGAAGATTCTGGCCAACGCAGACACCATGAAGGTGCTGGGAGTGCAGCGGCC TCTCCTACAGAGCACAATCATTGTGGAGAAGACAGTTCAAGACCTCCTGAACCTGATG CATGACTTGAGTGCATATTAGATCAATTCTCAACATGGTGTGCGTGAAGCTCCAGG AGTACAAGGACACCTGCAGCTTACAGGGGTATTGTCCAGTCAGAAGAAAACT TGTCAATCAGTGCATCCTGGGCAAAAGATGATGATATCAGCAGACTCTTGAATCTCTA CCAAACCTGGATGAATATGGCTCAACCCAAACAGCTGAGGCCAAAAAGAGAGGAGGAAG AAGATTTTATAAGGGCAGCTTTTGGCAAGGAGTCTGAAGTTCTTATTGGGAACCTGGG TGATAAATTAATCCCTCCACAAGACATCCTTCGTGACGTCAGTGACCTCAAAGCCTTG GCCAACATGCATGAAAGCCTGGAATGGTTGGCAAGTCGAACAAAGTCAGCTTTTCCCA ATCTTTCTACATCCAGATGCTTTCTCCTGCTCAAGACAGCCACACGAACCGGATCT CCCCCCAGTGTGAGAGCAGATCATGCAGACTCTCAGTGAACCTTGCCAAATCGTTCCAG GATATGGCTGACCGCTGCTTGCTTGTCTTACATCTGGAAGTGAGGGTTCACTGTTTCC ACTATCTTATCCCTCTTGCAAAGGAGGGGAATATGCCATTGTGGCTAATGTGGAAAG TATGGATTATGACCCCTGGTGGTCAAGCTCAACAAAGATATCAGCGCCATGAAGAG GCCATGAGCGCCAGCCTTCAGCAGCACAAGTCCAGTATATCTTGAAGCCTGGGCC ACCTGATCTCCTGCATCCTCATTAAATGGTGGCCAGTACTTCAGGCGCATCAGTGAGTC TGGCATCAAGAAAATGTGTAGGAACATTTTGTCTTCAGCAGAATTTGACCAACATC ACCATGTGCGGGAGGCAGACCTGGACTTTGCAAGGCAGTACTACGAGATGCTTACA ACACAGCTGACGAGCTCCTGAACCTGGTGGTGGACCAGGGTGTGAAGTACACGGAGCT GGAGTACATCCACGCTCTGACCTGTGACCGCAGCCAGACTGGGGTGGGGGAAGTGC ACCACCCAGAACACGAGCTGCAGAGGAGGCTCAAAGAGATCATCTGCGAGCAGGCTGC CATCAAGCAAGCCACCAAGGACAAGAAGATAACTACCGTTTAGCAGGGCGTACTGCGG TTGGTGACGGGGTCCCCCTCAGTCACACTCACTTTTTCCTC		
	ORF Start: ATG at 75 ORF Stop: TAA at 2988		
	SEQ ID NO: 160	971 aa	MW at 109984.9kD
NOV53a, CG59553-01 Protein Sequence	MAEEAAGGKYRSTVSKSDPSGLLISVIRTLSTSDVDRENEKGRLEEAYEKCDRLD DELIVQHYTELTTAIRTYSITERITNSRNKIKQVKENLLSCKMLLHCKRDELRLKI EGIEHKHVLNLLDEIENIKQVPQKLEQCMASKHYLSATDMLVSAVESLEGPLLQVEGL SDLRLLELHSSKMMNLHLVLIDELHRHLYIKSTSRVQRNKEKGKISSLVKDASVPLIDV TNLPTPRKFLDTSHYSTAGSSSVREINLQDIKEDLELDPEENSTLFMGILIKGLAKLK KIPETVKAIIERLEQELKQIVKRSTTQVADSGYQRGENVTVENQPRLLLELLELFDK FNAVAAHSSVVLGYLQDTVVTPLTQQEDIKLYDMADVWVKIQDVLQMLLLEYLDMKNT RTASEPSAQLSYASTGREFAAFFAKKKPQRPKNSLKFESSSHAISMSAYLREQRREL YSRSGELQGGPDDNLEGGGTFKVPCKPGARNITVIFHPLLRFIQEIEHALGLGPAKQC PLREFLTVYIKNIFLNQVLAEINKEIEGVTKTSDPLKILANADTMKVLGVQRPLLQST IIVEKTVQDLLNLMHDLAYSQDQFLNMVCVKLQEYKDTCTAAYRGIVQSEEKLVISAS WAKDDDISRLKSLPNWMNMAQPKQLRPKREEEEDFIRAAPGKSESVLIGNLGDKLIP PQDILRDVSDLKALANMHESLEWLASRTKSAFNSLSTSQMLSPAQDSHTNTDLPVSE QIMQTLSELAKSFQDMADRCLLVLHLEVRVHCFHYLIPLAKEGNYAIVANVESMDYDP LVVVLNKKDISAIEEAMSASLQHKFYIFEGLGHILSCILINGAQYFRRISESIGIKKM CRNIFVLQQLNTNITMSREADLDFARQYQYEMLYNTADELLNLVVDQGVKYTELEYIHA LTLHRSQTGVGELTTQNTSCRGGSKRSSASRLPSSKPPRTR		

Further analysis of the NOV53a protein yielded the following properties shown in Table 53B.

Table 53B. Protein Sequence Properties NOV53a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV53a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 53C.

Q62824	RSEC8 - Rattus norvegicus (Rat), 975 aa (fragment).	1..947 1..948	902/948 (95%) 925/948 (97%)	0.0
Q9P102	REC8 - Homo sapiens (Human), 637 aa (fragment).	339..947 2..610	609/609 (100%) 609/609 (100%)	0.0

PFam analysis predicts that the NOV53a protein contains the domains shown in the Table 53E.

Table 53E. Domain Analysis of NOV53a			
Pfam Domain	NOV53a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 54.

The NOV54 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 54A.

Table 54A. NOV54 Sequence Analysis			
	SEQ ID NO: 161	501 bp	
NOV54a, CG59545-01 DNA Sequence	<u>CAACACGAGGAACAATGTCTTCTTTACCCGTGCCATACAACTGCCTGTGTCTTTGTC</u> TGTTGGTTCTCTGCGTGATAATCAAAGGGACACTGATCGACTCTTCTATCAACGAACCA CAGCTGCAGGTGGATTCTACACTGAGATGAATGAGGACTCAGAAATTGCCTTCCATT TGCAGTGCACCTAGGCCGTCGTGTGGTCATGAACAGTCGTGAGTTGGGATATGGAT GTTGGAGGAGAATTTACACTATGTGCCCTTTGAGGATGGCAAACCATTTGACTTGCGC ATCTACGTGTGTCTCAATGAGTATGAGGTAAGGTAAATGGTGAATACATTTATGCCT TTGTCCATCGAATCCCGCCATCATATGTGAAGATGATTCAGTGTGGAGAGATGTCTC CCTGGACTCAGTGCTTGTCAACAATGGACGGAGATGATCACACTCCTCATTGTTGAGG <u>AAACCCTCTTTCTACCTGACCATGGGATTCTTAGAGC</u>		
	ORF Start: ATG at 15	ORF Stop: TGA at 441	
	SEQ ID NO: 162	142 aa	MW at 16511.9kD
NOV54a, CG59545-01 Protein Sequence	MSSLLPVPYKLPVSLVSGSCVLIKGTLDSSINEPQLQVDFYTEMNEDSEIAFHLRVHL GRRVVMNSREFGIWMLEENLHYVPFEDGKPFDLRIYVCLNEYEVKVNGEYIYAFVHRI PPSYVKMIQVRDVSLSVLVNNRR		

Further analysis of the NOV54a protein yielded the following properties shown in Table 54B.

Table 54B. Protein Sequence Properties NOV54a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV54a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 54C.

Table 54C. Geneseq Results for NOV54a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV54a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG66741	Human Charcot-Leyden crystal protein 5A (CLC5A) - Homo sapiens, 142 aa. [CN1302875-A, 11-JUL-2001]	1..142 1..142	139/142 (97%) 139/142 (97%)	2e-77
AAG66742	Human Charcot-Leyden crystal protein 5B (CLC5B) - Homo sapiens, 170 aa. [CN1302875-A, 11-JUL-2001]	6..142 34..170	136/137 (99%) 136/137 (99%)	3e-76
AAM79041	Human protein SEQ ID NO 1703 - Homo sapiens, 139 aa. [WO200157190-A2, 09-AUG-2001]	1..139 1..139	107/139 (76%) 116/139 (82%)	2e-56
AAY28350	Full Placental Protein 13 amino acid sequence - Homo sapiens, 139 aa. [WO9938970-A1, 05-AUG-1999]	1..139 1..139	107/139 (76%) 116/139 (82%)	2e-56
AAG78627	Human Charcot-Leyden crystal 4 CLC4 protein #2 - Homo sapiens, 167 aa. [CN1302876-A, 11-JUL-2001]	6..139 34..167	102/134 (76%) 111/134 (82%)	2e-53

- 5 In a BLAST search of public sequence databases, the NOV54a protein was found to have homology to the proteins shown in the BLASTP data in Table 54D.

Table 54D. Public BLASTP Results for NOV54a				
Protein Accession Number	Protein/Organism/Length	NOV54a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UHV8	PLACENTAL PROTEIN 13 (PLACENTA PROTEIN 13) - Homo sapiens (Human), 139 aa.	1..139 1..139	107/139 (76%) 116/139 (82%)	9e-56

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Q9NR03	PLACENTAL PROTEIN 13-LIKE PROTEIN - Homo sapiens (Human), 139 aa.	1..139 1..139	86/139 (61%) 107/139 (76%)	9e-45
A46523	Charcot-Leyden crystal protein - human, 142 aa.	1..142 1..142	76/142 (53%) 96/142 (67%)	7e-36
Q05315	Eosinophil lysophospholipase (EC 3.1.1.5) (Charcot-Leyden crystal protein) (Lysolecithin acylhydrolase) (CLC) (Galactin-10) - Homo sapiens (Human), 141 aa.	2..142 1..141	75/141 (53%) 95/141 (67%)	3e-35
Q96KD6	PLACENTAL PROTEIN 13-LIKE - Homo sapiens (Human), 104 aa (fragment).	1..104 1..104	66/104 (63%) 79/104 (75%)	1e-31

Pfam analysis predicts that the NOV54a protein contains the domains shown in the Table 54E.

Table 54E. Domain Analysis of NOV54a			
Pfam Domain	NOV54a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Gal-bind_lectin: domain 1 of 1	5..137	37/142 (26%) 106/142 (75%)	3.1e-28

Example 55.

The NOV55 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 55A.

Table 55A. NOV55 Sequence Analysis		
	SEQ ID NO: 163	2071 bp
NOV55a, CG59435-01 DNA Sequence	AAACTATTGTAGGCGCAGTCATGCAGGAAAACCTCAGATTGCTTCATCAGGAGATG ATATTTAAATATGGGATGCTTCATCTATGACATTGGTGGATAAATTCACCCACACAC ATCACCACATGGAATCAGCTCAATATGTTGGAGCAGCAATAGTAACCTTTTAGTAACA GCATCTTCCAGTGGCGACAAATAGTTGTCTCAAGTTGCAAATGTAACCTGTTCAC TTTTAGAGCTTGCTGAAGGGCAAAAGCAGACATGTGTCAATTTAAATCTACATCTAT GTATTTGGTAAGCGGAGGCCATAAATAACACTGTTAATATTGGGATTTAAATCAAAA AGAGTTTCATCGATCTCTAAGGATCATAAAGATCAAGTAACTTGTGTAACATACAAT GGAATGATTGCTACATTGCTTCTGGATCTCTAGTGGTGAAATTTATTTACACAGTGT AACCCTAATTTATCTAGTACTCCTTTTGCCATGGTAGTAACCAAGTTCCGGCACTTG AAGTACTCCTTGTTTAAAGAACTACTACTGGGCAGTGTTCGGATAATGGAATAGTAA CTCTCTGGGATGTAATAGTCAGAGTCCATACCATAAATTTGACAGTGTACACAAAGC TCCAGCGTCAGGCATCTGTTTTCTCCTGTCAATGAATTGCTCTTTGTAACCATAGGC TTGGATAAAAGAATCATCCTCTATGACACTTCAAGTAAGAAGCTAGTGAAAACCTTTAG TGGCTGACACTCCTCTAACTGCGGTAGATTTCATGCCTGATGGAGCCACTTTGGCTAT TGGATCTTCCCGGGGAAAATATATCAATATGATTAAAGAAATGTTGAAATCACCAGTT AAGACCATCAGTGCTCACAAGACATCTGTGCAGTGTATAGCATTTCAGTACTCCACTG TTCTTACTAAGTCAAGTTTAAATAAAGGCTGTTCAAATAAGCCACAAACAGTGAACAA ACGAAGTGTTAATGTGAATGCTGCTAGTGGAGGAGTTCAAGAAATCCGGAAATGTGAGA GAAGCACTGCCACGTCCATTGCCACAGTTCTACCACAACCTATGACATCAGCTATGG	

	GGAAAGGAACAGTTGCTGTTCAAGAAAAAGCAGGTTTGCCTCGAAGCATAAACACAGACACTTTATCTAAGGAAACAGACAGTGGAAAAATCAGGATTCTCCAGCTTTGATGATACTGGGAAAAGTAGTTTAGGTGACATGTTCTCACCTATCAGAGATGATGCTGTAGTTACAAGGGAAGTGATGAGTCCATAGGCAAAGGAGATGGCTTTGACTTTCTACCCGAGTTGAAGTCAAGTGTCTTCTCCAAGAAAAATCCAGTAACCTCAAGTACTTCAGTATTGCATCTAGTCTCTTAATGTTTTATGGGATCTCCAGGGAAGAGGAAAAATGAAAAACCGTGATCTAACAGCTGAGTCTAAGAAAAATATATATGGGAAAAACAGGAATCTAAAGACTCCTTCAAACAGTTAGCAAAGTTGGTCACATCTGGTGCTGAAAGTGGAATCTAAATACCTCTCCATCATCTAACCAAACAAGAAATCTTGAGAAATTTGAAAAGCCAGAGAATGAAATTTGAAGCCAGTTGATATGTGAACCCCAATCAATGGATCCTCAACTCCAAATCCAAAGATAGCATCTTCTGTCACTGCTGGAGTTGCCAGTTCACTCTCAGAAAAATAGCCGACAGCATTGGAAATAACCGGCAAAATGCACCATTGACTTCCATTCAAATTCGTTTTATTTCAGAACATGATACAGGAAACGTTGGATGACTTTAGAGAAGCATGCCATAGGGACATTGTGAATTTGCAAGTGGAGATGATTAAACAGTTTCATATGCAACTGAATGAAATGCATTCTTTGCTGGAAAGATACTCAGTGAATGAAGGTTTAGTGGCTGAAATTTGAAAGACTACGAGAAGAAAACAAAAGATTACGGGCCACTTTTGAAATTTCACTGAATACCTTAATGTTCTGTGTAATTTGGGAAGTTTCTGGCAACACAGAACTACATAGAATCAT		
	ORF Start: ATG at 22	ORF Stop: TGA at 1999	
	SEQ ID NO: 164	659 aa	MW at 71851.2kD
NOV55a, CG59435-01 Protein Sequence	MQENLRFASSGDDIKIWDASSMTLVDFKNPHTSPHGISSICWSSNSNFLVTASSSGDKIVVSSCKCKPVPPLLELAEGQKQTCVNLNSTSMYLVSGGLNNTVNIWDLKSKRVHRSLLKDHKQVTCVTYNWNCYIASGSLSGEII LHSVTTNLSSTPFGHGSNQVRHLKYSLFKKSLLSVSDNGIVTLWDVNSQSPYHNFDVSHKAPASGICFSPVNELEFVTIGLDRKIILYDTSSKKLVKTLVADTPLTAVDFMPDGATLAIGSSRGKIIYQYDLRMLKSPVKTI SAHKTSVQCIAPQYSTVLTKSSSLNKGCSENKPTTVNKRSVNVNAAAGGVQNSGIVREAPATSIATVLPQPMTSAMKGTVAQEKAGLPRSINTDTLSKETDSGKNQDFSSPDDTGKSSLGDMFSPIRDDAVVNKGSDESIGKGDGDFLPQLNSVFPFRKNPVTSSVLSHSSPLNVFMGSPGKEENENRDLTAESKKIYMGKQESKDSFKQLAKLVTSGAESGNLNTSPSSNQTRNSEKFEKPENEIEAQLICEPPINGSSTPNPKIASSVTAGVASSLSEKIADSIIGNRQNAPLTSIQIRFIQNMIQETLDDFREACHRDIVNLQVEMIKQFHMQLNEMHSLRLERYSVNEGLVAEIERLREENKRLRAHF		
	SEQ ID NO: 165	2009 bp	
NOV55b, CG59435-02 DNA Sequence	AAACTATTGTAGGCGCAGTCATGCAGGAAAACCTCAGATTGCTTCATCAGGAGATGATATATAAATATGGGATGCTTCATCTATGACATTGGTGGATAAATCAACCCACACACATCACCACATGGAATCAGCTCAATATGTTGGAGCAGCAATAATACTTTTAGTAAACACATCTTCCAGTGGCGACAAAATAGTTGTCTCAAGTTGCAAAATGAAACCTGTTCCACTTTTAGAGCTTGCTGAAGGGCAAAAGCAGACATGTTGCAATTTAAATTTCTACATCTATGTATTGGTAAGCGGAGGCCCTAAATAACACTGTTAATATTGGGATTTAAATCAAAAGAGTTTCATCGATCTCTTAAGGATCATAAAGATCAAGTAAGTGTGTAACATACAATGGAAATGATTGCTACATTGCTTCTGGATCTCTTAGTGGTGAATTAATTTACACAGTGTAAACCTAATTTATCTAGTACTCCTTTTGGCCATGGTAGTAACCACTCTGTTCCGCACTTGAAGTACTCTTGTTTAAGAAATCACTACTGGGCAGTGTTCGGATAATGGAAATAGTAACCTCTCTGGGATGTAATAGTCAGAGTCCATACCATAACTTTGACAGTGTACACAAAGCTCCAGCGTCAGGCATCTGTTTTCTCTGTCAATGAATTGCTCTTTGTAACCATAGGCTTGGATAAAAGAATCATCCTCTATGACACTTCAAGTAAGAAGCTGTGAAAACTTAGTGGCTGACACTCCTCTAACTGCGGTAGATTTTATGCCTGATGGAGCCACTTTGGCTATTGGATCTTCCCGGGGAAAAATATATCAATATGATTTAAGAATGTTGAATCACCA GTTAAGACCATCAGTGTCTACAAGACATCTGTGCAGTGTATAGCAATTCAGTACTCCA CTGTTCTTACTAAGTCAAGTTTAAATAAAGGCTGTTCAAATAAGCCACAACAGTGAA CAAACGAAGTGTTAATGTGAATGCTGCTAGTGGAGGAGTTCAGAATTCGGGAATGTGAGAGAAGCACCTGCCAGTCCATTGCCACAGTTCTACCACAACCTATGACATCAGCTA TGGGGAAGGAACAGTTGCTGTTCAGAAAAAGCAGGTTTGCCTCGAAGCATAAACACAGACACTTTATCTAAGGAAACAGACAGTGGAAAAATCAGGATTCTCCAGCTTTGATGATACTGGGAAAAGTAGTTTAGGTGACATGTTCTCACCTATCAGAGATGATGCTGTAGTTAACAAGGGAAGTGATGAGTCCATAGGCAAAGGAGATGGCTTTGACTTTCTACCGCATTTGAAGTCAAGTGTCTTCTCCAAGAAAAATCCAGTAACCTCAAGTACTTCAGTATTG CATTCTAGTCTCTTAATGTTTTATGGGATCTCCAGGGAAGAGGAAAAATGAAAAACGTGATCTAACAGCTGAGTCTAAGAAAAATATATATGGGAAAAACAGGAATCTAAAGACTCTTCAAACAGTTAGCAAAGTTGGTGCACATCTGGTGCTGAAAGTGGAATCTAAATACC TCTCCATCATCTAACCAAACAAGAAATCTGAGAAATTTGAAAAAGCCAGAGAAATGAAAT TGAAGCCAGTTGATATGTGAACCCCAATCAATGGATCCTCAACTCCAAATCCAAAGATAGCATCTTCTGTCACTGCTGGAGTTGCCAGTTCACTCTCAGAAAAATAGCCGACAGCATTTGAAATAACCGGCAAAATGCACATTGACTTCCATTCAAGATTCGTTTTATTCA GAACATGATACAGGAACGTTGGATGACTTTAGAGAAGCATGCCATAGGGACATTGTGAATTTGCAAGTGGAGATGATTAAACAGTTTCATATGCAACTGAATGAAATGCATTCTTTGCTGGAAAGATACTCAGTGAATGAAGGTTTAGTGGCTGAAATTTGAAAGACTACGAG AAGAAAAACAAAAGATTACGGGCCACTTTTGAAATTT		
	ORF Start: ATG at 22	ORF Stop: TGA at 2002	
	SEQ ID NO: 166	660 aa	MW at 71965.3kD
NOV55b,	MQENLRFASSGDDIKIWDASSMTLVDFKNPHTSPHGISSICWSSNNNFLVTASSSGDK		

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CG59435-02 Protein Sequence	IVVSSCKCKPVPLLELAEGQKQTCVNLNSTSMYLVSGGLNNTVNIWDLKSKRVHRSK DHKDQVTCVTYNWDCYIASGSLSGEII LHSVTTNLSSTPFGHGSNQSVRHLKYSLFK KSLLGSVSDNGIVTLWDVNSQSPYHNFDSVHKAPASGICFSPVNELLFVTIGLDKRII LYDTSSKLVKTLVADTPLTAVDMPDGATLAIGSSRGKIYQYDLRMLKSPVKTI SAH KTSVQCI AFQYSTVLTKSSLNKGCSNKPTTVNKRSVNVNAASGGVQNSGIVREAPATS IATVLPQPMTSAMGKGTAVQEKAGLPRSINTDTLSKETD SGKNQDFSSFDDTGKSSL GDMFSPIRD DAVVNKGSDSIGKGDGDFLPQLNSVFPKRKNPVTSSSTVLHSSPLNV FMGSPGKEENENRDLTAESKKIYMGKQESKDSFKQLAKLVTSGAESGNLNTSPSSNQ RNSEKFEKENEIEAQLICEPPINGSSTPNPKIASSVTAGVASSLSEKIADSI GNNRQ NAPLTSIQIRFIQNMIQETLDDFREACHRDI VNLQVEMIKQFHMQLNEMHSL LERYSV NEGLVAEIERLREENKRLRAHF
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 55B.

Table 55B. Comparison of NOV55a against NOV55b.		
Protein Sequence	NOV55a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV55b	1..659	658/660 (99%)
	1..660	659/660 (99%)

Further analysis of the NOV55a protein yielded the following properties shown in Table 55C.

5

Table 55C. Protein Sequence Properties NOV55a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV55a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 55D.

Table 55D. Geneseq Results for NOV55a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV55a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG74568	Human colon cancer antigen protein SEQ ID NO:5332 - Homo sapiens, 404 aa. [WO200122920-A2, 05-APR-2001]	256..659 1..404	399/404 (98%) 399/404 (98%)	0.0

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AAE10677	Human NEDD1-related protein - Homo sapiens, 208 aa. [WO200172955-A2, 04-OCT-2001]	453..611 2..159	145/159 (91%) 149/159 (93%)	4e-75
AAM70774	Human bone marrow expressed probe encoded protein SEQ ID NO: 31080 - Homo sapiens, 67 aa. [WO200157276-A2, 09-AUG-2001]	240..306 1..67	67/67 (100%) 67/67 (100%)	9e-31
AAM06190	Peptide #4872 encoded by probe for measuring breast gene expression - Homo sapiens, 67 aa. [WO200157270-A2, 09-AUG-2001]	240..306 1..67	67/67 (100%) 67/67 (100%)	9e-31
ABB23122	Protein #5121 encoded by probe for measuring heart cell gene expression - Homo sapiens, 65 aa. [WO200157274-A2, 09-AUG-2001]	307..371 1..65	65/65 (100%) 65/65 (100%)	3e-29

In a BLAST search of public sequence databases, the NOV55a protein was found to have homology to the proteins shown in the BLASTP data in Table 55E.

Table 55E. Public BLASTP Results for NOV55a				
Protein Accession Number	Protein/Organism/Length	NOV55a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
I60167	regulatory protein Nedd1 - mouse, 660 aa.	1..659 1..660	564/660 (85%) 607/660 (91%)	0.0
P33215	NEDD1 protein - Mus musculus (Mouse), 675 aa (fragment).	1..659 16..675	564/660 (85%) 607/660 (91%)	0.0
Q9CWK2	NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-REGULATED GENE 1 - Mus musculus (Mouse), 660 aa.	1..659 1..660	563/660 (85%) 606/660 (91%)	0.0
Q9FI89	SIMILARITY TO REGULATORY PROTEIN NEDD1 - Arabidopsis thaliana (Mouse-ear cress), 787 aa.	8..533 15..532	145/550 (26%) 246/550 (44%)	4e-40
BAB75165	WD-40 REPEAT PROTEIN - Anabaena sp. (strain PCC 7120), 1526 aa.	2..298 916..1208	92/307 (29%) 147/307 (46%)	2e-18

PFam analysis predicts that the NOV55a protein contains the domains shown in the Table 55F.

Table 55F. Domain Analysis of NOV55a

Pfam Domain	NOV55a Match Region	Identities/ Similarities for the Matched Region	Expect Value
WD40: domain 1 of 7	28..61	6/37 (16%) 27/37 (73%)	57
WD40: domain 2 of 7	70..105	10/37 (27%) 27/37 (73%)	0.062
WD40: domain 3 of 7	111..147	9/37 (24%) 28/37 (76%)	20
WD40: domain 4 of 7	153..190	10/38 (26%) 29/38 (76%)	3.4
WD40: domain 5 of 7	197..234	7/38 (18%) 25/38 (66%)	19
WD40: domain 6 of 7	240..275	14/37 (38%) 28/37 (76%)	3.1
WD40: domain 7 of 7	282..316	8/37 (22%) 26/37 (70%)	1.3e+03

Example 56.

The NOV56 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 56A.

Table 56A. NOV56 Sequence Analysis

	SEQ ID NO: 167	1771 bp
NOV56a, CG59439-01 DNA Sequence	GACTGTTTCACCATGCAGTGGCTAATGAGGTTCCGGACCCCTCTGGGGCATCCACAAAT CCTTCCACAACATCCACCCTGCCCTTCACAGCTGCGCTGCCGGTCTTTATCAGAATT TGGAGCCCCAAGATGGAATGACTATGAAGTACCGGAGGAATTTAACTTTGCAAGTTAT GTACTGGACTACTGGGCTCAAAGGAGAAGGAGGGCAAGAGAGGTCCAAATCCAGCTT TTTGGTGGGTGAATGGCCAAGGGATGAAGTAAAGTGGAGCTTCAGAGAGATGGGAGA CCTAACCCGCGGTGTAGCCAACGCTCTCACACAGACCTGTGGCTTACAACAGGGAGAC CATCTGGCCTTGATGCTGCCTCGAGTTCCTGAGTGGTGGCTGGTGGCTGTGGGCTGCA TGCGAACAGGGATCATCTTCATTCCTGCGACCATCTGTGAAGGCCAAAGACATTCT CTATCGACTACAGTTGTCTAAAGCCAAGGGCATTGTGACCATAGATGCCCTTGCCCTCA GAGGTGGACTCCATAGCTTCTCAGTGCCCTCTCTGAAAACCAAGCTCCTGGTGTCTG ATCACAGCCGTGAAGGGTGGCTGGACTTCCGATCGCTGGTTAAATCAGCATCCCCAGA ACACACCTGTGTTAAGTCAAAGACCTTGGACCCAATGGTTCATCTTCTCACCAGTGGG ACCACAGGCTTCCCCAAGATGGCAAACACTCCCCATGGGTGGGCTTACAAACCTCCT TCCCAGGAAGTAGGAAATTACGGAGCCTGAAGACATCTGATGTCTCCTGGTGCCTGTC GGACTCAGGATGGATTGTGGCTACCATTTGGACCCCTGGTGAACCATGGACAGCGGGT TGTACAGTCTTTATCCACCATCTGCCACAGTTTGACACCAAGGTATGGCATCACAATCAAAC TGTTGAAATACCCATTAAACACTTTTGGGGGGTATCATCTATATATCGAATGATTCT GCAGCAGGATTTACACAGCATCAGGTTCCCTGCCCTGGAGCACTGCTATACTGGCGGG GAGGTGCTGTGCCCCAAGGATCAGGAGGAGTGGAAGAACGACGACGGGCTTCTGTCTCT ACGAGAACTATGGGCAGTCGGAAACGGGACTAATTTGTGCCACCTACTGGGGAATGAA GATCAAGCCGGGTTTCATGGGGAAGGCCACTCCACCTACGACGTCCAGGTCAATTGAT GACAAGGGCAGCATCCTGCCACCTAACACAGAAGGAAACATTGGCATCACAATCAAAC CTGTCAGGCTGTGAGCCTTTCATGTGCTATGAGGGTGACCCAGAGAAGACAGCTAA AGTGAATGTGGGGACTTCTACAACACTGGGGACAGAGGTAAGATGGATGAAGAGGGC TACATTTGTTTCTGGGGAGGAGTGATGACATCATTAATGCCTCTGGGTATCGCATCG GGCCTGCAGAGGTTGAAAGCGCTTTGGTGGAGCACCCAGCGGTGGCGGAGTCAGCCGT GGTGGGCAGCCAGACCCGATTCGAGGGGAGGTGGTGAAGGCCCTTATTGTCTGACC	

	CCACAGTTCCTGTCCCATGACAAGGATCAGCTGACCAAGGAAGTGCAGCAGCATGTCA AGTCAGTGACAGCCCCATACAAGTACCAAGGAAGGTGGAGTTTGTCTCAGAGCTGCC AAAAACCATCACTGGCAAGATTGAACGGAAGGAAGTTCGGAAAAAGGAGACTGGTCAG ATGTAATCGGCAGTGAAGTCAAGACGCACTG		
	ORF Start: ATG at 13	ORF Stop: TAA at 1744	
	SEQ ID NO: 168	577 aa	MW at 65272.6kD
NOV56a, CG59439-01 Protein Sequence	MQWLMRFRTLWGIHKSFHNIHPAPSQLRCRSLSEFGAPRWNDYEVPEEFNFASYVL DYWAQKEKEGKRGPNPAFWVWNGQDEVKWSFREMGLTRRVANVFTQTCCGLQQGDHLAL MLPRVPEWWLVAVGCMRTGIIIFIPTATILLKAKDILYRLQLSKAKGIVTIDALASEVDS IASQCPSLTKLLVSDHSREGWLDFRSLVKSASPEHTCVKSKTLDPMVIFFTSGTTGF PKMAKSHGLALQPSFPGSRKLRSLKTSVSWCLSDSGWIVATIWTLVEPWTAGCTVF IHHLPPQFDTKVIIQTLLKYPINHFVGVSSIYRMILQQDFTSIRFPALEHCYTGGEVVL PKDQEEWKRRRTGLLLYENYQSQSETGLICATYWGMIKPGFMGKATPPYDVQVIDDKGS ILPNTTEGNIGIRIKPVRPVSLEFMCYEGDPEKTAKECGDFYNTGDRGKMDDEEYICF LGRSDDIINASGYRIGPAEVESALVEHPVAESAUVGSPDPIRGEVVKAFIVLTPQFL SHDKDQLTKELQHVKSVTAPYKYPRKVEFVSELPKTIITGKIERKELRKKETGQM		
	SEQ ID NO: 169	1659 bp	
NOV56b, CG59439-02 DNA Sequence	GTTTCACCATGCAGTGGCTAATGAGGTTCCGGACCCTCTGGGGCATCCACAAATCCTT CCACAACATCCACCTGCCCCCTTCACAGCTGCGCTGCCGGTCTTTTATCAGAATTTGGA GCCCAAGATGGAATGACTATGAAGTACCGGAGGAATTTAACTTTGCAAGTTATGTAC TGGACTACTGGGCTCAAAAGGAGAAGGAGGGCAAGAGAGTCCAAATCCAGCTTTTGT GTGGTGAATGGCCAAAGGGGATGAAGTAAAGTGGAGCTTCAGAGAGATGGGAGACCTA ACCCGCCGTGTAGCCAACGCTCTTCACACAGACCTGTGGCCTACAACAGGGAGACCATC TGGCCTTGATGCTGCCTCGAGTTCCTGAGTGGTGGCTGGTGGCTGTGGGCTGCATGCG AACAGGGATCATCTTCATTCCTGCGACCATCTGTGTAAGGCCAAAGACATTCTCTAT CGACTACAGTTGTCTAAAGCCAAGGGCATTGTGACCATAGATGCCCTTGCTCAGAGG TGGACTCCATAGCTTCTCAGTGCCCTCTCTGAAAACCAAGCTCTGGTGTCTGATCA CAGCGCTGAAGGGTGGCTGGACTTCCGATCGCTGGTTAAATCAGCATCCCCAGAACAC ACCTGTGTTAAGTCAAAGACCTTGGACCCAATGGTCATCTTCTCACCAGTGGGACCA CAGGCTTCCCCAAGATGGCAAAACACTCCCATGGGTTGGCCTTACAACCTCTCTCCC AGGAAGTAGGAAATTACGGAGCCTGAAGACATCTGATGTCTCCTGGTGCCTGTGCGAC TCAGGATGGATTGTGGCTACCATTTGGACCTGGTAGAACCATGGACAGCGGGTTGTA CAGTCTTTATCCACCATCTGCCACAGTTTGACACCAAGGTATCATACAGACATTGTT GAAATACCCCATTAACCACTTTTGGGGGGTATCATCTATATATCGAATGATTCTGCAG CAGGATTTACCAGCATCAGGTTCCCTGCCCTGGAGCACTGCTATCTGCGGGGAGG TCGTGTTGCCCAAGGATCAGGAGGAGTGGAAAAGACGGACGGGCTTCTGCTCTACGA GAACATATGGGCAGTCGGAAACGGGACTAATTTGTGCCACCTACTGGGGAATGAAGATC AAGCCGGGTTTCATGGGGAAGGCCACTCCACCCTACGACGTCCAGGGTGACCCAGAGA AGACAGCTAAAGTGGAAATGTGGGGACTTCTACAACACTGGGGACAGAGGAAAGATGGA TGAAGAGGGCTACATTTGTTTCTGGGGAGGAGTGATGACATCATTAATGCCTCTGGG TATCGCATCGGGCTGCAGAGGTTGAAAGTGCTTTGGTGGAGCACCCAGCGGTGGCGG AGTCAGCCGTGGTGGGCAGCCAGACCCGATTTCGAGGGGAGGTGGTGAAGGCCTTTAT TGTCTGACCCACAGTTCCTGTCCCATGACAAGGATCAGCTGACCAAGGAAGTGCAG CAGCATGTCAAGTCAGTGACAGCCCCATACAAGTACCCAAGGAAAGTGGAGTTTGTCT CAGAGCTGCCAAAACCATCACTGGCAAGATTGAACGGAAGGAAGTTCGGAAAAGGA GACTGGTCAGATGTAATCGGCAGTGAAGTCAAGAC		
	ORF Start: ATG at 9	ORF Stop: TAA at 1638	
	SEQ ID NO: 170	543 aa	MW at 61518.2kD
NOV56b, CG59439-02 Protein Sequence	MQWLMRFRTLWGIHKSFHNIHPAPSQLRCRSLSEFGAPRWNDYEVPEEFNFASYVL DYWAQKEKEGKRGPNPAFWVWNGQDEVKWSFREMGLTRRVANVFTQTCCGLQQGDHLAL MLPRVPEWWLVAVGCMRTGIIIFIPTATILLKAKDILYRLQLSKAKGIVTIDALASEVDS IASQCPSLTKLLVSDHSREGWLDFRSLVKSASPEHTCVKSKTLDPMVIFFTSGTTGF PKMAKSHGLALQPSFPGSRKLRSLKTSVSWCLSDSGWIVATIWTLVEPWTAGCTVF IHHLPPQFDTKVIIQTLLKYPINHFVGVSSIYRMILQQDFTSIRFPALEHCYTGGEVVL PKDQEEWKRRRTGLLLYENYQSQSETGLICATYWGMIKPGFMGKATPPYDVQGDPEKTA KVECGDFYNTGDRGKMDDEEYICFLGRSDDIINASGYRIGPAEVESALVEHPVAESA VVGSPDPIRGEVVKAFIVLTPQFLSHDKDQLTKELQHVKSVTAPYKYPRKVEFVSEL PKTIITGKIERKELRKKETGQM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 56B.

Table 56B. Comparison of NOV56a against NOV56b.		
Protein Sequence	NOV56a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV56b	1..577	543/577 (94%)
	1..543	543/577 (94%)

Further analysis of the NOV56a protein yielded the following properties shown in Table 56C.

Table 56C. Protein Sequence Properties NOV56a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4712 probability located in mitochondrial matrix space; 0.1737 probability located in mitochondrial inner membrane; 0.1737 probability located in mitochondrial intermembrane space
SignalP analysis:	Likely cleavage site between residues 23 and 24

A search of the NOV56a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 56D.

Table 56D. Geneseq Results for NOV56a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV56a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB43245	Human ORFX ORF3009 polypeptide sequence SEQ ID NO:6018 - Homo sapiens, 537 aa. [WO200058473-A2, 05-OCT- 2000]	46..573 1..527	309/529 (58%) 402/529 (75%)	0.0
AAM80008	Human protein SEQ ID NO 3654 - Homo sapiens, 302 aa. [WO200157190-A2, 09-AUG- 2001]	331..577 24..302	247/279 (88%) 247/279 (88%)	e-140
AAM80007	Human protein SEQ ID NO 3653 - Homo sapiens, 302 aa. [WO200157190-A2, 09-AUG- 2001]	331..577 24..302	247/279 (88%) 247/279 (88%)	e-140

AAM41894	Human polypeptide SEQ ID NO 6825 - Homo sapiens, 390 aa. [WO200153312-A1, 26-JUL-2001]	257..573 7..323	193/317 (60%) 246/317 (76%)	e-116
AAM79024	Human protein SEQ ID NO 1686 - Homo sapiens, 196 aa. [WO200157190-A2, 09-AUG-2001]	382..577 1..196	196/196 (100%) 196/196 (100%)	e-112

In a BLAST search of public sequence databases, the NOV56a protein was found to have homology to the proteins shown in the BLASTP data in Table 56E.

Table 56E. Public BLASTP Results for NOV56a				
Protein Accession Number	Protein/Organism/Length	NOV56a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96A20	MIDDLE-CHAIN ACYL-COA SYNTHETASE1 (MEDIUM-CHAIN ACYL-COA SYNTHETASE) - Homo sapiens (Human), 577 aa.	1..577 1..577	576/577 (99%) 576/577 (99%)	0.0
Q9TVB5	XENOBIOTIC/MEDIUM-CHAIN FATTY ACID:COA LIGASE FORM XL-III PRECURSOR - Bos taurus (Bovine), 577 aa.	1..576 1..576	439/576 (76%) 486/576 (84%)	0.0
Q9BEA2	LIPOATE-ACTIVATING ENZYME PRECURSOR - Bos taurus (Bovine), 577 aa.	1..576 1..576	438/576 (76%) 485/576 (84%)	0.0
Q91VA0	MEDIUM-CHAIN ACYL-COA SYNTHETASE (EC 6.2.1.2) (HYPOTHETICAL 64.8 KDA PROTEIN) - Mus musculus (Mouse), 573 aa.	1..577 1..573	406/577 (70%) 472/577 (81%)	0.0
O70490	KIDNEY-SPECIFIC PROTEIN - Rattus norvegicus (Rat), 572 aa.	1..573 1..567	315/580 (54%) 417/580 (71%)	0.0

PFam analysis predicts that the NOV56a protein contains the domains shown in the
5 Table 56F.

Table 56F. Domain Analysis of NOV56a

Pfam Domain	NOV56a Match Region	Identities/ Similarities for the Matched Region	Expect Value
AMP-binding: domain 1 of 1	87..499	106/425 (25%) 299/425 (70%)	2.5e-96

Example 57.

The NOV57 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 57A.

Table 57A. NOV57 Sequence Analysis

	SEQ ID NO: 171	2501 bp
NOV57a, CG59354-01 DNA Sequence	ACACCATGACCACCTTGATGATAAGTTGCTGGGGGAGAACTGCAGTACTACTATAG CAGCAGTGAGGATGAGGACAGTGACCACGAGGACAAGGACCGAGGCAGATGTGCCCCA GCCAGCAGTTCTGTGCCTGCAGAGGCTGAGCTGGCAGGCGAAGGCATCTCAGTTAACA CAATGACTCTGAAGGAGTTTGCCATAATGAATGAGGACCAAGATGATGAAGAGTTTCT GCAGCAGTACCGAAGCAGCGAATGGAAGAGATGCGGCAGCAGCTTCACAAGGGGCCC CAATTCAAGCAGGTTTTTGAGATCTCCAGTGGAGAAGGGTTTTAGACATGATTGATA AAGAACAGAAAAGCATTGTCTCATGTTTATTTATGAGGATGGCATTCCAGGGAC CGAAGCCATGAATGGTTGCATGATCTGCCTTGCCGAGAGTACCCAGCTGTCAAGTTC TGCAAGGTGAAGAGCTCAGTTATTGGCGCCAGCAGTCAGTTCACCGAAGATGCCCTTC CTGCCCTGCTGATCTATAAGGGGGTGAAATTGATCGGCAATTTTGTTCGTGTTACTGA CCAGCTGGGGGATGATTTCTTTGCTGTGGACCTTGAAGCTTTTCTCCAGGAATTTGGA TTACTCCCAAGAAAAGGAGTCTTGGTGTCTGACATCTGTGCGTAACCTGCCACGTGTCT ACAGTGAGGATAGCGACCTGGAAATAGATTGAACGTATAGTCTAGTTGCATAGATTTTC TCATTGTTTGGGTTGGAATACACGTCATTGTTTATTTTGTTCCTTTGCTCTTCGGCT TTTCAGCTGTTCTTTGTAGTCCCTTTTATTATGCATAAAATAAAGAAATTTTAGATT AAATCAGAAATGCTGAATAACCTTGTAAGTCTAGCAATAAGGTGACTTACAATTTGATAAA CAGGAAGCCAGGCTTTTGAACGTCTTACTTAAAGATTCTGTGGTGTGACATCTCTGTTA TTGTTTCCAGTCAATATTACAAAGCATCCTAAAGACAGGGTCTTGGAAATTTGCTTTC AGATGATCTTAGAGGTCTCTGCCAAGTCTGAGAGTATAATTCTGTAGGTATTGTGTTA TTTGCAACGTAATAGTGCATTTTCTTAATCAAATGATTGTAAATATATTTACTTGT AATCAGTTCCATAGCTTTAGACGGTGGTTAGATTTTCTTTTCCACACAGGGTCTTTG TTTAAAGGGGTGAGCCACCGCAGCCAGTCTGAGGGGTGGCCTCTGCTGCTGGATTTTC ATGTCTTCTCCAGCATGACTAAGTCTGGAACAGCAGGAAGGGTGTATGCTTACTGAC CTGGTGATGTTAGAAGCAAGTAGTTTATGGATTAAACATTAAGCTGGAGTGGGGC TGGAAATCTTTGTAAAGGAAGTCTTTTCAGTAAGATGCCCTGCTGTCTTTGTCTCT TTTTTGTTTAAACAAGGTAACCTTTTGTGTTAACAAGGTAACCTTTTGTGTTAACCTAGAT TTTTTTTAAACTTTTTTTTTTTTTCATATTGGAAAAGTAATTCATATTCAGTAGAGG AAAAGTGAACAAAACAGAAAGCAAAATAAGAAAATTAATAATCTCTAATCTCTACTA CCTAGAATAAAACACTATTAATATTTGGTCTGTTTCTGCAAGGTGTTTTCTGTGT ATACATGGATATTTGTTGTTTAAACAAAACGATGGGATCATTTCTGAACATACTG TTCTATAGTATGGTCAGCTAATAATATATCAGACCTTTTTTTTATATTATTAATATT CTACAACCTTTTTAAAAATGTCTATTAATATTCATCGTATAGATGTGATATAATTTGC TTGATGGTGTCTCTTAAAAAGAAAGATAGCAAAATCTTTTTTAAATTACAAAAGTG ATAGATGTTCAATTGTAGAAAATGTAATAAACAAGTCTAAGACTTAAAGCCATATAAT TCCACCAACCAAAATTAATCCCTTTTGTCTATTTCTAGTCATTTTATAGCCTTTTTT TTTCTATGTATTATAATAATTATCATTGCGTTTTTTTCTTTTAACTTTTAAAA ATGTATATTCTAGGGTCAGGGGAAATGTAATCTGGAATTAATATTAGCCTTAAATTT CACAAATTTGATTTTCTGGCTTTTCAGGAATTGACTAAGTGTAAAAGAGTCTTGAAA GTATTTAGTCAACAAACAGAGTGCATTTTTTTTTTTTGTGACTAAGAAAGCTCGTTGTG GTAGAAAAGGGTGAATGATTGAAAATATTAGAAGCAGGGAAGTATTGTTAGTCTAG CTTATTTCTTTTCTAGTCTTTTTTCAATATTTTATAAACATTGAGTACTTACTGAATT TAGTTCTGTGCTCTTCTTATTAGTGTGTATCATAAATACTTTGATGTTTCAAAACA TTCTAAATAAATAATTTTCAGTGGCTTCATAATAAAAAAAAAAAAAAAAAAAAAA AAAAAA	
	ORF Start: ATG at 6	ORF Stop: TGA at 726
	SEQ ID NO: 172	240 aa MW at 26866.9kD
NOV57a,	MTTLDDKLLGEKLQYYYSSSEDESDHEDKDRGRCAPASSSVPAEELAGEGIVNTM TLKEFAIMNEDQDEEFLQYRQRMEEMLRQLHKGQPFQVFEISSGEGFLDMIDKE	

CG59354-01 Protein Sequence	QKSIVIMVHIYEDGIPGTEAMNGMICLAAEYPAVKFCKVKSSVIGASSQFTRNALPALLIYKGGELIGNFVRVTDQLGDDFFAVDLEAFLQEFGLLPEKEVLVLTSVRNSATCHSEDSLEID		
	SEQ ID NO: 173	893 bp	
NOV57b, CG59354-02 DNA Sequence	<u>CACCATGACCACCTGTATGATAAGTTGCTGGGGGAGAACTGCAGTACTACTATAGC</u> AGCAGTGAAGATGAGGACAGTGACCACGAGGACAAGGACCGAGGCATCTCAGTTAACA CAGGCCCAAAGGTGTGATCAATGACTGGCGCGCTTCAAGCAGTTGGAGACAGAGCA GAGGGAGGAGCAGTGCCGGGAGATGGAAAGGCTGATCAAGAAGCTGTCAATGACTTGC AGGTCCCATCTGGATGAAGAGGAGGAGCAACAGAAACAGAAAGACCTCCAGGAGAAGA TCAGTGGGAAGATGACTCTGAAGGAGTTTGCCATAATGAATGAGGACCAAGATGATGA AGAGTTTCTGCAGCAGTACCGGAAGCAGCGAATGGAAGAGATGCGGCAGCAGCTTCAC AAGGGCCCCCAATTCAAGCAGGTTTTTGAGATCTCCAGTGGAGAAGGGTTTTAGACA TGATTGATAAAGAACAGAAAAGCATTGTTCATCATGGTTTCATATTTATGAGGATGGCAT CAGGGACCGAAGCCATGAATGGTTGCATGATCCGCCTTGAAGGGGGGTGAATTGATC GGCAATTTTGTTTCGTGTACTGACCAGCTGGGGGATGATTTCTTTGCTGTGGACCTTG AAGCTTTTCTCCAGGAATTTGGATTACTCCAGAAAAGGAAGTCTTGGTGCTGACATC TGTGCGTAACTCTGCCACGTGTACAGTGAGGATAGCGACCTGGAAATAGATTGA <u>ACT</u> GATAGTCTAGTTGCATATAGATTCTCATTGTTTGGGTTGGAATACACCATTGTTTAT TTTTGTTCTTTGTCTTCTGGCTTTTCAGCTGTTCTTTGTAGTCCCTTTTATTATGCA TAAATAAAGAAATCTTAGATT		
	ORF Start: ATG at 5	ORF Stop: TGA at 749	
	SEQ ID NO: 174	248 aa	MW at 29227.4kD
NOV57b, CG59354-02 Protein Sequence	MTTLYDKLLGEKLQYYYSSSEDESDHEDKDRGISVNTGPKGVIINDWRRFKQLETEQR EEQCREMERLIKKLSMTCRSHLDEEEQKQKDLQEKISGKMTLKEFAIMNEDQDDEE FLQYRKRQMEEMRQQLHKGPPQKQVFEISSGEGFLDMIDKEQKSIVIMVHIYEDGIR DRSHEWLHDPCKGGELIGNFVRVTDQLGDDFFAVDLEAFLQEFGLLPEKEVLVLTSV RNSATCHSEDSLEID		
	SEQ ID NO: 175	891 bp	
NOV57c, CG59354-03 DNA Sequence	<u>CACCATGACCACCTGTATGATAAGTTGCTGGGGGAGAACTGCAGTACTACTATAGC</u> AGCAGTGAAGATGAGGACAGTGACCACGAGGACAAGGACCGAGGCATCTCAGTTAACA CAGGCCCAAAGGTGTGATCAATGACTGGCGCGCTTCAAGCAGTTGGAGACAGAGCA GAGGGAGGAGCAGTGCCGGGAGATGGAAAGGCTGATCAAGAAGCTGTCAATGACTTGC AGGTCCCATCTGGATGAAGAGGAGGAGCAACAGAAACAGAAAGACCTCCAGGAGAAGA TCAGTGGGAAGATGACTCTGAAGGAGTTTGCCATAATGAATGAGGACCAAGATGATGA AGAGTTTCTGCAGCAGTACCGGAAGCAGCGAATGGAAGAGATGCGGCAGCAGCTTCAC AAGGGGCCCAATTCAAGCAGGTTTTTGAGATCTCCAGTGGAGAAGGGTTTTTAGACA TGATTGATAAAGAACAGAAAAGCATTGTTCATCATGGTTTCATATTTATGAGGATGGCAT TCCAGGGACCGAAGCCATGAATGGTTGCATGATCCGCCTTGCCGAGAGTACCCAGCT GTCAAGTTCTGCAAGGTGAAGAGCTCAGTTATTGGCGCCAGCAGTCAGTTCACCAGGA ATGCCCTTCTGCCCTGCTGATCTATAAGGGGGGTGAATTGATCGGCAATTTTGTTCG TGTTACTGACCAGCTGGGGGATGATTTCTTTGCTGTGGACCTTGAAGCTTTTCTCCAG GAATTTGGATTACTCCAGAAAAGGAAGTCTTGGTGCTGACATCTGTGCGTAACTCTG CCAGTGTACAGTGAGGATAGCGACCTGGAAATAGATTGA <u>ACT</u> GATAGTCTAGTTGC ATAGATTTCTCATTGTTTGGG		
	ORF Start: ATG at 5	ORF Stop: TGA at 851	
	SEQ ID NO: 176	282 aa	MW at 32598.5kD
NOV57c, CG59354-03 Protein Sequence	MTTLYDKLLGEKLQYYYSSSEDESDHEDKDRGISVNTGPKGVIINDWRRFKQLETEQR EEQCREMERLIKKLSMTCRSHLDEEEQKQKDLQEKISGKMTLKEFAIMNEDQDDEE FLQYRKRQMEEMRQQLHKGPPQKQVFEISSGEGFLDMIDKEQKSIVIMVHIYEDGIP GTEAMNGCMIRLAAEYPAVKFCKVKSSVIGASSQFTRNALPALLIYKGGELIGNFVRV TDQLGDDFFAVDLEAFLQEFGLLPEKEVLVLTSVRNSATCHSEDSLEID		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 57B.

Table 57B. Comparison of NOV57a against NOV57b through NOV57c.		
Protein Sequence	NOV57a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV57b	58..240 100..248	138/183 (75%) 140/183 (76%)
NOV57c	58..240 100..282	182/183 (99%) 182/183 (99%)

Further analysis of the NOV57a protein yielded the following properties shown in Table 57C.

Table 57C. Protein Sequence Properties NOV57a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV57a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 57D.

Table 57D. Geneseq Results for NOV57a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV57a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE03537	Human secreted protein variant, SEQ ID NO: 228 - Homo sapiens, 301 aa. [WO200132675-A1, 10-MAY-2001]	1..240 1..301	226/301 (75%) 230/301 (76%)	e-117
AAY99657	Human GTPase associated protein-8 - Homo sapiens, 301 aa. [WO200031263-A2, 02-JUN-2000]	1..240 1..301	226/301 (75%) 230/301 (76%)	e-117
AAE02004	Fruitfly viral IAP-associated factor (VIAF) - Drosophila melanogaster, 240 aa. [WO200134798-A1, 17-MAY-2001]	55..214 59..213	52/161 (32%) 86/161 (53%)	3e-14

AAE02003	Zebrafish viral IAP-associated factor (VIAF) - Brachydanio rerio, 239 aa. [WO200134798-A1, 17-MAY-2001]	21..236 2..237	69/241 (28%) 117/241 (47%)	5e-13
AAE02002	Mouse viral IAP-associated factor (VIAF) - Mus musculus, 240 aa. [WO200134798-A1, 17-MAY-2001]	58..240 52..240	59/195 (30%) 99/195 (50%)	4e-12

In a BLAST search of public sequence databases, the NOV57a protein was found to have homology to the proteins shown in the BLASTP data in Table 57E.

Table 57E. Public BLASTP Results for NOV57a				
Protein Accession Number	Protein/Organism/Length	NOV57a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96AF1	HYPOTHETICAL 34.3 KDA PROTEIN - Homo sapiens (Human), 301 aa.	1..240 1..301	226/301 (75%) 230/301 (76%)	e-117
Q13371	Phosducin-like protein (PHLP) - Homo sapiens (Human), 301 aa.	1..240 1..301	225/301 (74%) 230/301 (75%)	e-116
T17321	hypothetical protein DKFZp564M1863.1 - human, 301 aa.	1..240 1..301	225/301 (74%) 230/301 (75%)	e-116
Q923E8	RIKEN CDNA 1200011E13 GENE - Mus musculus (Mouse), 301 aa.	1..240 1..301	210/301 (69%) 223/301 (73%)	e-109
Q63737	Phosducin-like protein (PHLP) - Rattus norvegicus (Rat), 301 aa.	1..240 1..301	210/301 (69%) 223/301 (73%)	e-108

PFam analysis predicts that the NOV57a protein contains the domains shown in the

5 Table 57F.

Table 57F. Domain Analysis of NOV57a

Pfam Domain	NOV57a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Phosducin: domain 1 of 2	35..57	14/23 (61%) 21/23 (91%)	8.7e-08
Phosducin: domain 2 of 2	58..240	133/183 (73%) 174/183 (95%)	9.7e-148

Example 58.

The NOV58 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 58A.

Table 58A. NOV58 Sequence Analysis

	SEQ ID NO: 177	756 bp	
NOV58a, CG59319-01 DNA Sequence	GGATCCCAATGAAGATACAGAATGGAATGACATTTTAAGAGATTTCGGCATTCTTCCTCCTAAAGAAGAGTCAAAAGATGAAATTGAAGAAATGGTTTACGTTTACAGAAAGAAGCAATGGTGAAACCATTTGAAAAGATGACTCTTGACAGCTAAAGGAAGCTGAAGATGATTTCGATGAAGAAGATATGCAGGCTGTTGAAACATATAGAAAGAAGCGGTTACAGGAAATGGAAAGCTCTTAAGAAAAACAAAAATTTGGAGAATTAAGAGAAATTTCTGGAAATCAGTATGTGAATGAAGTCACAAATGCAGAAGAAGATGTGTGGGTTATAATTTCATCTATACAGATCAAGCATCCCAATGTGTTTGTGGTTAACCAGCATCTTAGTCTTCTAGCAAGAAGTTTCCAGAACTAAATTTGTTAAAGCCATCGTGAATAGCTGTATTCAACACTACCATGACAATTGTTTACCAACAATTTTGTGTATAAAAAATGGTCAGATAGAAGCCAAATTCATTGGAATTATAGAATGTGGAGGGATAAATCTCAAGCTGGAAGAACTTGAATGGAAGCTAGCAGAAGTTGGAGCAATACAGACTGATTGGAAGAAAACCCAGAAAGACATGGTAGATATGATGGTATCTTCAATTAGAAACACTTCTATTTCATGATGACAGTGATAGCTCCAACAGTGATAATGATACCAAAATAGAGAGAAATATTCAATAAATAGCTTTTAGTAAAAAA		
	ORF Start: GAT at 2	ORF Stop: TAG at 719	
	SEQ ID NO: 178	239 aa	MW at 27811.3kD
NOV58a, CG59319-01 Protein Sequence	DPNEDTEWNDILRDFGILPPKEESKDEIEEMVLRQLQKEAMVKPFKMTLAQLKEAEDEFDEEDMQAVETYRKKRLQEWKALKKKQKFGELREISGNQYVNEVTNAEDVWVVIHLYRSSIPMCLLVNQHLSSLARKFPETKFVKAI VNSCIQHYHDNCLPTIFVYKNGQIEAKFIGIIECGGINLKEELEWKLAEVGAIQTDLEENPRKDMVMMVSSIRNTSIHDDSDSSNSDNDTK		
	SEQ ID NO: 179	745 bp	
NOV58b, CG59319-02 DNA Sequence	GGATCCCAATGAAGATACAGAATGGATCCCAATGAAGATACAGAATGGAATGACATTTTAAGAGATTTCGGCATTCTTCTCCTAAAGAAGAGTCAAAAGATGAAATTGAAGAAATGGTTTACGTTTACAGAAAGAAGCAATGGTGAAACCATTTGAAAGATGACTCTTGCA CAGCTAAAGGAAGCTGAAGATGAATTTGATGAAGAAGATATGCAGGCTGTTGAAACATATAGAAAGAAGCGGTTACAGGAATGGAAGCTCTTAAGAAAAACAAAAATTTGGAGATTAAAGAGAAATTTCTGGAAATCAGTATGTGAATGAAGTCACAAATGCAGAAGAAGATGTGTGGGTTATAATTCATCTATACAGATCAAGCATCCCAATGTGTTTGTGGTTAACCAGCATCTTAGTCTTCTAGCAAGAAAGTTTCCAGAACTAAATTTGTTAAAGCCATCGTGAATAGCTGTATTCAACACTACCATGACAATTTGTTTACCAACAATTTTGTGTATAAA AATGGTCAGATAGAAGCCAAATTCATTGGAATTATAGAATGTGGAGGGATAAATCTCAAGCTGGAAGAAGCTTGAATGGAAGCTAGCAGAAGTTGGAGCAATACAGACTGATTGGAAGAAAACCCAGAAAAGACATGGTAGATATGATGGTATCTTCAATTAGAAACACTTCTATCCATGATGACAGTGATAGCTCCAACAGTGATAATGATACCAATAGAA		
	ORF Start: ATG at 22	ORF Stop: TAG at 742	
	SEQ ID NO: 180	240 aa	MW at 27942.5kD

NOV58b, CG59319-02 Protein Sequence	MDPNEDTEWNDILRDFGILPPKEESKDEIEEMVLRLQKEAMVKPFKMTLAQLKEAED EFDEEDMQAVETYRKKRLQEWKALKKKQKFGELREISGNQYVNEVTNAEEDVWVI IHL YRSSIPMCLLVNQHLSSLARKFPETKFKVKAIVNSCIQHYHDNCLPTIFVYKNGQIEAK FIGIIECGGINLKLEELWKLAIEVGAIQTDLEENPRKDMVDMMVSSIRNTSIHDDSDS SNSDNDTK
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 58B.

Table 58B. Comparison of NOV58a against NOV58b.		
Protein Sequence	NOV58a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV58b	1..239	216/239 (90%)
	2..240	216/239 (90%)

Further analysis of the NOV58a protein yielded the following properties shown in Table 58C.

Table 58C. Protein Sequence Properties NOV58a	
PSort analysis:	0.8800 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV58a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 58D.

Table 58D. Geneseq Results for NOV58a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV58a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE02003	Zebrafish viral IAP-associated factor (VIAF) - Brachydanio rerio, 239 aa. [WO200134798-A1, 17-MAY-2001]	1..237 3..239	133/238 (55%) 181/238 (75%)	3e-75
AAU27979	Mouse contig polypeptide sequence #132 - Mus musculus, 243 aa. [WO200164834-A2, 07-SEP-2001]	1..231 7..240	137/234 (58%) 176/234 (74%)	2e-74

AAU27807	Human full-length polypeptide sequence #132 - Mus musculus, 239 aa. [WO200164834-A2, 07-SEP-2001]	1..231 3..236	137/234 (58%) 176/234 (74%)	2e-74
AAE02001	Human viral IAP-associated factor (VIAF) - Homo sapiens, 239 aa. [WO200134798-A1, 17-MAY-2001]	1..231 3..236	137/234 (58%) 176/234 (74%)	2e-74
AAB68507	Human GTP-binding associated protein #7 - Homo sapiens, 239 aa. [WO200105970-A2, 25-JAN-2001]	1..231 3..236	137/234 (58%) 176/234 (74%)	2e-74

In a BLAST search of public sequence databases, the NOV58a protein was found to have homology to the proteins shown in the BLASTP data in Table 58E.

Table 58E. Public BLASTP Results for NOV58a				
Protein Accession Number	Protein/Organism/Length	NOV58a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9CQU4	1700010B22RIK PROTEIN - Mus musculus (Mouse), 240 aa.	1..239 3..240	208/239 (87%) 229/239 (95%)	e-121
Q9WUP3	PDCL2 - Mus musculus (Mouse), 238 aa (fragment).	1..239 1..238	207/239 (86%) 228/239 (94%)	e-121
Q9DA99	1700016K07RIK PROTEIN - Mus musculus (Mouse), 192 aa.	47..239 1..192	165/193 (85%) 183/193 (94%)	3e-94
CAC40345	SEQUENCE 5 FROM PATENT WO0134798 - Brachydanio rerio (Zebrafish) (Zebra danio), 239 aa.	1..237 3..239	133/238 (55%) 181/238 (75%)	1e-74
Q9H2J4	HTPHLP (UNKNOWN) (PROTEIN FOR MGC:3062) - Homo sapiens (Human), 239 aa.	1..231 3..236	137/234 (58%) 176/234 (74%)	8e-74

PFam analysis predicts that the NOV58a protein contains the domains shown in the

5 Table 58F.

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Table 58F. Domain Analysis of NOV58a			
Pfam Domain	NOV58a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Phosducin: domain 1 of 1	60..175	32/120 (27%) 55/120 (46%)	5.8

Example 59.

The NOV59 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 59A.

Table 59A. NOV59 Sequence Analysis			
	SEQ ID NO: 181	981 bp	
NOV59a, CG59576-01 DNA Sequence	GCCACCGCGCCAGCTGGCTTTTGTGTTTTTATCCTTCTGCTCCTCATTTACCTATTCA CCATCATTTGGTAGTCTTATGGTGTCTTTGGCCATCAAACCTGGATTCTGCCTGCACAG CTCCTTCTATTTCTTCATCAGTGTCTCTCCTTCTAGAGATCTGGTATACCACCATC ACCATCCCCAAGATGTTCTTCAACCTAGCCAGTGAGCAGAAGACCACCTCCCTGGATG GTTGCCTATTGCAGATGTATTTCTTTACTCCCTCGGCATCACTGAGGTTTGCTTGCT CACCACGAGGCTATGGACAGATACCTGGCCATCTGTAATCACCTTTGCTACCCCCACA GTCAAGACACCTCAGCTCTACACTCAGGTGATTCTAGGTTGTTGCATCTGTGGCTTCT TCACGCTGCTCCCTGAGATTGCTTGGATATCCCACTGCCATTTTGTGGTCCAAATCA AATCCACAACATTTTCTGTGACCTTGATCCTATCCTGAATCTAGCATGTGTAGACACT GGCCCAGTTGTTTTAAATCAAGGTTGTGGACATTGTACATGCTGTGGAGATCATCACAG CTATAATGCTTGTGACTTTGGCTTACGTCCAAATTATTGCAGTGATCCTAAGAAACTG CTCTGCTGATGGATGCCAAAAGGCATTTTCTACCTATGCTTTCCACCTTGCTATTTTC TTAATCTTTTTTGGAAAGTGTAGCCCTGATGTACCTGCTCTTCTGTGCCAAGTACTCCT TTTTCTGGGACACAACCATCAGCCTAATGTTTGCAGTGCTGTCAACCGACAACAATCAT CTGTAGTCTGAGGAATAAAGAGATAAAGGAAGCAATAAAAAAGCACATGTGCCAATCA ATGATATGCACACATCATGTCAAATAAGACCAAATACACACCTCTTAATTACCAAAGA ATATTATACAAATATTACATTAATACGTTCAAGTGTGTTTGTGCTGCTGTG		
	ORF Start: GCC at 1	ORF Stop: TAA at 895	
	SEQ ID NO: 182	298 aa	MW at 33780.0kD
NOV59a, CG59576-01 Protein Sequence	ATAPSWLLFFILLLLIYLFITIGSLMVFFAIKLDLFLHSSFYFFISVLSFLEIWTITI TIPKMFNLASEQKTTSLDGLLQMYFFYSLGITEVCLLTTRAMDRLAICNHLCYPT VTPQLYTVQVILGCCICGFFLLPEIAWISTLPFCGPNQIHNI FCDLDPILNLACVDT GPVVLIKVVDIVHAVEIITAIMLVTLAYVQIIAVILRNCSADGCQKAFSTYAFHLAIF LIFFGSVALMYLFSKYSFFWDTTISLMFAVLSPTTIICSLRNKEIKEAIKKHMCQS MICTHHVK		

- 5 Further analysis of the NOV59a protein yielded the following properties shown in Table 59B.

Table 59B. Protein Sequence Properties NOV59a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 25 and 26

A search of the NOV59a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 59C.

Table 59C. Geneseq Results for NOV59a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV59a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72586	Human OR-like polypeptide query sequence, SEQ ID NO: 2267 - Homo sapiens, 289 aa. [WO200127158-A2, 19-APR-2001]	7..295 1..289	286/289 (98%) 286/289 (98%)	e-167
AAG71784	Human olfactory receptor polypeptide, SEQ ID NO: 1465 - Homo sapiens, 289 aa. [WO200127158-A2, 19-APR-2001]	7..295 1..289	286/289 (98%) 286/289 (98%)	e-167
AAG71785	Human olfactory receptor polypeptide, SEQ ID NO: 1466 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	5..292 20..311	175/293 (59%) 217/293 (73%)	6e-95
AAU24721	Human olfactory receptor AOLFR220 - Homo sapiens, 343 aa. [WO200168805-A2, 20-SEP-2001]	7..283 53..328	170/279 (60%) 212/279 (75%)	4e-94
AAG71808	Human olfactory receptor polypeptide, SEQ ID NO: 1489 - Homo sapiens, 317 aa. [WO200127158-A2, 19-APR-2001]	7..283 29..304	170/279 (60%) 212/279 (75%)	4e-94

- 5 In a BLAST search of public sequence databases, the NOV59a protein was found to have homology to the proteins shown in the BLASTP data in Table 59D.

Table 59D. Public BLASTP Results for NOV59a				
Protein Accession Number	Protein/Organism/Length	NOV59a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96R35	OLFACTORY RECEPTOR - Homo sapiens (Human), 216 aa (fragment).	50..267 1..216	107/218 (49%) 146/218 (66%)	7e-55

CG59557-01 Protein Sequence	YFFHSLGVTEALVLTVMADRCVAICNPLRYAITMSPRLCIQLSTGSCIFGFLMLLPE IVCISTLPFCGANQIHLFCDFEPVLQLACTDTYIILVEDVIRAISSILTSVSVITLFY LRIITVILRIPSGESRQKAFPTCAAHIAIFLLFFGSVSLMYLRFVTFPPLLDKAIAL MFAVLALLFNPVIYSLRNKDMKNATKKILCSQKMFNASGS
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Further analysis of the NOV60a protein yielded the following properties shown in Table 60B.

Table 60B. Protein Sequence Properties NOV60a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 67 and 68

A search of the NOV60a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 60C.

Table 60C. Geneseq Results for NOV60a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV60a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG71807	Human olfactory receptor polypeptide, SEQ ID NO: 1488 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	16..330 1..315	313/315 (99%) 314/315 (99%)	e-180
AAG71803	Human olfactory receptor polypeptide, SEQ ID NO: 1484 - Homo sapiens, 315 aa. [WO200127158-A2, 19-APR-2001]	16..329 1..314	219/314 (69%) 259/314 (81%)	e-129
AAU24658	Human olfactory receptor AOLFR156 - Homo sapiens, 331 aa. [WO200168805-A2, 20-SEP-2001]	9..329 10..330	218/321 (67%) 259/321 (79%)	e-128
AAU24721	Human olfactory receptor AOLFR220 - Homo sapiens, 343 aa. [WO200168805-A2, 20-SEP-2001]	20..329 33..342	196/310 (63%) 234/310 (75%)	e-111
AAG71808	Human olfactory receptor	20..323 9..312	195/304 (64%) 232/304 (76%)	e-111

	Homo sapiens, 317 aa. [WO200127158-A2, 19-APR-2001]			
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Protein Accession Number	Protein/Organism/Length	NOV60a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9WU86	ODORANT RECEPTOR S1 - Mus musculus (Mouse), 324 aa.	15..324 8..320	135/315 (42%) 188/315 (58%)	4e-67
Q9EPG2	M51 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	20..325 5..311	129/307 (42%) 189/307 (61%)	4e-65
P23270	Olfactory receptor-like protein I7 - Rattus norvegicus (Rat), 327 aa.	24..319 10..310	126/301 (41%) 182/301 (59%)	8e-65
Q9QWU6	OLFACTORY RECEPTOR I7 - Mus musculus (Mouse), 327 aa.	16..319 1..310	128/310 (41%) 184/310 (59%)	9e-64
O13036	CHICK OLFACTORY RECEPTOR 7 - Gallus gallus (Chicken), 323 aa.	16..319 1..305	122/305 (40%) 187/305 (61%)	1e-63

Pfam Domain	NOV60a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	56..304	45/270 (17%) 172/270 (64%)	2.4e-21

The NOV61 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 61A.

Table 61A. NOV61 Sequence Analysis			
	SEQ ID NO: 185	1061 bp	
NOV61a, CG59555-01 DNA Sequence	CAATCTGGTCTCTAAGTGATCTTTTTCTTTTTCACAGGGAAATGGGGGAAAATCAGACA ATGGTCACAGAGTTCTCTCTACTGGGATTTCTCCTGGGCCCAAGGATTCAGATGCTCC TCTTTGGGCTCTTCTCCCTGTTCTATATCTTCACCTGCTGTGGGGAACGGGGCCATCCT GGGGCTCATCTCACTGGACTCCAGACTCCACACCCCATGTACTTCTTCTCTCACAC CTGGCTGTGCTGCACATCGCCTACACCCGCAACACGGTGCCCGAGATGCTGGCGAACCC TCCTGCATCCAGCCAAGCCCATCTCCTTTGCTGGCTGCATGACGCAGACCTTCTCTG TTTGAGTTTTGGACACAGCGAATGTCTCCTGCTGGTGTGATGTCCTACGATCGTTAC GTGGCCATCTGCCACCCTCTCCGATACTCCGTCACTCATGACCTGGAGAGTCTGCATCA CCCTGGCCGTCACTTCTTGGACGTGTGGCTCCCTCCTGGCTCTGGCCATGTGGTTCT CATCCTAAGACTGCCCTTCTCTGGGCCTCATGAAATCAACCACTTCTTCTGTGAAATC CTGTCTGTCTCCTCAGGCTGGCCTGTGCTGACACCTGGCTCAACAGAGTGGTCATCTTTG CAGCCTGCGTGTCTTCTCCTGGTGGGGCCACCCAGCCTGGTGTCTGTCTCTACTCGCA CATCTCTGGCGGCCATCCTGAGGATCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCC ACCTGCTCCTCCACCTCTGCGTGGTGGGACTCTTCTTTGGCAGTGCCATCATCATGT ACATGGCCCCAAGTCCCGCCATCCTGAGGAGCAGCAAAAGGTCTTTTCTATTTTA CAGTTTTTTCAACCCAACACTTAACCCCTGATTACAGCCTGAGGAACGGAGAGGTC AAGGGTGCCCTGAGGAGAGCACTGGGCAAGGAAAGTCATTCTTAAGTGGTGTGACATT TGACTCTCCCTCCTCAGTCATCTCCTGGAATCTTGGTACCAAATACCACCTAAGTTCA CTACTCTTTTATATCA		
	ORF Start: ATG at 41	ORF Stop: TAA at 971	
	SEQ ID NO: 186	310 aa	MW at 34713.8kD
NOV61a, CG59555-01 Protein Sequence	MGENQTMVTEFLLGLFLGPRIQMLLFGFLSLFYIFTLLNGAAILGLISLDSRLHTPM YFFLSHLAVVDIAYTRNTVPQMLANLLHPAKPISFAGCMQTQFLCLSFHSECLLLVL MSYDRYVAICHPLRYSVIMTWRCITLAVTSWTCGSLALAHVVLILRLPFSGPHEIN HFFCEILSVLRLACADTWNQVVIFAACVFFLVGPPSLVLVSVSHILAAILRIQSGEG RRKAFSTCSSHLCVVGLFFGSAIIMYMAPKSRHPPEEQKVFFLFYSFFNPNTLNPLIYS LRNGEVKGALRRALGKESH		

Further analysis of the NOV61a protein yielded the following properties shown in Table 61B.

Table 61B. Protein Sequence Properties NOV61a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 43 and 44

A search of the NOV61a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 61C.

Table 61C. Geneseq Results for NOV61a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV61a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM29935	Peptide #3972 encoded by probe for measuring placental gene expression - Homo sapiens, 311 aa. [WO200157272-A2, 09-AUG-2001]	1..310 2..311	310/310 (100%) 310/310 (100%)	0.0
AAM17409	Peptide #3843 encoded by probe for measuring cervical gene expression - Homo sapiens, 311 aa. [WO200157278-A2, 09-AUG-2001]	1..310 2..311	310/310 (100%) 310/310 (100%)	0.0
AAG72949	Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2631 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	1..310 2..311	310/310 (100%) 310/310 (100%)	0.0
AAG72187	Human olfactory receptor polypeptide, SEQ ID NO: 1868 - Homo sapiens, 310 aa. [WO200127158-A2, 19-APR-2001]	1..310 1..310	310/310 (100%) 310/310 (100%)	0.0
AAU04577	Human G-protein coupled receptor like protein, GPCR #11 - Homo sapiens, 308 aa. [WO200153454-A2, 26-JUL-2001]	1..310 1..308	288/310 (92%) 294/310 (93%)	e-165

In a BLAST search of public sequence databases, the NOV61a protein was found to have homology to the proteins shown in the BLASTP data in Table 61D.

Table 61D. Public BLASTP Results for NOV61a				
Protein Accession Number	Protein/Organism/Length	NOV61a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96R46	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..283 1..217	217/217 (100%) 217/217 (100%)	e-125
O95047	Olfactory receptor 2A4 - Homo sapiens (Human), 310 aa.	1..307 1..307	217/307 (70%) 250/307 (80%)	e-122

Q9NQNO	DJ1005H11.1 (7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE) PROTEIN)) - Homo sapiens (Human), 272 aa (fragment).	39..307 1..269	187/269 (69%) 216/269 (79%)	e-103
Q9Z1V2	OLFACTORY RECEPTOR B12 - Mus musculus (Mouse), 223 aa (fragment).	63..285 1..223	172/223 (77%) 190/223 (85%)	9e-98
O43888	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..282 1..217	173/217 (79%) 188/217 (85%)	1e-97

PFam analysis predicts that the NOV61a protein contains the domains shown in the Table 61E.

Table 61E. Domain Analysis of NOV61a			
Pfam Domain	NOV61a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	40..289	65/269 (24%) 188/269 (70%)	1.1e-45

Example 62.

The NOV62 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 62A.

Table 62A. NOV62 Sequence Analysis			
	SEQ ID NO: 187	1201 bp	
NOV62a, CG59551-01 DNA Sequence	AGTTGGTTGTAATAATTCTGCTTATATTACCTACAGAGTAAACATTATAGCATTATC ACTCCAGAATCCTTTGTTTCTATGGTTTCCAGATGTTTCCAATGTCTAGATGTTCCAG CTGCCCATCTCTGAGAAATCCAGCTGTGTCTCACAATGGATGCCACAGCCTGTAATGA ATCAGTGGATGGCTCACCCGCTCTTCTATCTATTGGGCATCCCCCTCTCTGCCAGAGACC TTCTTCTCCCTGTGTTTTTATTTTCTCTCTCTTCTACCTTCTCATCTGATGGGTA ATGCCCTGATCCTGGTGGCCGTGGTGGCAGAGCCAGCCTCCACAAGCCCATGTACTT CTTTCTGATCAATCTCTCCACCTTGGACATCCTTTTACCACAACCACTGTCCCAAG ATGCTGTCTTATTCTTGCTTGGGGACCGCTTCTCAGCTTTTCTCTGCTTACTGC AGATGTACCTCTTCAAAGTTTACATGTTTCTCAGAAGCCTTCATCCTGGTGGTATGGC CTATGACCGCTATGTGGCTATCTGCCACCCACTGCACTACCCCTGTCTCATGAACCCA CAGACCAATGCTACCTTGGCAGCCAGTGCCTGGCTAACTGCCCTCCTCTGCCCATCC CAGCAGTAGTAAGGACCTCCAGATGGCATATAACAGCATTGCCTACATCTACCACTG CTTCTGTGATCATCTGGCTGTGGTCCAGGCCTCTGCTCTGACACCAACCCCGAGACC CTCATGGGCTTCTGCATCGCCATGGTGGTGTCTTCTCTCCCTTCTCTCTGGTGTCTT TCTCCTATGTCCACATCCTGGCCTCAGTGTCTCGCATCAGTTCCTTAGAAGGACGGGC AAAAGCCTTCTCCACCTGCAGCTCCACCTTCTGGTCTGGGGACCTACTACTCATCT ATTGCCATAGCCTACGTGGCTACAGGGCTGACCTGCCCTTGACTTCCATATCATGG GCAATGTGGTATATGCCATTCTCACACCAATTCTCAACCCCTCATTTACAGCTGAG AAACAGGGATGTAAAGGCAGCCATCACAAAATCATGTCTCAAGACCCAGGCTGTGAC AGGAGCATTTGACCTTTAAATGCAGCTAACTCTGCTTCCAGGACACCAATAACAGTG CTTAGCACAGAGAAAGGACTCAATACATGATAATGAAATAA		
	ORF Start: ATG at 152	ORF Stop: TGA at 1112	
	SEQ ID NO: 188	320 aa	MW at 35502.6kD

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NOV62a, CG59551-01 Protein Sequence	MDATACNESVDGSPVFYLLGIPSLPETFFLPVFFIPLLFYLLILMGNALILVAVVAEP SLHKPMYFFLINLSTLDILFTTTTVPKMLSLFLLGDRFLSFSSCLLQMYLFQSFTCSE AFILVVMAYDRYVAICHPLHYPLMNPQTNATLAASAWLTALLLPIPAVVRTSQMAYN SIAYIYHCFCDHLAVVQASCSDTTPQTLMGFCIAMVVSFLPLLLVLLSYVHILASVLR ISSLEGRAKAFSTCSSHLLVVGTYSSIAIAYVAYRADLPDLDFHIMGNVVYAILTPIL NPLIYTLRNRDVKAAITKIMSQDPGCDRSI
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Further analysis of the NOV62a protein yielded the following properties shown in Table 62B.

Table 62B. Protein Sequence Properties NOV62a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	Likely cleavage site between residues 57 and 58

A search of the NOV62a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 62C.

Table 62C. Geneseq Results for NOV62a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV62a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72119	Human olfactory receptor polypeptide, SEQ ID NO: 1800 - Homo sapiens, 295 aa. [WO200127158-A2, 19-APR-2001]	35..290 2..257	213/256 (83%) 228/256 (88%)	e-119
AAU24639	Human olfactory receptor AOLFR134 - Homo sapiens, 325 aa. [WO200168805-A2, 20-SEP-2001]	16..308 17..308	129/293 (44%) 186/293 (63%)	6e-67
AAG72479	Human OR-like polypeptide query sequence, SEQ ID NO: 2160 - Homo sapiens, 324 aa. [WO200127158-A2, 19-APR-2001]	16..308 17..308	129/293 (44%) 186/293 (63%)	6e-67
AAG71590	Human olfactory receptor polypeptide, SEQ ID NO: 1271 - Homo sapiens, 324 aa. [WO200127158-A2, 19-APR-2001]	16..308 17..308	129/293 (44%) 186/293 (63%)	6e-67
AAG71632	Human olfactory receptor	16..315 13..312	126/300 (42%) 179/300 (59%)	3e-64

	Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]			
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In a BLAST search of public sequence databases, the NOV62a protein was found to have homology to the proteins shown in the BLASTP data in Table 62D.

Table 62D. Public BLASTP Results for NOV62a				
Protein Accession Number	Protein/Organism/Length	NOV62a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z236	OLFACTORY RECEPTOR - Rattus norvegicus (Rat), 221 aa (fragment).	70..289 2..221	187/220 (85%) 202/220 (91%)	e-104
CAB43131	OLFACTORY RECEPTOR - Stenella coeruleoalba (Striped dolphin), 172 aa (fragment).	69..240 1..172	136/172 (79%) 148/172 (85%)	1e-73
Q9EPG2	M51 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	16..310 12..305	131/295 (44%) 191/295 (64%)	2e-67
Q9H208	HP4 OLFACTORY RECEPTOR - Homo sapiens (Human), 317 aa (fragment).	16..312 12..308	127/297 (42%) 180/297 (59%)	3e-65
Q920G5	OLFACTORY RECEPTOR P3 - Mus musculus (Mouse), 324 aa.	16..308 19..311	126/295 (42%) 180/295 (60%)	1e-62

5 PFam analysis predicts that the NOV62a protein contains the domains shown in the Table 62E.

Table 62E. Domain Analysis of NOV62a			
Pfam Domain	NOV62a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	46..295	58/268 (22%) 179/268 (67%)	4.6e-38

Example 63.

The NOV63 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 63A.

Table 63A. NOV63 Sequence Analysis			
	SEQ ID NO: 189		1042 bp
NOV63a, CG59540-01 DNA Sequence	GACCTTTTCATCACACTCTGGTCATTTACAAACTGTTATTAAGGAATGGGGGACAAGCA GCCCTGGGTCACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGCAGAGATGGAGATC TTTCTCTCTTGCATCTTCTCCCTGTTATATCTCTTCAGTCTACTGAGGAATGGCATGA ACATGGGACTCATCTGTCTGGATCCCAGACTACACACCCCATATACTTCTTCTGTGTC ACACTTGGCCGTCATTGACATATACTATGCTTCCAACAATTTGCTCAACATGCTGGAA AACCTAGTGAAACACAAAAAACTATCTCGTTTCACTCTTGCAATTATGCAGATGGCTT TGTATTTGACTTTTGCTGCTGTCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAG ATTTGTGGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAACGGAGAGTGTGC ACAGTACTGGCTATTACTTCTTGGGATGTGGATTTTCCCTGGCCCTCATAAATCTTAA TTCTCCTTCTAAGGCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGA AATTCTGTCTGTCTCTCAAACCTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTGTC TTTGCTGGTGGTGTGTTTGTCTTAGTCGGGCCCTTTCCTTGATGCTGATCTCCTACA TGCGCATCTCTTGGCCATCTGAAGATCCAGTCAGGCGAGGGCCACAGAAAGGACTT CTCTACCTGCTCCTCCCACCTCTGTGTGGTGGGGTTCTTCTTTGCCAACGCCATTGTGTC ATGTACATGGCCCCCAAGTCCGCGCCATCCGAGGAGCAGCAGAAGGTCCTTCCCTGTG TTTGAGCCTTTTGAATCAGGTGCTGAACCCCTCTGATCTACAGCTTGAGGAATGTC AGAGGTCAAGAGTGCCCCACAAGAGGGCCACTGAAGAAGGAGAGGCTGATGTTACAAT CTCAAAGGCACCACGAGGAGAGGGCCTGCTCCGACAAATGGGGAAGTTGGCTTTT		
	ORF Start: ATG at 45		ORF Stop: TGA at 960
	SEQ ID NO: 190		305 aa MW at 34554.8kD
NOV63a, CG59540-01 Protein Sequence	MGDKQPWVTEFILVGFQLSAEMEIFLSCIFSLLYLFSLLRNGMNMGLICLDPRLHTPI YFFLSHLAVIDIYYASNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVV MSYDRFVAICHPLHYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVN HFFGEILSVLKLACADTWINEIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSSEG HRKDFSTCSSHLCVVGFFFANAIVMYMAPKSRHPPEEQKVLSLFCSLWNQVLNPLLIY SLRNAEVKSAPEQGH		

Further analysis of the NOV63a protein yielded the following properties shown in Table 63B.

Table 63B. Protein Sequence Properties NOV63a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	Likely cleavage site between residues 43 and 44

A search of the NOV63a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 63C.

Table 63C. Geneseq Results for NOV63a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV63a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU24758	Human olfactory receptor	1..300 1..299	258/300 (86%) 275/300 (91%)	e-146

	[WO200168805-A2, 20-SEP-2001]			
AAG72952	Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634 - Homo sapiens, 310 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	255/300 (85%) 272/300 (90%)	e-144
AAG72377	Human OR-like polypeptide query sequence, SEQ ID NO: 2058 - Homo sapiens, 312 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	255/300 (85%) 272/300 (90%)	e-144
AAG72169	Human olfactory receptor polypeptide, SEQ ID NO: 1850 - Homo sapiens, 312 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	255/300 (85%) 272/300 (90%)	e-144
AAG71994	Human olfactory receptor polypeptide, SEQ ID NO: 1675 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	225/300 (75%) 256/300 (85%)	e-129

In a BLAST search of public sequence databases, the NOV63a protein was found to have homology to the proteins shown in the BLASTP data in Table 63D.

Table 63D. Public BLASTP Results for NOV63a				
Protein Accession Number	Protein/Organism/Length	NOV63a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O95047	Olfactory receptor 2A4 - Homo sapiens (Human), 310 aa.	1..299 1..298	173/299 (57%) 217/299 (71%)	2e-92
O43885	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..281 1..216	154/216 (71%) 182/216 (83%)	5e-88
O43888	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..281 1..216	153/216 (70%) 182/216 (83%)	8e-88
Q96R48	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..281 1..216	153/216 (70%) 181/216 (82%)	2e-87
Q96R47	OLFACTORY RECEPTOR - Homo sapiens (Human), 215 aa (fragment).	67..281 1..214	149/215 (69%) 175/215 (81%)	3e-84

PFam analysis predicts that the NOV63a protein contains the domains shown in the Table 63E.

Table 63E. Domain Analysis of NOV63a			
Pfam Domain	NOV63a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	47..290	55/270 (20%) 174/270 (64%)	9.7e-25

Example 64.

The NOV64 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 64A.

Table 64A. NOV64 Sequence Analysis			
	SEQ ID NO: 191	973 bp	
NOV64a, CG59280-01 DNA Sequence	AGGCACTAAATGAATATCTGTTTAATTCATAAAGTAACAGAGTTTCTCTTCTCTGGAT TCCCACAGTTTGAAGATGGTAGCCTCCTCTTCTTCATTCCATTGTTTGTATCTACAT ATTTCATTGTCATTGGGAATCTTATTGTATTTTTCAGTCAGGGTGGATACCCGCTCTC CACAAACCCATGTATAATTTTATCAGCATTTTCTCATTTCTGGAGATCTGGTACACAA CTGCCACAATTCCCAAGATGCTCTCCATCCTCATCAGCAGGCAGAGGACCATCTCCAT GGTTGGTTGCCTCTTGACAGATGACTTCTTCCATTCACTGGGAAATTCAGAGGGGATT TTGTTGACCAACCATGGCCATTGATAGGTACGTTGCCATCTGTAACCCCTCTCCGCTACC CAACCATCATGACCCCCGGGCTCTGTGTTTCAGCTCTCTGTGGGCTCTGTCATCTTTGG CTTTCTTGTGTTGCTCCCAGAGATTGCATGGATTTCACACTGCCCTTCTGTGGACCC AACCAAATCCACCAGATCTTCTGTGATTTTGAACCTGTGCTGCGCTTGGCCTGTACAG ACACGTCATGATTCTGATTGAGGATGTGATCCATGCTGTGGCCATTGTATTCTCTGT CCTGATTATTGCCTTTTCTTATATCAGAATCATCACTGTAATCCTGAGGATTCCCTCT GTTGAAGGCCGCCAGAAGGCCTTTTCTACCTGTGCGGCCCATCTTAGTGTCTTTCTGA TGTTCTATGGCAGTGTATCCCTCATGTACCTGCGTTTCTCTGCCACTTTCCACCGAT TTTGGACACAGCTGTTGCACTGATGTTTGCACTTCTTGCTCCCTTTTCAACCCTATC ATCTATAGCTTTAGAAATAAGGACATGAAGATTGCAATTAAGGCTTTTCTGCCCTC AGAAGATGGTTAATTTATCTGTAGATTAAATGCTAGCTCATAGGCA		
	ORF Start: ATG at 10	ORF Stop: TAA at 955	
	SEQ ID NO: 192	315 aa	MW at 35741.4kD
NOV64a, CG59280-01 Protein Sequence	MNICLIHKVTEFLFSGFPQFEDGSLFFIPLFVIYIFIVIGNLIVFFAVRVDTRLHNP MYNFISIFSFLEIWTYTTATIPKMLSILISQRTISMVGCLLQMYFFHSLGNSEGI LLT TMAIDRYVAICNPLRYPTIMTPGLCVQLSVGSCIFGFLVLLPEIAWISLFPFCGNQI HQIFCDFEPVLR LACTDTSMILIEDVIHAVAIVFSVLI IAFSYIRIITVILRIPSVEG RQKAFSTCAHLSVFLMFYGSVSLMYLRFSATFPPI LDTAVALMFVLAFFFNPIIYS FRNKDMKIAIKKLFQPKMNVLSVD		
	SEQ ID NO: 193	929 bp	
NOV64b, CG59280-02 DNA Sequence	TCTTCTTCATTCCATTGTTTGTATCTACATATTTCATTGTCATTGGGAATCTTATTGT ATTTTTTGCACTCAGGTGGATACCCGCTCTCCACAACCCCATGTATAATTTTATCAGC ATTTTCTCATTTCTGGAGATCTGGTACACAACCTGCCACAATCCCAAGATGCTCTCCA TCCTCATCAGCAGGCAGAGGACCATCTCCATGGTTGGTTGCCTCTTGACAGATGACTT CTTCCATTCACTGGGAAATTAGAGGGGATTTTGTGACCAACCATGGCCATTGATAGG TACGTTGCCATCTGTAACCCCTCTCCGCTACCCAACCATCATGACCCCCGGGCTCTGTG TTCAGCTCTCTGTGGGGTCTGTCATCTTTGGCTTCTTGTGTTGCTCCCAGAGATTGC ATGGATTTCCACACTGCCCTTCTGTGGACCAACCAAATCCACCAGATCTTCTGTGAT TTTGAACCTGTGCTGCGCTTGGCCTGTACAGACACGTCATGATTCTGATTGAGGATG TGATCCATGCTGTGGCCATTGTATTCTCTGTCTGATTATTGCCTTTTCTTATATCAG AATCATCACTGTAATCCTGAGGATTCCCTCTGTTGAAGGCCGCCAGAAGGCCCTTTTCT ACCTGTGCCGCCCATCTTAGTGTCTTCTGATGTTCTATGGCAGTGTATCCCTCATGT ACCTGCGCTTCTCTGCACTTTCCACCGATTTTGGACACAGCTGTTGCACTGATGTT TGCAGTTCTTGCTCCCTTTTCAACCCTATCATCTATAGCTTTAGAAATAAGGACATG AAGATTGCAATTAAGGCTTTTCTGCCCTCAGAAGATGGTTAATTTATCTGTAGATT AATGCTAGCTCATAGGCACCTTTCACTGTGGATTACTCTAACACAATAAACCATAT		

AAG71803	Human olfactory receptor polypeptide, SEQ ID NO: 1484 - Homo sapiens, 315 aa. [WO200127158-A2, 19-APR-2001]	9..311 9..311	243/303 (80%) 267/303 (87%)	e-143
AAU24658	Human olfactory receptor AOLFR156 - Homo sapiens, 331 aa. [WO200168805-A2, 20-SEP-2001]	9..311 25..327	240/303 (79%) 264/303 (86%)	e-140
AAG71807	Human olfactory receptor polypeptide, SEQ ID NO: 1488 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	9..313 9..313	222/305 (72%) 259/305 (84%)	e-131
AAU24721	Human olfactory receptor AOLFR220 - Homo sapiens, 343 aa. [WO200168805-A2, 20-SEP-2001]	9..308 37..336	209/300 (69%) 242/300 (80%)	e-119

In a BLAST search of public sequence databases, the NOV64a protein was found to have homology to the proteins shown in the BLASTP data in Table 64E.

Table 64E. Public BLASTP Results for NOV64a				
Protein Accession Number	Protein/Organism/Length	NOV64a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9EPG2	M51 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	1..302 4..303	137/303 (45%) 194/303 (63%)	2e-71
Q9EPV0	M50 OLFACTORY RECEPTOR (OLFACTORY RECEPTOR M50) - Mus musculus (Mouse), 316 aa.	6..302 4..301	132/298 (44%) 191/298 (63%)	3e-71
Q9EPG1	M50 OLFACTORY RECEPTOR - Mus musculus (Mouse), 316 aa.	6..302 4..301	130/298 (43%) 190/298 (63%)	2e-70
Q9WU86	ODORANT RECEPTOR S1 - Mus musculus (Mouse), 324 aa.	1..310 12..321	133/313 (42%) 190/313 (60%)	4e-69
Q96KK4	DJ994E9.5 (OLFACTORY RECEPTOR, FAMILY 10, SUBFAMILY C, MEMBER 1 (HS6M1-17)) - Homo sapiens (Human), 306 aa.	9..314 2..306	137/307 (44%) 189/307 (60%)	9e-68

PFam analysis predicts that the NOV64a protein contains the domains shown in the

Table 64F. Domain Analysis of NOV64a			
Pfam Domain	NOV64a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	41..289	51/269 (19%) 179/269 (67%)	2.2e-33

Example 65.

The NOV65 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 65A.

Table 65A. NOV65 Sequence Analysis			
	SEQ ID NO: 195	972 bp	
NOV65a, CG59568-01 DNA Sequence	GCATGGTGATCCTGTCTCTGGGAAAACCAAACGATGAGAGTGAATTCGTGCTTCAAGG ATTCTCTTCCATCAGACAGTAAATATTTTCCTCTTTATGATAATTTTAGTCTTCTAC ATCTTAACGTGTTCTGGAAACATCCTCATTGTCTCTAGTTTCTAGTCAGACATCATC TCCACACCCCTATGTACTTCTCTCTGGTGAACCTGTCTGTCTGGAGATCTGGTATAC CTCTAACATCATCCCCAAATGTTGCTGATTATCATAGCTGAAGAGAAGACTATCTCT GTGGCTGGCTGGCTGGCACAATCTACTTCTTCGGATCCCTGGCTGCCACGGAGTGCC TCTTGCTCACTGTGATGTCTTATGATCGCTACCTAGCCATCTGCCAGCCTCTTTGCTA CCGTGTCCTCATGACTGGCCCCCTTTGCATCAGGCTAGCTGCTGGCTCTTGGTCTGC TGCTTCCTCCTTACAGCAATCACCATGGTCTTGCTATGTAGACTAACCTTCTGTGGAC CCTATGAACTGATCACTTCTTTGTGACTTCACCCCTCTGGTTTCTATCTCTCTGCAT GGATACCTCAGTGACTGAGACCATTGCCTTTGCCACCTCTTCTGCAGTAACTCTGATC CCATTTCTCCTCATTGTAGCCTCCTACTCCTGCGTCTTTCTGCTATCCTAAGAATCC CATCTTGACAGGCCAGAAAAAGGCCTTCTCCACCTGCTCTTCCACCTCACTGTGGT CATAGTGTTTTATGGGACACTGATTGCCACATACCTTGTGCCCTCAGCCAACCTATCC CAACTCTTGTGCAAAGGGTCTCTCTGCTCTACATCATCTGACACCCATGTTTAAAC CCATCATTTATAGCCTGAGAAATAGAGACATCCATGAAGCTCTGAAGAAGTGCTTGAG GAAGAAGTCAGGTGTTTGCCTTAGATAATACGAAAAGGAAAAA		
	ORF Start: ATG at 3	ORF Stop: TAA at 954	
	SEQ ID NO: 196	317 aa	MW at 35713.4kD
NOV65a, CG59568-01 Protein Sequence	MVILSWENQTMREVFVLQGFSSIRQLNIFLFMIILVFYILTVSGNIIIVLLVLRHHL HTPMYFLLVNLSCLEIWTYSNIIIPKMLLIIEEKTISVAGWLAQFYFFGSLAATECI LLTVMSYDRYLAICQPLCYRVLMTGPLCIRLAAGSWFCCFLITMTVLLCRLTFCG YETDHFCDFTPLVHLSCMDTSVTETIAFATSSAVTLIPFLLIVASYSVLSAILRIE SCTGQKKAFTSCSSHLTVVIVFYGTLIATYLVPSANSSQLLCKGSSLLYIILTPMFNP IIYSLRNRIHEALKKCLRKKSGVCLR		

Further analysis of the NOV65a protein yielded the following properties shown in

5 Table 65B.

Table 65B. Protein Sequence Properties NOV65a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3888 probability located in mitochondrial inner membrane; 0.3030 probability located in mitochondrial intermembrane space
SignalP analysis:	Likely cleavage site between residues 45 and 46

A search of the NOV65a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 65C.

Table 65C. Geneseq Results for NOV65a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV65a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72527	Human OR-like polypeptide query sequence, SEQ ID NO: 2208 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..316 1..316	315/316 (99%) 315/316 (99%)	0.0
AAG72231	Human olfactory receptor polypeptide, SEQ ID NO: 1912 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..316 1..316	315/316 (99%) 315/316 (99%)	0.0
AAG72084	Human olfactory receptor polypeptide, SEQ ID NO: 1765 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..316 1..316	315/316 (99%) 315/316 (99%)	0.0
AAG72700	Murine OR-like polypeptide query sequence, SEQ ID NO: 2382 - Mus musculus, 314 aa. [WO200127158-A2, 19-APR-2001]	1..308 3..308	154/308 (50%) 208/308 (67%)	2e-83
AAG71814	Human olfactory receptor polypeptide, SEQ ID NO: 1495 - Homo sapiens, 317 aa. [WO200127158-A2, 19-APR-2001]	8..311 5..308	142/304 (46%) 208/304 (67%)	7e-79

5 In a BLAST search of public sequence databases, the NOV65a protein was found to have homology to the proteins shown in the BLASTP data in Table 65D.

Table 65D. Public BLASTP Results for NOV65a				
Protein Accession Number	Protein/Organism/Length	NOV65a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9GZK7	Olfactory receptor 11A1 (Hs6M1-18) - Homo sapiens (Human), 315 aa.	1..308 1..306	147/308 (47%) 202/308 (64%)	4e-77

O13036	CHICK OLFACTORY RECEPTOR 7 - Gallus gallus (Chicken), 323 aa.	7..311 4..308	139/305 (45%) 198/305 (64%)	1e-76
Q9JKA6	OLFACTORY RECEPTOR P2 - Mus musculus (Mouse), 315 aa.	4..313 1..311	143/311 (45%) 194/311 (61%)	1e-75
Q9WU86	ODORANT RECEPTOR S1 - Mus musculus (Mouse), 324 aa.	14..308 21..315	144/295 (48%) 189/295 (63%)	2e-75
Q9UGF6	Olfactory receptor 5V1 (Hs6M1-21) - Homo sapiens (Human), 321 aa.	7..305 4..302	138/299 (46%) 199/299 (66%)	5e-75

PFam analysis predicts that the NOV65a protein contains the domains shown in the Table 65E.

Table 65E. Domain Analysis of NOV65a			
Pfam Domain	NOV65a Match Region	Identities/ Similarities for the Matched Region	Expect Value
granulin: domain 1 of 1	144..155	7/13 (54%) 11/13 (85%)	1.7
Trypan_glycop: domain 1 of 1	218..241	6/24 (25%) 21/24 (88%)	7.9
7tm_1: domain 1 of 1	44..293	53/268 (20%) 172/268 (64%)	1.5e-31

Example 66.

The NOV66 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 66A.

Table 66A. NOV66 Sequence Analysis		
	SEQ ID NO: 197	987 bp
NOV66a, CG59224-01 DNA Sequence	CATCTTCCTATGTGTCATGTCTCCTCTTAATGACACAAAAATGGAAGTCCTTAGATTCTCCTTATCGGGATCACTGGACTGGAGAAAAGTCGCACCTGGATATCCATTCTTTCTTATCTGTGTACCTTCTTCTTGGATGGGTAATTTACCGTCCTCTTTTATCAAGACAGAGCAAAGCCTCCATGAACCTATGTATTATTGCTTCCATGCTCTCCATCTGTGACTAGGGCTGTCTGTCTTCTTACCCATCACTTTGGGACTATTCTATTTGATGTCCATGAAATTCATGCAGCTCCATGCTTTGCCAGGAATTTTATCCATCTGTTACAGTCAGTGAAGCCTCTGTACTGTCTGTAATGGCATTGACTGGTATGTGGCAATCCACAGTCCTTTGAGATACAGCACTATCTTAAGTAGTCCAGAGCCATCAAAACAGGGGTTCTTCTGACTTCCAAGAATGTTCTTTGATCCTTCCACTGCCCTTCTCTTGCAAAGGCTGAGATATTGTCATCAAAACCTGCTCTCCACTCCTATTGTCTCCACCAGGATGTCATGAAGCTGATGTGTTCTGACAAACACAGTCAATGTTGTCTACGGACTCTGTGCAGGACTTTCTACTATGCTGGACTTGGTGTATTACCTTCTCCTATATGATTTTAAGGGCTGTACTGGGCTGTGCTTATCTTCTATGTGCCCACGCTGAGTGTGCCATGCTCCACAGTTTGCCAAGGATGTGTCTCTATGATCCACGTCCTCATGGCTGATATTTTCTGCTGGTGCCACCCTGTGTAATCCCATCGTGTACTGTGTGAAGACCCACCAATCCGAGAAAAGTTGTG	

	GGGAAACTTTGTCCAAAAGTAAGTTGATCAAAGGAATGAGAAAGGGAATGAATGTATA A		
	ORF Start: ATG at 17		ORF Stop: TGA at 953
	SEQ ID NO: 198	312 aa	MW at 35250.7kD
NOV66a, CG59224-01 Protein Sequence	MSPLNDTKMEVLRFLIGITGLEKSRTWISIPFLSVYLLSWMGNTVLFFIKTEQSLH EPMYYLLSMLSISDLGLSLSSLPITLGLFLFDVHEIHAAPCFAQEFFIHLFTVSEASV LSVMAFDWYVAIHSPLRYSTILTSPIRAIKTGVLTSKNVLLILPLPFLQLRLRYCHQN LLSHSYCLHQDVMKLMCSNTNVVYGLCAGLSTMLDLVFTFSYMLRAVLGIATPR QQFKALNTCISHICAVLIFYVPTLSAAMLHQFARDVSPMIHVLMAIDFLVLPPLLNPI VYCVKTHQIREKVVGKLCPEKVS		

Further analysis of the NOV66a protein yielded the following properties shown in Table 66B.

Table 66B. Protein Sequence Properties NOV66a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.2007 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 50 and 51

- A search of the NOV66a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 66C.

Table 66C. Geneseq Results for NOV66a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV66a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72488	Human OR-like polypeptide query sequence, SEQ ID NO: 2169 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	309/313 (98%) 309/313 (98%)	e-176
AAG71557	Human olfactory receptor polypeptide, SEQ ID NO: 1238 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	309/313 (98%) 309/313 (98%)	e-176
AAU24573	Human olfactory receptor AOLFR63 - Homo sapiens, 313 aa. [WO200168805-A2, 20-SEP-2001]	1..310 1..311	186/311 (59%) 246/311 (78%)	e-109
AAG71558	Human olfactory receptor	1..310 1..311	185/311 (59%) 245/311 (78%)	e-108

	Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]			
AAU24682	Human olfactory receptor AOLFR181 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	1..307 1..306	188/308 (61%) 237/308 (76%)	e-106

In a BLAST search of public sequence databases, the NOV66a protein was found to have homology to the proteins shown in the BLASTP data in Table 66D.

Table 66D. Public BLASTP Results for NOV66a				
Protein Accession Number	Protein/Organism/Length	NOV66a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	14..304 11..303	141/293 (48%) 199/293 (67%)	2e-77
O88628	Olfactory receptor 51E2 (G-protein coupled receptor RA1c) - Rattus norvegicus (Rat), 320 aa.	14..304 11..303	141/293 (48%) 200/293 (68%)	2e-77
CAC38935	SEQUENCE 9 FROM PATENT WO0131014 - Homo sapiens (Human), 318 aa.	5..304 6..306	145/302 (48%) 206/302 (68%)	2e-77
CAC37756	SEQUENCE 1 FROM PATENT WO0125434 - Homo sapiens (Human), 317 aa.	5..304 5..305	145/302 (48%) 206/302 (68%)	3e-77
Q9H255	Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor) (HPRAJ) - Homo sapiens (Human), 320 aa.	14..304 11..303	139/293 (47%) 198/293 (67%)	2e-76

PFam analysis predicts that the NOV66a protein contains the domains shown in the
5 Table 66E.

Table 66E. Domain Analysis of NOV66a			
Pfam Domain	NOV66a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 2	43..151	30/111 (27%) 73/111 (66%)	6.3e-14

7tm_1: domain 2 of 2	212..292	16/92 (17%) 52/92 (57%)	0.052
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Example 67.

The NOV67 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 67A.

Table 67A. NOV67 Sequence Analysis			
	SEQ ID NO: 199	994 bp	
NOV67a, CG59222-01 DNA Sequence	<u>CACAATGTCGTCTTCAATAGTTCTGCCTTATACCCTCGCTTCCTCCTAACGGGCCTCTCAGGCCTTGAAAGCAGATATGACTTGATTTCCCTGCCCATCTCTTGGTTTATGCCACCTCAATTGCCGGGAACATTAGCATCCTCTTCATTATCAGAACTGAGTCTTCCCTCCCAACCCGATGTATTACTTTCTGTCAATGCTGGCATTCACTGACCTGGGCCTATCTAACACTACCTTACCTACCATGTTCACTGTCTTCTGGTTCCATGCCCGGAGATCTCCTTCAATGCTTGTCTGGTCCAAATGTACTTCATTGTTTTCTCGATTATTGAGTCAGCTGTACTCCTGGCTATGGCCTTTGACTGCTTTATAGCAATCTGTGAACCTTGGCGCTATGCCCATCCTAACCAATGATGTAATCATTGGGATTGGGTTGGCAATTGCTGGAAGGGCCTTGGCTCTGGTCTTTCCAGCTTCTTTCTCTCTTGAAGAGGCTTCAATATCATGATGTCAATATTCTGTCTACCTCTTCTGCCTGCACCAGGACCTCATAAAGACGACTGTATCCAATGTCGAGTCAGCAGCATCTATGGCCTCATGGTGGTCACTGTGCCATGGGACTTGATTCAGTGCTTCTCCTCTCTCCATGTCTCTCATCCTGGGCACAGTGTGAGTATAGCCTCAAGGCAGAGAGAGTGAGAGCCCTCAATACTTGCACTCTCCACATCTGTGCTGTACTCACCTTCTATACACCAATGATTGGGCTATCTATGATCCATCGCTATGGACAGAATGCTTCTCAATTGTCCATGTGCTGATGGCCAATGTCTACTTGTGGTTCCACCTCTCATGAACCCCGTTGTCTACAGTGTAAAGACCAAGCAGATTCTGTGACAGAATCTTCAATAAATTC</u> <u>AAGAAACATGAAGTGTAGATGACAGAGATTCTGAAACATAACTTTCCTCCATTCCCCATATATTT</u>		
	ORF Start: ATG at 5	ORF Stop: TAG at 944	
	SEQ ID NO: 200	313 aa	MW at 35044.2kD
NOV67a, CG59222-01 Protein Sequence	MSVFNSSALYPRFLTGLSGLESRYDLISLPFLVYATSIAGNISILFIIRTESSLHQPMYYFLSMLAFTDLGLSNTTLPMTFVSFVWFHAREISFNACLVQMYFIHVFSIIESAVL LMAFDCFIACEPLRYAAILTNDVIIGIGLAIAGRALALVFPASFLLKRLQYHDVNI LSYLFCLHQDLIKTTVSNCRVSSIYGLMVVICSMGLDSVLLLLSVVLILGTVLSIASK AERVRALNTCISHICAVLTFYTPMIGLSMIHRYGQNASSIVHVLMAVYLLVPLMPNE VVYSVKTKQIRDRIFNFKKHEV		

Further analysis of the NOV67a protein yielded the following properties shown in
5 Table 67B.

Table 67B. Protein Sequence Properties NOV67a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4047 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3480 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV67a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 67C.

Table 67C. Geneseq Results for NOV67a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV67a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72605	Human OR-like polypeptide query sequence, SEQ ID NO: 2286 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAG71519	Human olfactory receptor polypeptide, SEQ ID NO: 1200 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAU24683	Human olfactory receptor AOLFR182 - Homo sapiens, 314 aa. [WO200168805-A2, 20-SEP-2001]	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102
AAG71715	Human olfactory receptor polypeptide, SEQ ID NO: 1396 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102
ABB44526	Human GPCR4a polypeptide SEQ ID NO 11 - Homo sapiens, 315 aa. [WO200174904-A2, 11-OCT-2001]	5..308 6..309	169/304 (55%) 227/304 (74%)	2e-96

In a BLAST search of public sequence databases, the NOV67a protein was found to have homology to the proteins shown in the BLASTP data in Table 67D.

Table 67D. Public BLASTP Results for NOV67a

Protein Accession Number	Protein/Organism/Length	NOV67a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H344	Olfactory receptor 5112 (HOR5'beta12) - Homo sapiens (Human), 312 aa.	13..308 12..307	154/296 (52%) 221/296 (74%)	2e-91
Q9H2C8	ODORANT RECEPTOR HOR3'BETA1 - Homo sapiens (Human), 321 aa.	2..308 10..316	160/307 (52%) 216/307 (70%)	5e-89
Q9H343	Olfactory receptor 5111 (HOR5'beta11) - Homo sapiens (Human), 314 aa.	5..312 5..313	156/309 (50%) 223/309 (71%)	9e-89

AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	13..309 11..307	148/297 (49%) 207/297 (68%)	2e-86
Q924X8	OLFACTORY RECEPTOR S85 - Mus musculus (Mouse), 314 aa.	2..304 3..305	150/303 (49%) 221/303 (72%)	1e-85

PFam analysis predicts that the NOV67a protein contains the domains shown in the Table 67E.

Table 67E. Domain Analysis of NOV67a			
Pfam Domain	NOV67a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	42..138	24/99 (24%) 67/99 (68%)	7.8e-14

Example 68.

- 5 The NOV68 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 68A.

Table 68A. NOV68 Sequence Analysis			
	SEQ ID NO: 201	981 bp	
NOV68a, CG59220-01 DNA Sequence	GCAATGAGAAACCGCAGTGTTGTCCCTGAGTTTGTCTCCTCGGGCTGTCAGCTGGCC CCCAGACCCAGACTCTGCTCTTTGTGCTGTTTCGTGGTGATTGCTCCTCGACTGTGAT GGGAAACCTGCTGCTGCTGGTGGTGAATTAATGCTGATTCTTGCCTCCACACACCCATG TACTTCTTCTCTGGGACAATTGCTCTTCTTGGATCTCTGCCATTCTCTGTCACTGCAC CTAAGCTGTTGGAGAACCTCCTGTCTGAGAAGAAAACCATCTCAGTAGAGGGCTGCAT GGCTCAGGTCTTCTTTGTGTTTGGCACTGGGGGCACTGAATCCTCCCTGCTTGTCTGTG ATGGCCTATGACCGCTATGTTGCCATCAGCTCTCCTTTGCTCTATGGCCAAGTGATGA ACAGACAGCTGTGTTTCAAGGCTGGTGGGGGCTCATGGGGCTTGGCTTTTCTGGATGC CCTCATCAATATCCTTGTAGCTCTCAATTTAGACTTCTGTGAGGCTCAAAATATCCAC CACTTCAGCTGTGAGCTGCCCTCTCTCTATCCTTTGTCTTGTCTGTAGTGTGTCAAGCAA GTTTTACCACCCCTGCTCTGCTCCAGCTTCTGCAATTTCTTTGAAATTTTCTCATGAT ATTCTTGTCTTATATTTGCATTTTGTCCACCATCCTGAGGATCAGCTCCACTACAGGC AGAAGCAAAGCCTTCTCCACCTGCTCCTCCACCTCACTGCAGTGATTTTCTTTTATG GCTCCGGATTACTCCGCTATCTCATGCCAAATTCAGGATCCATTCAAGAGCTGATCTT CTCCTTGCAGTACAGCGTGATCACTCCCATGCTGAATCTCCTCATTTACAGCGCTGAAG AACAGGGAGGTGAAGGCAGCTGTGAGAAGAACATTGAGAAAATATTTCTAGTGTGTTCA ATAGACTTATGAAATCAGAATGATGAGGGAAGTGGATAGAACTGCAACAAGCA		
	ORF Start: ATG at 4	ORF Stop: TAG at 919	
	SEQ ID NO: 202	305 aa	MW at 33732.3kD
NOV68a, CG59220-01 Protein Sequence	MRNRSVVPFVLLGLSAGPQTQLLFVLFVVICLLTVMGNLLLLLVVINADSLHTPMY FFLGQLSFLDLCHSSVTAPKILENLLSEKKTISVEGCMQVFFVFATGGTESSLLAVM AYDRYVAISSPLLYGQVMNRQLCSGLVGGSWGLAFLDALINILVALNLDCEAQNIHH FSCELPSLYPLSCSDVSASFSTLLCSSFLHFFGNFLMIFLSYICILSTILRISSTGR SKAFSTCSSHLTAVIFFYSGLLRLYMPNSGSIQELIFSLQYSVITPMLNLLIYSLKN REVKAAVRRTLRLKYF		

Further analysis of the NOV68a protein yielded the following properties shown in Table 68B.

Table 68D. Public BLASTP Results for NOV68a				
Protein Accession Number	Protein/Organism/Length	NOV68a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JM36	OLFACTORY RECEPTOR - Mus musculus domesticus (western European house mouse), 214 aa (fragment).	66..279 1..214	144/214 (67%) 169/214 (78%)	5e-78
Q9QZ18	OLFACTORY RECEPTOR - Mus musculus (Mouse), 312 aa.	3..299 5..303	142/299 (47%) 193/299 (64%)	2e-72
Q9EPG6	B1 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	3..299 5..303	140/299 (46%) 196/299 (64%)	2e-72
P23266	Olfactory receptor-like protein F5 - Rattus norvegicus (Rat), 313 aa.	3..305 5..309	142/305 (46%) 196/305 (63%)	9e-72
Q9EQA3	ODORANT RECEPTOR K30 - Mus musculus (Mouse), 311 aa.	3..305 5..310	143/306 (46%) 202/306 (65%)	2e-71

PFam analysis predicts that the NOV68a protein contains the domains shown in the Table 68E.

Table 68E. Domain Analysis of NOV68a			
Pfam Domain	NOV68a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	39..286	54/268 (20%) 169/268 (63%)	1.7e-29

Example 69.

- 5 The NOV69 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 69A.

Table 69A. NOV69 Sequence Analysis		
	SEQ ID NO: 203	957 bp
NOV69a, CG59218-01 DNA Sequence	GTCCACAATGGCCAATCAGACTGTGGTGACTGAGTTCTTCTCTCCAAGGCCTGACGGAT ACCAAAGAGCTTCAGGTGGCTGTTTTTCTGCTCCTGCTGCTTGCTACCTTGTGACTG TCTCTGGGAACCTGATCATCATCAGCCTGACCTTGCTGGACACCCGCTGCAGACATC TATGTACTTATTTCTCCAGAATCTGTCTGCTTAGAAATTGGTTCCAGACAGTCATC GTGCCCAAGATGCTGCTCAACATTGCCATGGGGACCAAGACCGTTAGCTTTGCTGGGT GCATTACCCAGGACTTTTCTTCCACATCTTCTGGGGGCCACAGAGTTCTTCTCCT CACAGCCATGGCCTATGACCAGTATATTGCCATCTGCAAGCCCCCTCACTACCCCATG CTCATAAGTAGTAGAGTGCACACAGCTCATCCTCACCTGCTGGCTACTAGGTTTTCT CCTTCATCATCATGCCTGTCATCCTGACCAGTCAGCTTCCATTCTGTGATACCCACAT CAAGCATTCTTCTGTGACTACACGCCTCTAATGGAGGTGGTCTGCAGTGGGCCAAG GTGCTGGAGATGGTGGATTTTACCCTGGCCTTAGTAGACTGTTTGGCACCTTGGTAC	

	TCATCACCTGTCTATGTCCAGATCATCCAGACAATTGTCAGAATCCCCGCTGTCCA GGAGAGGAAGAAGGCTTTCTCTACCTGTTCTCTCATGTGTCATTATGGTTACCATGTGT TATGACAGCTGCTCTTTATGTATGTCAAGCCCTCTCCAGGAAAGTGGGTGATGTCA ACAAGGGAGTGTCTAATCAATACAATTATTGCCCACTGTTAAATCCCTTCATCTG TACTCTGAGGAACCAACAAGTTAAGCAGGTAATGAAAGACCTAGTCAGAAAAATGACT TTGTTCCAAAATAAATAAGGGCCCTAAAA		
	ORF Start: ATG at 8	ORF Stop: TAA at 944	
	SEQ ID NO: 204	312 aa	MW at 35358.1kD
NOV69a, CG59218-01 Protein Sequence	MANQTVVTEFFLQGLTDTKEQVAVFLLLLAYLVTVSGNLI I ISLTLLDTRLQTSMY LFLQNLSCLEIWFQTVIVPKMLLNIAMGKT VSFAGCITQDFFPHLLGATEFFLLTA MAYDQYIAICKPLHYPLISSRVCTQLILTCWLLGFSFIIMPVILTSQLPFCDTIHKH FFCDYTPLMEVVCSPKVL E MVDFTLALVALFGTLVLITLSYVQIIQTIVRIPAVQER KKAFSTCSSHVIMVTMCYDSCFFMYVKPSPGKWVDVNKGVS LINTIIAPLLNPFICTL RNQOVKQVMKDLVRKMTL FQNK		

Further analysis of the NOV69a protein yielded the following properties shown in Table 69B.

Table 69B. Protein Sequence Properties NOV69a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 40 and 41

A search of the NOV69a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 69C.

Table 69C. Geneseq Results for NOV69a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV69a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72538	Human OR-like polypeptide query sequence, SEQ ID NO: 2219 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	284/317 (89%) 293/317 (91%)	e-157
AAG72229	Human olfactory receptor polypeptide, SEQ ID NO: 1910 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	284/317 (89%) 293/317 (91%)	e-157
AAU24761	Human olfactory receptor AOLFR112B - Homo sapiens, 309	1..306 1..306	173/307 (56%) 227/307 (73%)	2e-96

	2001]			
AAU24765	Human olfactory receptor AOLFR225B - Homo sapiens, 309 aa. [WO200168805-A2, 20-SEP-2001]	1..306 1..306	166/307 (54%) 227/307 (73%)	2e-94
AAG66353	GPCR partial protein sequence - Unidentified, 313 aa. [WO200155179-A2, 02-AUG-2001]	1..309 1..310	160/311 (51%) 209/311 (66%)	4e-87

In a BLAST search of public sequence databases, the NOV69a protein was found to have homology to the proteins shown in the BLASTP data in Table 69D.

Table 69D. Public BLASTP Results for NOV69a				
Protein Accession Number	Protein/Organism/Length	NOV69a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z1V0	OLFACTORY RECEPTOR C6 - Mus musculus (Mouse), 313 aa.	1..309 1..310	160/311 (51%) 209/311 (66%)	2e-86
CAC88326	SEQUENCE 18 FROM PATENT WO0164879 - Homo sapiens (Human), 331 aa.	8..306 12..311	142/301 (47%) 200/301 (66%)	4e-78
CAC88328	SEQUENCE 22 FROM PATENT WO0164879 - Homo sapiens (Human), 331 aa.	8..306 12..311	142/301 (47%) 198/301 (65%)	2e-77
CAC88327	SEQUENCE 20 FROM PATENT WO0164879 - Homo sapiens (Human), 331 aa.	8..306 12..311	141/301 (46%) 198/301 (64%)	8e-77
O70270	OLFACTORY RECEPTOR-LIKE PROTEIN - Rattus norvegicus (Rat), 327 aa.	3..308 11..316	136/307 (44%) 208/307 (67%)	4e-76

PFam analysis predicts that the NOV69a protein contains the domains shown in the

5 Table 69E.

Table 69E. Domain Analysis of NOV69a			
Pfam Domain	NOV69a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	39..244	47/214 (22%) 147/214 (69%)	1.9e-25

Example 70.

The NOV70 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 70A.

Table 70A. NOV70 Sequence Analysis			
	SEQ ID NO: 205	962 bp	
NOV70a, CG59216-01 DNA Sequence	CATCTTCCTATGTGTCATGTCTCCTCTTAATGACACAAAAATGGAAGTCCTTAGATTCTCCTCTTATCGGGATCACTGGACTGGAGAAAAGTCGCACCTGGATATCCATTCCCTTTCTATCTGTGTACCTTCTTTCTTGGATGGGTAATTTTACCGTCCTCTTTTTATCAAGACAGAGCAAAGCCTCCATGAACCTATGTATTATTGCTTTCCATGCTCTCCATCTCTGACCTAGGGCTGTCTCTGTCTTCTTACCACATCACTTTGGGACTATTCTTATTTGATGTCCATGAAATTCATGCAGTCCATGCTTTGCCAGGAATTTTTATCCATCTGTTTACAGTCAGTGAAGCCTCTGTACTGTCTGTAATGGCATTTGACTGGTATGTGGCAATCCACAGTCCTTTGAGATACAGCACTATCTTAAGTAGTCCCAGAGCCATCAAACAGGGGTTCTTCTGACTTCCAAGAATGTTCTTTTGATCCTTCCACTGCCCTTCTCTTGCAAAGGCTGAGATATTGTGCATCAAACCTGCTCTCCCACTCCTATTGTCTCCACCAGGATGTGATGAAGCTGATGTGTTCTGACAAACAGTCAATGTTGTCTACGGACTCTGTGCAGGACTTTCTACTATGCTGGACTTGGTGTTTATTACCTTCTCCTATATTATGATTTTAAGGGCTGTACTGGGAATTGCTACCCCGACAGACAGTTC AAGGCCCTCAACACGTGCATCTCTCACATCTGTGCTGTGCTTATCTTCTATGTGCCACGCTGAGTGTGCCATGCTCCACCAGTTTGCAGGGATGTGTCTCCTATGATCCACGTCCTCATGGCTGATATTTTCTGCTGGTGCCACCCCTGTGTAATCCCATCGTGTACTGTGTGAAGACCCACCAATCCGAGAAAAGTTGTGGGGAAACTTTGTCCAAAAGTAAGTTGATCAA		
	ORF Start: ATG at 17	ORF Stop: TGA at 956	
	SEQ ID NO: 206	313 aa	MW at 35363.9kD
NOV70a, CG59216-01 Protein Sequence	MSPLNDTKMEVLRFLLLIGITGLEKSRTWISIPFLSVYLLSWMGNFTVLFFIKTEQSLHEPMYYLLSMLSISDLGLSLSLPITLGLFLFDVHEIHAAPCFQAQEFFIHLFTVSEASVLSVMAFDWYVAIHSPLRYSTILTSAPRAIKTGVLVTSKNVLLILPLPFLQLRLRYCHQNLLSHSYCLHQDVMKLMCSNDTVNVVYGLCAGLSTMLDLVFTFSYIMILRAVLGIATPQQFKALNTCISHICAVLIFVYPTLSAAMLHQFARDVSPMIHVLMAIDIFLLVPPLNPIVYCVKTHQIREKVVGKLCPKVS		

- 5 Further analysis of the NOV70a protein yielded the following properties shown in Table 70B.

Table 70B. Protein Sequence Properties NOV70a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.2007 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 50 and 51

A search of the NOV70a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 70C.

Table 70C. Geneseq Results for NOV70a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV70a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72488	Human OR-like polypeptide query sequence, SEQ ID NO: 2169 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..313 1..313	310/313 (99%) 310/313 (99%)	e-178
AAG71557	Human olfactory receptor polypeptide, SEQ ID NO: 1238 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..313 1..313	310/313 (99%) 310/313 (99%)	e-178
AAU24573	Human olfactory receptor AOLFR63 - Homo sapiens, 313 aa. [WO200168805-A2, 20-SEP-2001]	1..311 1..311	186/311 (59%) 246/311 (78%)	e-110
AAG71558	Human olfactory receptor polypeptide, SEQ ID NO: 1239 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..311 1..311	185/311 (59%) 245/311 (78%)	e-109
AAU24682	Human olfactory receptor AOLFR181 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	1..308 1..306	188/308 (61%) 238/308 (77%)	e-107

- 5 In a BLAST search of public sequence databases, the NOV70a protein was found to have homology to the proteins shown in the BLASTP data in Table 70D.

Table 70D. Public BLASTP Results for NOV70a				
Protein Accession Number	Protein/Organism/Length	NOV70a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC38935	SEQUENCE 9 FROM PATENT WO0131014 - Homo sapiens (Human), 318 aa.	5..305 6..306	145/302 (48%) 207/302 (68%)	5e-79

AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	14..305 11..303	141/293 (48%) 199/293 (67%)	7e-79
CAC37756	SEQUENCE 1 FROM PATENT WO0125434 - Homo sapiens (Human), 317 aa.	5..305 5..305	145/302 (48%) 207/302 (68%)	7e-79
O88628	Olfactory receptor 51E2 (G-protein coupled receptor RA1c) - Rattus norvegicus (Rat), 320 aa.	14..305 11..303	141/293 (48%) 200/293 (68%)	7e-79
Q9H255	Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor) (HPRAJ) - Homo sapiens (Human), 320 aa.	14..305 11..303	139/293 (47%) 198/293 (67%)	7e-78

PFam analysis predicts that the NOV70a protein contains the domains shown in the Table 70E.

Table 70E. Domain Analysis of NOV70a			
Pfam Domain	NOV70a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 2	43..151	30/111 (27%) 73/111 (66%)	6.3e-14
YCF9: domain 1 of 1	208..262	10/59 (17%) 31/59 (53%)	7.5
7tm_1: domain 2 of 2	212..293	18/93 (19%) 55/93 (59%)	0.00034

Example 71.

The NOV71 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 71A.

Table 71A. NOV71 Sequence Analysis		
	SEQ ID NO: 207	995 bp
NOV71a, CG59214-01 DNA Sequence	GCACAATGCTCTGTCTTCAATAGTTCTGCCTTATACCTCGCTTCTCCTAACGGGCCT CTCAGGCCTTGAAAGCAGATATGACTTGATTCCCTGCCCATCTTCTTGGTTTATGCC ACCTCAATTGCCGGGAACATTAGCATCCTCTTCATTATCAGAACTGAGTCTTCCCTCC ACCAACCGATGTATTACTTTCTGTCAATGCTGGCATTCACTGACCTGGGCCTATCTAA CACTACCTTACCTACCATGTTCAAGTGTCTTCTGGTTCCATGCCCGGAGATCTCCTTC AATGCTTGTCTGGTCCAAATGTACTTCATTATGTTTCTCGATTATTGAGTCAGCTG TACTCCTGGCTATGGCCTTTGACTGCTTTATAGCAATCTGTGAACCTTGCGCTATGC AGCCATCCTAACCAATGATGTAATCATTGGGATTGGGTTGGCAATTGCTGGAAGGGCC TTGGCTCTGGTCTTCCAGCTTCTTCTCTTGAAGAGGCTTCAATATCATGATGTCA ATATTCTGTCCTACCTCTTCTGCCTGCACAGGACCTCATAAAGACGACTGTATCCAA CTGTGCGATCAGCAGCATCTATGGCCTCATGGTGGTCATCTGTTCCATGGGACTTGAT TCAGTGTCTCTCTCTCTCTATGTCTCATCTGGGCACAGTGTGAGTATAGCCT	

	CCAAGGCAGAGAGAGTGAGAGCCCTCAATACTGTCATCTCCACATCTGTGCTGTACT CACCTTCTATACACCAATGATTGGGCTATCTATGATCCATCGTATGGACAGAAATGCT TCCTCAATTGTCCATGTGCTGATGGCCAATGTCTACTTGCTGGTTCCACCTCTCATGA ACCCCGTTGTCTACAGTGTAAAGACCAAGCAGATTCTGACAGAATCTTCAATAAATT CAAGAAACATGAAGTGTAGATGACAGAGATTCTGAAACATAACTTCCCTCCATTCCC CATATATTT		
	ORF Start: ATG at 6	ORF Stop: TAG at 945	
	SEQ ID NO: 208	313 aa	MW at 35044.2kD
NOV71a, CG59214-01 Protein Sequence	MSVFNSSALYPRFLTGLSGLESRYDLISLPFLVYATSIAGNISILFIIRTESSLHQ PMYYFLSMLAFTDLGLSNTTLPMTFSVFWFHAREISFNACLVQMYFIHVFSIIESAVL LAMAFDCFIAICEPLRYAAILTNDVIIGIGLAIAGRALALVFPASFLLKRLQYHDVNI LSYLFCLHQDLIKTTSNCRVSSYGLMVVICSMGLDSVLLLSYVLILGTVLSIASK AERVRALNTCISHICAVLTFYTPMIGLSMIHRYGQNASSIVHVLMAVNYLLVPLPMNP VVYSVKTKQIRDRIFNKFKKHEV		

Further analysis of the NOV71a protein yielded the following properties shown in Table 71B.

Table 71B. Protein Sequence Properties NOV71a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4047 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3480 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV71a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 71C.

Table 71C. Geneseq Results for NOV71a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV71a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72605	Human OR-like polypeptide query sequence, SEQ ID NO: 2286 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAG71519	Human olfactory receptor polypeptide, SEQ ID NO: 1200 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAU24683	Human olfactory receptor	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102

	aa. [WO200168805-A2, 20-SEP-2001]			
AAG71715	Human olfactory receptor polypeptide, SEQ ID NO: 1396 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102
ABB44526	Human GPCR4a polypeptide SEQ ID NO 11 - Homo sapiens, 315 aa. [WO200174904-A2, 11-OCT-2001]	5..308 6..309	169/304 (55%) 227/304 (74%)	2e-96

In a BLAST search of public sequence databases, the NOV71a protein was found to have homology to the proteins shown in the BLASTP data in Table 71D.

Table 71D. Public BLASTP Results for NOV71a				
Protein Accession Number	Protein/Organism/Length	NOV71a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H344	Olfactory receptor 5112 (HOR5'beta12) - Homo sapiens (Human), 312 aa.	13..308 12..307	154/296 (52%) 221/296 (74%)	2e-91
Q9H2C8	ODORANT RECEPTOR HOR3'BETA1 - Homo sapiens (Human), 321 aa.	2..308 10..316	160/307 (52%) 216/307 (70%)	5e-89
Q9H343	Olfactory receptor 5111 (HOR5'beta11) - Homo sapiens (Human), 314 aa.	5..312 5..313	156/309 (50%) 223/309 (71%)	9e-89
AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	13..309 11..307	148/297 (49%) 207/297 (68%)	2e-86
Q924X8	OLFACTORY RECEPTOR S85 - Mus musculus (Mouse), 314 aa.	2..304 3..305	150/303 (49%) 221/303 (72%)	1e-85

PFam analysis predicts that the NOV71a protein contains the domains shown in the

5 Table 71E.

Table 71E. Domain Analysis of NOV71a			
Pfam Domain	NOV71a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	42..138	24/99 (24%) 67/99 (68%)	7.8e-14

Example 72.

The NOV72 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 72A.

Table 72A. NOV72 Sequence Analysis			
	SEQ ID NO: 209	1004 bp	
NOV72a, CG59211-01 DNA Sequence	CTTCTCATCTTTTCCCTCAAATACTGGGATGTCCATTCTCAATACCTCTGAAATGGAA ATCTCTATTTTCTACTTGGTTGGGATCCCAGGTTTGGAGCATGCCAATATTTGGATCT CTATCCCCATATGTCTCATGTACACTGTTGCTATCCTAGGGAATTGTACCATTCTGTT TTTCATAAAAACAGAGCCTTCTTTGCATGAGCCCATGTACTATTTTCTCTCCATGTTG GCTCTCTCTGACCTGGGACTATCCCTCTCCTCTCTCCCTACCATGTTAAGGATTTTCC TGTTCATGCTCCAGGAATTTCCCTGATGCCTGTATTGCTCAAGAGTTTTCATCCA TGGATTCTCAGCTATGGAGTCATCTGTACTTCTTATAATGTCTTTGATCGCTTTATT GCCATCTGCAACCCCTGAGATACACTTCCATCCTCACCAGTGCCAGAGTCATTCAAA TTGGGCTTGCTTTTCTCTCAAAAATGTTTGTGATCCTCCCATTTCTTTCACTCT AAAACATCTAAAATATTGTAAGAAGAACCTCCTGTCCCAATCCTACTGCCTCCATCAA GATGTCATGAAACTGGCCTGCACTGACAACAAGGTCAACATCATCTATGGCTTATTTG TGGCTCTCACAGGCATCCTAGACTTGACATTTATTTCATGTCCTACATGTTGATACT GAAAGCAGTGTGAGCATAGCATCAAGAAAAGAAAAGGCTCAAGGTCCTCAATACATGT GTTTCCCACATCTGTGCTGTGCTCATCTTCTATGTGCCATTATCTCCCTAGCTGTCA TCTACCGGTTTGCCAAACACAGTTTCCCAATCACTAGGATCCTCATAGCTGATGCTTT TCTGCTGGTGCCTCCATTGATGAACCCCATTTGTATACTGTGTGAAGAGCCAGCAGATA AGAAATCTTGTCTTAGAAAACTGTGCCAGAAGCAAAGCTGAAGCGGATGCTTAACCA CATGATGCTTAACCCAAA		
	ORF Start: ATG at 29	ORF Stop: TGA at 968	
	SEQ ID NO: 210	313 aa	MW at 35313.1kD
NOV72a, CG59211-01 Protein Sequence	MSILNTSEMEISIFYLVGIPGLEHANIWISIPICLMYTVAILGNCTILFFIKTEPSLH EPMYFFLSMLALSDLGLSLSLPTMLRIFLNFAPGISPDACIAEFFIHGFSAMESSV LLIMSFDRFIAICNPLRYTSILTSARVIQIGLAFSLKNVLLILPPFTLLKHLKYCKKN LLSQSYCLHQDVMKLACTDNKVNIIYGLFVALTGILDLTIFIMSYMILLKAVLSIASR KKRLKVLNLCVSHICAVLIFVVPISLAVIYRFKHSFPIIRILIADAFLLVPPLMNP IVYCVKSQLIRNLVLEKLCQKQS		

- 5 Further analysis of the NOV72a protein yielded the following properties shown in Table 72B.

Table 72B. Protein Sequence Properties NOV72a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 44 and 45

A search of the NOV72a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 72C.

Table 72C. Geneseq Results for NOV72a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV72a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG71564	Human olfactory receptor polypeptide, SEQ ID NO: 1245 - Homo sapiens, 322 aa. [WO200127158-A2, 19-APR-2001]	1..313 5..317	312/313 (99%) 312/313 (99%)	e-177
AAU24573	Human olfactory receptor AOLFR63 - Homo sapiens, 313 aa. [WO200168805-A2, 20-SEP-2001]	1..312 1..312	225/312 (72%) 272/312 (87%)	e-131
AAG71721	Human olfactory receptor polypeptide, SEQ ID NO: 1402 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..311 1..311	236/312 (75%) 267/312 (84%)	e-131
AAU24682	Human olfactory receptor AOLFR181 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	1..308 1..306	224/308 (72%) 265/308 (85%)	e-131
AAG71701	Human olfactory receptor polypeptide, SEQ ID NO: 1382 - Homo sapiens, 312 aa. [WO200127158-A2, 19-APR-2001]	1..308 1..306	224/308 (72%) 265/308 (85%)	e-131

- 5 In a BLAST search of public sequence databases, the NOV72a protein was found to have homology to the proteins shown in the BLASTP data in Table 72D.

Table 72D. Public BLASTP Results for NOV72a				
Protein Accession Number	Protein/Organism/Length	NOV72a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H344	Olfactory receptor 5112 (HOR5'beta12) - Homo sapiens (Human), 312 aa.	12..304 10..303	152/294 (51%) 219/294 (73%)	6e-90

Q9EQQ7	MOR 3'BETA4 - Mus musculus (Mouse), 319 aa.	1..309 1..310	159/310 (51%) 219/310 (70%)	9e-89
Q9H343	Olfactory receptor 5111 (HOR5'beta11) - Homo sapiens (Human), 314 aa.	4..313 4..314	154/311 (49%) 226/311 (72%)	9e-89
CAC38935	SEQUENCE 9 FROM PATENT WO0131014 - Homo sapiens (Human), 318 aa.	5..305 6..306	153/302 (50%) 217/302 (71%)	2e-87
CAC37756	SEQUENCE 1 FROM PATENT WO0125434 - Homo sapiens (Human), 317 aa.	5..305 5..305	153/302 (50%) 217/302 (71%)	3e-87

PFam analysis predicts that the NOV72a protein contains the domains shown in the Table 72E.

Table 72E. Domain Analysis of NOV72a			
Pfam Domain	NOV72a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF40: domain 1 of 1	109..134	10/26 (38%) 20/26 (77%)	0.38
7tm_1: domain 1 of 2	43..144	27/107 (25%) 71/107 (66%)	1.6e-15
7tm_1: domain 2 of 2	212..293	16/93 (17%) 56/93 (60%)	4.7
Sina: domain 1 of 1	300..311	7/12 (58%) 10/12 (83%)	1

Example 73.

5 The NOV73 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 73A.

Table 73A. NOV73 Sequence Analysis		
	SEQ ID NO: 211	1581 bp
NOV73a, CG59276-01 DNA Sequence	CTGGTGGGTTGGCGGCTAAGGGGCGGAGACAAGAGGGGCGGCCACCATCTCCTCCAAT GGAAGGGGAGACAGGGGCGGGCTTAATGACGGAAGGAGCATGGCGTGGAGACACCTGAA AAAGCGGGCCAGGATGCTGTGATCATCTGGGGGAGGAGGACTTCTCTTCGCCTCC TACCTGATGGCCACGGGAGATGAGCGTTTCTATGCTGAACACCTGATGCCGACTCTGC AGGGGCTGCTGGACCCGAGTCAGCCACAGACTGGCTGTTTCGTTCCACCTCCCTGGG GCTCCTTCCACGGGCCAGATTCAAGACTCTGACATGCTGGAAGTGAGAGTTCTGGGC CATAAATTCGAAATCCAGTAGGAATTGCTGCAGGATTGACAAGCATGGGGAAGCCG TGGACGGACTTTATAAGATGGGCTTTGGTTTGTGAGATAGGAAGTGTGACTCCAAA ACCTCAGGAAGGAAACCCTAGACCCAGAGTCTTCCGCCCTCCCTGAGGACCAAGCTGTC ATTAACAGGTATGGATTAAACAGTCACGGGCTTTCAGTGGTGAACACAGGTTACGGG CCAGACAGCAGAAGCAGGCCAAGCTCACAGAAGATGGACTGCCTCTGGGGGTCAACT	

	GGGGAAGAACAAGACCTCAGTGGACGCCGCGGAGGACTACGCAGAAGGGGTGCGCGTA CTGGGCCCCCTGGCCGACTACCTGGTGGTGAATGTGTCCAGCCCCAACACTGCCGGGC TGCGGAGCCTTCAGGGAAGGCCGAGCTGCGCCGCCTGCTGACCAAGGTGCTGCAGGA GAGGGATGGCTTGCAGAGAGTGCACAGGCCGCGCAGTCTGGTGAAGATCGCTCCTGAC CTCACCAGCCAGGATAAGGAGGACATTGCCAGTGTGGTCAAAGAGTTGGGCATCGATG GGCTGATTGTACGAACACCACCGTGAGTCGCCCTGCGGGCCTCCAGGGTGCCCTGCG CTCTGAAACAGGAGGGCTGAGTGGGAAGCCCCCTCCGGGATTATCAACTCAAACATT CGGGAGATGTATGCACTACCCAAGGCAAGGTTTCCCGTCGAGTTCCCATAAATTGGGG TTGGTGGTGTGAGCAGCGGGCAGGACGCGCTGGAGAAGATCCGGGCAGGGGCCCTCCT GGTGACGCTGTACACGGCCCTCACCTTCTGGGGGCCACCGTTGTGGGCAAAGTCAAG CGGGAAGTGGAGGCCCTTCTGAAGGAGCAGGGCTTTGGCGGAGTCACAGATGCCATTG GAGCAGATCATCGGAGGATGAGGAAACGGGCAGAGAAGCGGCTGATTGTCCAGTCCCC CTGCGTGGAGGCTGCTTGGCTGGGCTCGAGCCAGCGGTGGTGGGTGAGTGGGACCT GGTGGTCTGCTGGTGGTCAAGTGGGAATTTCCAGGTACGATTGTTTTCAGGCACTGT TCTTTGACTTGGTGCAGAAAAACAGATTTTGCAACACTTTCCAAGGACACAGTGTTA CCACTCCCTCACCTGCCATGGCCTCTTGGTCTGCTTTAACTTCTGAGCCTCAGG AGTCCATCTTGTCTG		
	ORF Start: ATG at 97		ORF Stop: TGA at 1555
	SEQ ID NO: 212	486 aa	MW at 52982.6kD
NOV73a, CG59276-01 Protein Sequence	MAWRHLKKRAQDAVILGGGGLLFASYLMATGDERFYAEHLMPTLQGLLDPEAHRLA VRFTSLGLLPRARFQSDMLEVRVLGHKFRNPVGLAAGFDKHGEAVDGLYKMGFGFVE IGSVTPKQEGNPRPRVRLPEDQAVINRYGFNSHGLSVVEHRLRARQQKAKLTEDG LPLGVNLGKNKTSVDAEDYAEGVRLGLADYLVVNVSSPNTAGLRSLQGKAELELRL LTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDIA SVVKELGIDGLIVTNTTVSRPA GLQGALRSETGGLSGKPLRDLSTQTI REMYALTQGVSRVP IIGVGVSSGQDALEK IRAGASLVQLYTALTFWGPVVGKVKRELEALLKEQFGGVTDAIGADHRRMRKRAEK RLIVQSPCEAAWLGSSPAVVGQLGPGGLLVVSLGISRYDCFQALFFDLVAEKQILQH FPRTQCYHSLTLPWPLGSAFNF		

Further analysis of the NOV73a protein yielded the following properties shown in Table 73B.

Table 73B. Protein Sequence Properties NOV73a	
Psort analysis:	0.8110 probability located in plasma membrane; 0.6400 probability located in endoplasmic reticulum (membrane); 0.3700 probability located in Golgi body; 0.1839 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV73a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 73C.

Table 73C. Geneseq Results for NOV73a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV73a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB70780	Tobacco dihydro-ornithine decarboxylase protein - Nicotiana tabacum, 458 aa. [WO200118190-A2, 15-MAR-2001]	36..398 81..458	199/383 (51%) 257/383 (66%)	e-101

Q9FZM9	DIHYDROOROTATE DEHYDROGENASE - <i>Oryza sativa</i> (Rice), 468 aa.	29..398 79..468	206/394 (52%) 261/394 (65%)	e-101
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Pfam analysis predicts that the NOV73a protein contains the domains shown in the Table 73E.

Table 73E. Domain Analysis of NOV73a			
Pfam Domain	NOV73a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DHodehase: domain 1 of 1	77..381	183/331 (55%) 282/331 (85%)	1.9e-169

Example 74.

- 5 The NOV74 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 74A.

Table 74A. NOV74 Sequence Analysis		
	SEQ ID NO: 213	1875 bp
NOV74a, CG59268-01 DNA Sequence	<p>ATGGCCGCGAGCCTCGCCTCTGCGGACTGCCAGGCTGGAAGGATGCGAGGCTCCCGC TCTCCACCACAAGCAACGAAGCCTGCAAGCTGTTGATGCCACGCTGACCCAGTATGT AAAATGGACCAATGACAAGAGTCTCGGTGGCATCGAGGGCTGCCTGTCAAAGCTCAAA GCAGCAGATCCAACTTTGTGATGGGCCACGCCATGGCTACTGGCCTTGTGCTGATTG GCACTGGAAGCTCCGTGAAGCTGGACAAAGAGCTGGACCTGGCTGTGAAGACAATGGT GGAGATTTCAAGAACCCAGCCGCTGACAAGGCGGGAGCAGCTGCACGTGTCTGCAGTA GAGACATTTGCCAATGGGAACCTTCCGAAAGCCTGTGAACATATGGGAACAGATTCTCC AGGACCACCCGACAGACATGTTGGCCCTGAAATTTCCCATGATGCTTATTTTTACCT GGGCTATCAGGAACAGATGAGAGATTCTGTTGCTCGAATTACCCCTTCTGGACACCT GACATCCCCCTAAGCAGCTATGTGAAAGGCATCTACTCTTTGGCTTGATGGAACCA ACTTCTACGACCAGGCAGAAAACTCGCCAAAGAGGCACCAACTCTTTGTCTTCAACA CCAGCACCCACAGACAACTACTGGGCAGGAAAAGCAGGCTGTGATGGGGCCAGGAGT GGTAACACATGGGCTCTGTGTCTGCAGCCCCAGGCTGACGCATGGTCCGTGCACACCG TCGCTCACATCCAGAGATGAAAGCAGAGATCAAGGATGGGTTGGAATTCATGCAGCA CTCAGAGACCTTCTGGAAGGACTCTGATATGTTGGCTTGTCATAACTATTGGCACTGG GCTTTATATCTGATTGAGAAGGTTTAATAAGGAGAAGTTATTTCTCCAGGGCGAAT ATGAGGCCGCGCTGACCATCTACGATACCCACATCCTTCCAGCTGCAGGCCAACGA TGCAATGTGAGCGTGGTGGACAGCTGCTCCATGCTTACCGCCTGCAGATGGAAGGA GTGCTGTGGGCCAGCGGTGGCAGGATGCTGCTGTGGCCCGGAAGCACAGCCGAG ACCACATCCTGCTGTTCAATGACGCACACTTCCTGATGGCATCCCTGGGTGCACACGA CCCCCAGACCACAGGAGCTGCTGACCACCCTGCGGGAGCCAGCGAGTATGCAGAG GGGCTTCTCGGGGTGGGGTCTCACCCTGCCGAGAGGTGCCAGGCCCTTGGCTGTGTA TTATCAGCAATCCTGACGGTTCTGTTAGATTGGCACTGTTATGCTGCTTACAGATGA GCAAACCTGAGGCTGGAAGATCCCCAGGGGAGAACTGCCAGCACCTCCTGGCCCCGAG GTGGGGCTGCCCTGTGCCAGGCCCTGGTGGAGGCTGAGGACGGGAACCCTGACCGCG TCCTGGAGCTGCTGCCATCCGCTACCGGATCCGTCAGCTCGGTGGGAGCAATGC CCAGAGAGACGTCTTCAACAGCTGCTGATTACGCGGCTTAAACTGCACCTCCAGC GTCCATAAGAACGTAGCCCGGAGCCTTCTGATGGAGCGTGATGCCTTGAAGCCCACT CGCCCTGACCGAGCGGCTCATCCGCAAGGCAGCTACCGTCCACCTCATGCAGAAGCC TTCTACCGCCCAACCCCACTGCAGGCTGCTCTCCATGGAAGGAGGCGGCGGCGC GATGAGCCTTCAGCCTGCCGGGCAGGGGACGTGAACATGGATGACCTAAGAAGGAAG GCAAGTCCTTGTGCTGCGGCGCTGTTGTTGTTTCAGGATGTTACGTAGAGATGGAGGG TGATTTAATGTTCCCTGA</p>	
	ORF Start: ATG at 1	ORF Stop: TGA at 1873

	SEQ ID NO: 214	624 aa	MW at 69393.3kD
NOV74a, CG59268-01 Protein Sequence	MAAASPLRDCQAWKDARLPLSTTSNEACKLFDATLTQYVKWINDKSLGGIEGCLSKLK AADPTFVMGHAMATGLVLIGTGSSVKLDKELDLAVKTMVEISRTQPLTRREQHVS AV ETFANGNFPKACELWEQILQDHPDMLALKFSHDAYFYLG YQE QMRDSVARIYPFWTP DIP LSSYVKG IYSFGLMETNFYDQAEKLAKEAPTLC LQH QHPTDNYWAGKAGCDGARS GNTWALCLQPQADAWSVHTVAHIHEMKAEIKDGL EFMQHSETFWKDSDMLACHNYWHW ALY LIEKGLIRRTLFFQGEYEALTIYDTHILPSLQANDAMLDVVDSCSMLYRLQMEG VSVGQRWQDVLVPARKHSRDHILLFNDAHFLMASLGAHDPQT TQELLTTLRDASEYAE GPSRGGGPHPAERCQAFACIISNPDGSVRLALLCLLTDEQTEAGRSPGENCQHLLARD VGLPLCQALVEAEDGNPDRVLELLLP IRYRIVQLGGSNAQRDVFNQLLIHAA LNTCTSS VHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQKPSTRQPPLQAALSMEGGGGR DEPSACRAGDVNMDDPKKEGKSLLLRCCCSGCSVEMEGDLMFP		

Further analysis of the NOV74a protein yielded the following properties shown in Table 74B.

Table 74B. Protein Sequence Properties NOV74a	
PSort analysis:	0.4328 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1137 probability located in mitochondrial inner membrane; 0.1137 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV74a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 74C.

Table 74C. Geneseq Results for NOV74a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV74a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41338	Human polypeptide SEQ ID NO 6269 - Homo sapiens, 478 aa. [WO200153312-A1, 26-JUL-2001]	1..559 10..478	463/559 (82%) 466/559 (82%)	0.0
AAM39552	Human polypeptide SEQ ID NO 2697 - Homo sapiens, 453 aa. [WO200153312-A1, 26-JUL-2001]	1..529 1..439	434/529 (82%) 437/529 (82%)	0.0
AAG02871	Human secreted protein, SEQ ID NO: 6952 - Homo sapiens, 104 aa. [EP1033401-A2, 06-SEP-2000]	1..102 1..102	102/102 (100%) 102/102 (100%)	1e-52

AAM40893	Human polypeptide SEQ ID NO 5824 - Homo sapiens, 746 aa. [WO200153312-A1, 26-JUL-2001]	568..604 1..37	32/37 (86%) 32/37 (86%)	2e-10
AAM40892	Human polypeptide SEQ ID NO 5823 - Homo sapiens, 746 aa. [WO200153312-A1, 26-JUL-2001]	568..604 1..37	32/37 (86%) 32/37 (86%)	2e-10

In a BLAST search of public sequence databases, the NOV74a protein was found to have homology to the proteins shown in the BLASTP data in Table 74D.

Table 74D. Public BLASTP Results for NOV74a				
Protein Accession Number	Protein/Organism/Length	NOV74a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH18918	HYPOTHETICAL 45.7 KDA PROTEIN - Homo sapiens (Human), 404 aa.	66..559 1..404	399/494 (80%) 402/494 (80%)	0.0
Q9NWP8	KAIA2372 PROTEIN - Homo sapiens (Human), 336 aa.	1..352 1..310	305/352 (86%) 308/352 (86%)	e-172
Q9XW02	Y54G11A.4 PROTEIN - Caenorhabditis elegans, 497 aa.	4..556 6..458	165/557 (29%) 256/557 (45%)	3e-61
Q9XW01	Y54G11A.7 PROTEIN - Caenorhabditis elegans, 407 aa.	4..347 6..305	122/347 (35%) 177/347 (50%)	7e-53
Q98CS1	MLR5032 PROTEIN - Rhizobium loti (Mesorhizobium loti), 440 aa.	60..553 46..435	145/496 (29%) 215/496 (43%)	1e-43

5 PFam analysis predicts that the NOV74a protein contains the domains shown in the Table 74E.

Table 74E. Domain Analysis of NOV74a			
Pfam Domain	NOV74a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Monooxygenase: domain 1 of 1	225..410	28/238 (12%) 121/238 (51%)	6.4

Example 75.

The NOV75 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 75A.

Table 75A. NOV75 Sequence Analysis			
	SEQ ID NO: 215	1851 bp	
NOV75a, CG59549-01 DNA Sequence	<div>CAGCTACAGCAAACATCGTTTCGAGATGTCCCACCAAGAGGGCAGCACAGGTGGCTTAC</div> <div>CAGACTTAGTGACTGAAAGCCTGTTTCAGCAGCCAGAGGAGCAGTCTGGAGTAGCAGCG</div> <div>GGTGACGGCGGCCTCCTCAGACATTGAAATGGCAGCCACAGAGCCATCGACCGGAGAT</div> <div>GGTGGTGATACCAGGGATGGTGGTTTTCTGAACGATGCCAGCACAGAAAAACAAACA</div> <div>CAGACTCAGAAAAGTTCAAGTGAAGACGTGCAACTTGAAAGCATGGGTGAAGGTTTATT</div> <div>TGGTTACCCGTTAGTGGGAGAGGAGACAGAAAGGGAGGAGGAAGAAGAGATGGAG</div> <div>GAGGAAGGGGAGGAGGAAGAACAGCCTCGGATGTGTCCACGATGCGGTGGCACCAACC</div> <div>ATGATCAGTGTTTTGTTAGACGAGGATCAGGCGTTGGAGGAGTGGATTTCTCAGAGAC</div> <div>ATCTGCCCTGCCCGATCTCGCTGGCAAGTCCTTACTGCTCTTCGCCAGCGGCAGCTG</div> <div>GGTTCAGTGCCCGCTTTGTATATGAGGCCCTGTGGGGCAAGAACCCTTTGTGCAGCGTT</div> <div>TCCGCTGCAGTATCTTCTTGAAGCCATGCCGGTTCTGTCTAGTACCATAACACTTTAA</div> <div>CCAGCGTGGCACCCGACTGGCCAGTAGCGGTGATGACTTAAGGGTGATAGTGTGGGAC</div> <div>TGGGTGCGGCAGAAAGCCAGTACTGAACTTTGAGAGTGGTCACGATATTAAATGTCATCC</div> <div>AGGCTAAGTTCTTTCCTAACTGTGGTGATTCACCTCTGGCCATGTGTGGCCATGATGG</div> <div>ACAGGTACGGGTAGCAGAACTAATTAATGCATCATATTGCGAGAATACTAAGCGTGTG</div> <div>GCCAAGCACAGGGGACCTGCCACGAGTTGGCTCTGGAGCCAGACTCTCCTTATAAGT</div> <div>TCCTCACTTCAGGTGAAGATGCCGTTGTGTTACCATTTGACCTCAGGCAAGACCGGCC</div> <div>AGCTTCAAAAGTTGTGGTAACAAGAGAAAATGATAAGAAAGTCGGACTGTATACAATC</div> <div>TCTATGAATCCTGCCAATATTTACCAATTTGCAGTGGGTGGACATGATCAGTTTGTAA</div> <div>GGATTATGACCAGAGGAGAATTGATAAGAAAGAAAAACATGGAGTACTCAAGAAATT</div> <div>CACTCCTCATCATCTGGTTTATTGTGATTTCCCAACAAACATCACCTGCCGTTGTGTAC</div> <div>AGCCACGATGGCACAGAGCTCCTGGCCAGCTACAATGATGAAGATATTTACCTCTTCA</div> <div>ACTCCTCTCTCAGTGATGGTGTCTCAATATGTTAAGAGATATAAGGGGCACAGAAATAA</div> <div>TGACACAATCAAATGTGTTAATTTCTATGGCCCCCGGAGTGAGTTTGTCTGTAGCGGT</div> <div>AGTGATTGTGGGCACGCTCTTCTTCTGGGAGAAATCATCCTCCAGATCATCCAGTTCA</div> <div>TGGAGGGGGACAGAGGAGATATAGTAAACTGTCTTGAACCCACCCCTTACCTACCTGT</div> <div>GTTGGCGACAGTGGCCTAGATCAGCATGTCAGGATCTGGACACCCACAGCTAAAACT</div> <div>GCCACTGAGCTTACTGGGTTAAAAGATGTGATTAAAGAAGAACAAGCAGGAGCGAGATG</div> <div>AAGACAACCTTGAATATACGGAAGCTCGTTTGACAACCGCATGCTTCGGTTCTTCGTGCG</div> <div>TCACCTGTTACAGAGAGCTCATCAACCCGCTGGAGAGATCATGGAGCTGAGTTCCCA</div> <div>GATGAAGAAGAGTTGGATGAGTCTTCCAGCACCTCAGATACATCCGAGGAGGAGGGCC</div> <div>AAGATCGAGTGCAGTGCATACCATCCTGAAGGCCTCATATCCAGTCCAGCTAG</div>		
	ORF Start: ATG at 25	ORF Stop: TGA at 1825	
	SEQ ID NO: 216	600 aa	MW at 67372.4kD
NOV75a, CG59549-01 Protein Sequence	<div>MSHQEGSTGGLPDLVTESLFSSPEEQSGVAAVTAASSDIEMAATEPSTGDGGDTRDGG</div> <div>FLNDASTENQNTDSESSSEDVELESMEGLFGYPLVGEETEREEEEEMEEEGEEEEEQ</div> <div>PRMCPRCGNTNHDQCLLEDDQALEEWISSETALPRSRWQVLTALRQRLGSSARFVY</div> <div>EACGARTFVQRFRLQYLLGSHAGSVSTIHFNRQGRTRLASSGDDLRVIVWDWVRQKPV</div> <div>NFESGHDINVIQAKFFPNCGDSTLAMCGHDGQVRVAELINASYCENTKRVAKHRGPAH</div> <div>ELALEPDSPYKFLTSGEDAVVFTIDLRQDRPASKVVVVTRENDKKVGLYTI SMNPANIY</div> <div>QFAVGGHDQFVRIYDQRRIDKKENNGVLKKFTPHHLVYCDFPTNITCVVYSHDQTELL</div> <div>ASYNDEDIYLFNSSLSDGAQYVKRYKGRNNDTIKCVNFYGPREFVVS GSDCGHVFF</div> <div>WEKSSSQIIQFMEGDRGDIVNCLEPHYPYLPVLATSLDQHVRIWTPAKTATELTGLK</div> <div>DVIKKNQERDEDNLNYTDSFDNRMLRFFVRHLLQRAHQPGWRDHGAEPDEEELDES</div> <div>SSTSDTSEEGQDRVQCIPS</div>		

Further analysis of the NOV75a protein yielded the following properties shown in Table 75B.

Table 75B. Protein Sequence Properties NOV75a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0442 probability located in microbody (peroxisome)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV75a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 75C.

Table 75C. Geneseq Results for NOV75a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV75a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR85870	WD-40 domain-contg. Mus musculus protein - Mus musculus, 816 aa. [WO9521252-A2, 10-AUG-1995]	95..589 333..815	295/495 (59%) 372/495 (74%)	e-179
AAM73935	Human bone marrow expressed probe encoded protein SEQ ID NO: 34241 - Homo sapiens, 164 aa. [WO200157276-A2, 09-AUG-2001]	1..157 8..164	157/157 (100%) 157/157 (100%)	2e-87
AAM61216	Human brain expressed single exon probe encoded protein SEQ ID NO: 33321 - Homo sapiens, 164 aa. [WO200157275-A2, 09-AUG-2001]	1..157 8..164	157/157 (100%) 157/157 (100%)	2e-87
AAM34114	Peptide #8151 encoded by probe for measuring placental gene expression - Homo sapiens, 164 aa. [WO200157272-A2, 09-AUG-2001]	1..157 8..164	157/157 (100%) 157/157 (100%)	2e-87
AAB57007	Human prostate cancer antigen protein sequence SEQ ID NO:1585 - Homo sapiens, 214 aa. [WO200055174-A1, 21-SEP-2000]	408..600 22..214	144/194 (74%) 162/194 (83%)	2e-80

In a BLAST search of public sequence databases, the NOV75a protein was found to have homology to the proteins shown in the BLASTP data in Table 75D.

Table 75D. Public BLASTP Results for NOV75a				
Protein Accession Number	Protein/Organism/Length	NOV75a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q12839	H326 PROTEIN - Homo sapiens (Human), 597 aa.	1..600 1..597	408/604 (67%) 471/604 (77%)	0.0
Q01078	PROTEIN PC326 - Mus musculus (Mouse), 747 aa.	95..589 264..746	295/495 (59%) 372/495 (74%)	e-178
Q9W091	CG8001 PROTEIN - Drosophila melanogaster (Fruit fly), 748 aa.	68..587 209..711	178/533 (33%) 280/533 (52%)	1e-77
Q96E00	UNKNOWN (PROTEIN FOR MGC:9478) - Homo sapiens (Human), 273 aa.	1..246 1..243	141/249 (56%) 173/249 (68%)	8e-66
Q9M1E5	HYPOTHETICAL 54.0 KDA PROTEIN - Arabidopsis thaliana (Mouse-ear cress), 481 aa.	183..536 42..419	136/382 (35%) 209/382 (54%)	2e-62

PFam analysis predicts that the NOV75a protein contains the domains shown in the Table 75E.

Table 75E. Domain Analysis of NOV75a			
Pfam Domain	NOV75a Match Region	Identities/ Similarities for the Matched Region	Expect Value
WD40: domain 1 of 7	188..224	13/37 (35%) 29/37 (78%)	0.0016
WD40: domain 2 of 7	231..269	12/39 (31%) 26/39 (67%)	11
WD40: domain 3 of 7	278..315	9/38 (24%) 24/38 (63%)	2.2e+02
WD40: domain 4 of 7	326..363	8/38 (21%) 27/38 (71%)	8.8
WD40: domain 5 of 7	382..418	5/37 (14%) 27/37 (73%)	12
WD40: domain 6 of 7	429..466	6/38 (16%) 26/38 (68%)	18
WD40: domain 7 of 7	473..509	11/37 (30%) 22/37 (59%)	0.51

Example 76.

The NOV76 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 76A.

Table 76A. NOV76 Sequence Analysis		
	SEQ ID NO: 217	7497 bp
NOV76a, CG59641-01 DNA Sequence	<p>ATGGTCTTGCTTCTTTGTCTATCTTGTCTGATTTTCTCCTGTCTGACCTTTTCCTGGT TAAAAATCTGGGGGAAAATGACGGACTCCAAGCCGATCACCAGAGTAAATCAGAAGC AAACCTCATCCCGAGCCAGGAGCCCTTTCCAGCCTCTGATAACTCAGGGGAGACACCG CAGAGAAATGGGGAGGGCCACACTCTGCCCAAGACACCCAGCCAGGCCAGCCAGCCT CCCACAAAGGCCCAAGATGCCGGTCGGCGGAGAACTCCCTACCACCTCCCACCA GAAGCCCCAAGAAACCCCTTTCTTCCAGTGACGCAGACCCCTCCCAGAGCTTCAA GCCAACGGGACTGGGACACAAGTCTGGAGGCCACAGATACCAATGGCCTGTCTCCT CAGCCAGGCCCCAGGGCCAGCAAGCTGGCTCCCCCTCCAAAGAAGACAAGAAGCAGGC AAACATCAAGAGGCAGCTGATGACCAACTTCATCTGGGCTCTTTTGATGACTACTCC TCCGACGAGGACTCTGTTGCTGGCTCATCTCGTGAGTCTACCCGGAAGGGCAGCCGGG CCAGCTTGGGGCCCTGTCCCTGGAGGCTTATCTGACCACAAGCCGAGCATGTCCGG ACTCCACCTGGTGAAGAGGGGACGGGAACACAAGAAGCTGGACCTGCACAGAGACTTT ACCGTGGCTTCTCCCGCTGAGTTGTGACACGCTTTGGGGGGGATCGGGTTCATCGAGA AGGTGCTTATGCCAACAACGGGATTGCCCGCTGAAGTGCATGCGCTCCATCCGCGAG GTGGCCCTATGAGATGTTCCGCAACGAGCGGGCCATCCGGTTTGTGATGGTGACC CCCGAGGACCTTAAGGCCAACGAGAGTACATCAAGATGGCGGATCATTACGTCCCCG TCCCAGGAGGGCCCAATAACAACAATATGCCAACGTGGAGCTGATTGTGGACATTGC CAAGAGAATCCCCGTGCAGGCGGTGTGGGCTGGCTGGGGCCATGCTTCAGAAAAACCT AAACTTCCGGAGCTGCTGTGCAAGAATGGAGTTGCTTCTTAGGCCCTCCAGTGAGG CCATGTGGGCTTAGGAGATAAGATCGCCTCCACCGTTGTCGCCAGACGCTACAGGT CCCCACCTTGCCTGGAGTGGAGCGGCTGACAGTGGAGTGGACAGAAGATGATCTG CAGCAGGGAAAAAGAATCAGTGTCCCAGAAGATGTTATGACAAGGGTTGCGTGAAG ACGTAGATGAGGGCTTGGAGGCAGCAGAAAGAATTGGTTTTCCATTGATGATCAAAGC TTCTGAAGTGGCGAGGGAAGGAATCCGGAAGGCTGAGAGTGGGAGGACTTCCCG ATCCTTTTCAGACAAGTACAGAGTGAATCCAGGCTCGCCCATCTTCTCATGAAGC TGGCCAGCACGCCCCTCACCTGGAAGTTCAGATCCTCGCTGACCAATGTTGGAATGC TGTGCTCTGTTTGGTCCGACTGCTCCATCCAGCGCGGCTGACAGTGGAGTGGTGTAG GAAGCACCAGGCCACCATCGCCCCGCTGGCCATATTGAGTTCATGGAGCAGTGTGCCA TCCGCTTGGCCAGACCCGCTGGGCTATGTGAGTGCAGGACAGTGAATACCTCTATAG TCAGGATGGCAGCTTCCACTTCTGGAGCTGAATCCTCGCTTGCAAGTGGAAACATCCC TGACAGAAATGATTGCTGATGTTAATCTGCGCGGCCCGCAGCTACAGATCGCCATGG CGGTGCCACTGCACCGGCTGAAGGATATCCGGCTTCTGTATGGAGATCACCATGGGG AGTGACTCCCATTTCTTTGAAACCCCTCAAACCCCTCCCTCGCCGAGGCCACGTC ATTGCCGCGAGAATCACCAGCGAAAACCCAGACGAGGGTTTAAAGCCGAGCTCCGGGA CTGTCCAGGAATGAATTTCCGGAGCAGCAAGAACGTGTGGGGTTACTTCAGCGTGGC CGCTACTGGAGGCTGCACGAGTTTGGCGATTCCCAATTTGGGCACTGCTTCTCTGG GGAGAGAACCGGGAAGAGGCCATTTGAAACATGGTGGTGGCTTTGAAGGAATGTCCA TCCGAGGCGACTTAGGACTACCGTGAATACCTCATTAACTCCTGGAGACCGAGAG CTTCAGAACACGACATCGACACCGGGTGGTTGGACTACCTCATTGTGAGAAAGTG CAGGCGGAGAAACCGGATATCATGCTTGGGGTGGTATGCGGGGCTTGAACGTGGCCG ATGCGATGTTCAGAACGTGCATGACAGATTTCTTACACTCCCTGGAAGGGGCCAGGT CCTCCAGCGGATTCCTACTGAACCTCGTAGATGTGGAATTAATTTACGAGGTGTT AAGTACATTTCTAAGGTGGCCCGGAGTCTCTGACCATGTTCTGTTCTCATCATGAATG GCTGCCACATCGAGATTGATGCCACCGGCTGAATGATGGGGGCTCCTGCTCTCCTA CAATGGGAACAGCTACCCACCTACATGAAGGAAGAGGTTGACAGTTACCGAATTACC ATCGGCAATAAGACGTGTGTGTTGAGAAGGAGAAGCATCTACAGTCTGAGATCCC CCTCGGCTGGGAAGCTGACACAGTACACAGTGGAGGATGGGGGCCAGTTGAGGCTGG GAGCAGCTACGCTGAGATGGAGGTGATGAAGATGATCATGACCCCTGAACGTTACAGAA AGAGGCCGGGTGAAGTACATCAAGCGTCCAGGTGCCGTGCTGGAAGCAGGCTGCGTGG TGGCCAGGCTGGAGCTCGATGACCCCTTCTAAAGTCCACCGGCTGAACCGTTACAGG AGAACTCCCTGCCAGCAGACACTGCCATCCTCGGAGAGAACTGCACCGGATCTTC CACAGCGTCTTGAAAACCTCACCACGTGATGAGTGGCTTTTGTCTGCCAGAGCCCG TTTTTAGCATAAAGCTGAAGGAGTGGGTGAGAAAGCTCATGATGACCTCCGGCACCC GTCACTGCCGCTGCTGGAGCTGCAGGAGATCATGACAGCGTGGCAGGCGGACCTCCC GCCCTGTGGAGAAGTCTGTCCGAGGGTATGGCCAGTATGCCAGCAACATCACCT CGGTGCTGTGCCAGTTCCCCAGCCAGCAGATAGCCACCATCTGGACTGCCATGCAGC CACCTGCGAGCGGAAGGCTGATCGAGAGGCTTCTTCAACACCCAGAGCATCGTG CAGTTGGTCCAGAGATACCGCAGCGGATCCGCGCTATATGAAAACAGTGGTGTGG ATCTCCTGAGAAGATACTTGGCTGTGAGAGCAAGGCAAGAGATGCTGATGCCAACAC CAGTGGGATGGTGGGGGCGTGAGGAGCCTGAGCTTTACCTCTGTGTGGTGTTTTGTG TCCCCGAAATCCCACTACGACAAGTGTGTGATAAACCTCAGGAGCAGTTCAAGCCAG ACATGTCCAGGTGCTGGACTGCATCTTCTCCACGCACAGGTGGCCCAAGAAGAACCA GCTGGTGATCATGTTGATCGATGAGCTGTGTGGCCAGACCTTCCCTGTGCGGACGAG CTGATCTCCATCTCAACGAGCTCACTCAGCTGAGCAAAAGCGAGCACTGCAAGTGG</p>	

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	<p>CCCTCAGAGCCCGGCAGATCCTGATTGCTCCACCTCCCCTCCTACGAGCTGCGGCA TAACCAGGTGGAGTCCATTTCTGTCTGCCATTGACATGTACGGCCACCAGTTCTGC CCCGAGAACTCAAGAAATTAATACTTTCGGAAACAACCATCTTCGACGCTCTGCCTA CTTTCTTCTATCAGCAAACAAGTCGTGTGCATGGCGTCTTGGAGGTTTACGTGCG GAGGGGCTACATCGCCTATGAGTTAAACAGCCTGCAGCACCGGCAGCTCCCGGACGGC ACCTGCGTGGTAGAATTCAGTTCATGCTGCCGTCTCCCAACCAACCGGATGACCG TGCCCATCAGCATCACCACCTGACCTGCTGAGGCACAGCACAGAGCTCTTCATGGA CAGCGGCTTCTCCCACTGTGCCAGCGCATGGGAGCCATGGTAGCCTTCAGGAGATT GAGGACTTCACCAGAAATTTGATGAAGTCATCTCTGCTTCGCCAACGTGCCCAAAG ACACCCCTCTTTCAGCGAGGCCCGCACCTCCCTATACTCCGAGGATGACTGCAAGAG CCTCAGAGAAGAGCCATCCACATTCGAATGTGTCCATCCAGTGTGCAGACCACTG GAGGATGAGGCACCTGGTGCCGATTTTACGGACATTCTGACAGTCCAAGAAAATATCC TTGTGGATTATGGACTCCGACGAATCACATTCTTGATTGCCAAGAGTTTGAGAAGA TCGCATTTACCGTCACTTGGAACCTGCCCTGGCCTTCCAGCTGGAACCTTAACCGGAT CGTAACCTCGATCTGACCGCGTGCCTGTGCCAACCAAGATGACACCTTTACCTGG GTGCTGCCAAGGTGAAGGAAGGTGTGGAAGTGACGGACCATAGGTTCTTCATCCGCGC CATCATCAGGCACCTGACCTGATCAAAAGGAAGCCTCCTTCAATACCTGCAGAAC GAGGGTGAGCGGCTGCTCTGGAGGCCATGGACGAGCTGGAGGTGGCGTTCAATAAAC CCAGCGTGCGCACCGACTGCAACCACATCTTCTCAACTTCGTGCCACTGTGCATCAT GGACCCCTTCAAGATCGAGGAGTCCGTGGCTACATGGTTATGCGCTACCGGACCGCG CTGTGGAACCTCCGTGTGCTACAGGCTGAGGTCAAGATCAACATCCGCAAGACCA CCGGCAGTGCCGTTCCCATCCGCTGTTCATCACCATGAGTCGGGCTACTACCTGGA CATCAGCCTTCAAAAGAGTGACTGACTCCAGATCTGGAATATCATGTCTTCACTCC TTCCGCAACAAGCAAGGCCCGCAGCACGGGATGCTGATCAATCTCCCTACGTCACT AGGATCTGCTCCAGGCCAAGCGATTCCAGGCCCAGACCTGGGAACCACTACATCTA TGACTTCCCGAAATGTTTCAGGCAGGCAAGTCCGGCGGCTCAGACGCGGTACATGTG CACAAATGTGCAAGCTCTCTTTAACTGTGGGGCTCCCGAGACAGTATCCCAAAGACA TCCTGACATACACTGAATTAGTGTGGACTCTCAGGCCAGCTGGTGGAGATGAACCG ACTTCTGTGTGGAATGAGGTGGGCATGGTGGCCTTCAAAATGAGGTTTAAAGACCCAG GAGTACCCGGAAGGACGGATGTGATCGTCATCGGCAATGACATCACTTCGATTTG GATCCTTTGGCCCTGGAGAGGACCTTCTGTACTCTGCGGGCATCCGAGATGGCCCGGGC AGAGGGCATTTCCAAAATTTACGTGGCAGCAACAGTGGCGCCCTATTGGCATGGCA GAGGAGATCAACACATGTTCCACGTGGCTTGGGTGGACCCAGAACCCCAAGAAA AAAAAAAACAGTGGCTTTCAGTGCAGGGAAGTGGATTCTGAGCCTCACTAAAGTATT TTTTAAGGGATTTAAATACCTGTACCTGACTCCCCAAGACTACACCAAGATCAGCTCC CTGAACCTCGTCCACTGTAAACACATCGAGGAAGGAGGAGATCCAGATACATCA CGGATATCATCGGAAGGATGATGGCTTGGGCGTGGAGAATCTGAGGGGCTCAGGCAT GATTGTGGGGAGTCTCTCTGGCTTACGAAGAGATCGTCACCATTAGCTTGGTGACC TGCCGAGGATCAAGGATTGGGGCTACTTGGTGAGGCTGGGCGAGGATTCCTTGACC TGGAGAATTTCCACATCATCCTCACAGGAGCAAGTCTCTCAACAAGGCTCTGGGAAG AGAGGTCTACACATCCAACAACCAAGTGGGTGGCGTTTCAGATCATGCAATACATGTT GTCTCCCATCATACCGTGCAGATGACTTTGAGGGGTTTATACCATCTGGAGTGGC TGCTCTATATGCCAAAGGATAATCACAGCCCTGTCCCTATCATCACACCACTGACCC CATTGACAGAGAAATGAATTCCTCCCATCCAGAGCTCCCTACGACCCCGGTGGATG CTTGCAAGGAAGGCTCACCCAACTCTGAAGGGAACGTGGCAGAGCGGATTCTTTGACC ACGGCAGTTTCAAGGAATCATGGCACCTGGGCGCAGACCGTGGTGACAGGACGAGC AAGGCTTGGGGGATTCCCGTGGGAGTGATTGCTGTGGAGACAGCGGATGTGGAGGTG GCAGTCCCTGCAAGCCCTGCCAACCTGGATTCTGAGGCCAAGATAATTGACAGGCAG GACAGGTGTGGTTCCAGACTCAGCCTACAAAACCGCCAGGCCGTCAAGGACTTCAA CCGGGAGAAGTTGCCCTGATGATCTTTGCCAACTGGAGGGGTTCTCCGGTGGCATG AAAGACATGTATGACAGGTGCTGAAGTTTGGAGCCTACATCGTGGACGATCCAGTCA AATACAAACAGCCCATCTGATCTATATCCGCCCCTATGCGGAGCTCCGGGGAGGCTC CTGGGTGGTCAATAGATGCCACCATCAACCCGCTGTGCATAGAAATGTATGCAGACAAA GAGAGCAGGGGTGGTGTCTGGAACCAAGGGGACAGTGGAGTTAAGTTCCGAAAGA AAGATCTGATAAAGTCCATGAGAAGGATCGATCCAGCTTACAAGAAGCTCATGGAACA GCTAGGGGAACCTGATCTCTCCGACAAGGACCGAAAGGACCTGGAGGGCCGGCTAAAG GCTCGCGAGGACCTGCTGCTCCCATCTACCACAGGTGGCGGTGACGTTCCGCGACT TCCATGACACACCCCGCCGATGCTGGAGAAGGGCGTATATCTGACATCCTGGAGTG GAAGACCGCAGCACCTTCTGTATTGGCGTCTGCGCCGCTCCTCCTGGAGGACGAG GTCAAGCAGGAGATCCTGCAGGCCAGCGGGAGCTGAGTCACGTGACATCCAGTCCA TGCTGCGTCTGCTGTTCTGTGGAGACGGAGGGGCTGTCAAGGCCTACTTGTGGGACAA CAACCAGGTGGTTGTGCACTGGCTGGAACAGCACTGGCAGGCAGGGGATGGCCCGCGC TCCACCATCGTGAAGAACATCACGTACCTGAAGCAGCACTGTCTTCAAGACCATCC GAGGCCTGGTTGAAGAAAACCCGAGGTGGCCGTGGACTGTGTGATATACCTGAGCCA GCACATCAGCCAGCTGAGCGGGCGCAGGTGCTTACCTGCTGTCTACCATGGACAGC CCGCGCTCCACCTGA</p>
	<div>ORF Start: ATG at 1</div> <div>ORF Stop: TGA at 7495</div>
	<div>SEQ ID NO: 218</div> <div>2498 aa</div> <div>MW at 280484.4kD</div>
NOV76a, CG59641-01 Protein Sequence	<p>MVLLCLSLIFSLTFSWLKIWKMTDSKPIITKSKSEANLIPSEQEPFASDNSGETP QRNGEGHTLPKTPSQAEPAASHKGPDKAGRRRNSLPSSHQKPPRNPLSSSDAAPSPELQ ANGTGTQGLEATDNLSSARPQGGQAGSPSKEDKQANIKRQLMTNFIILGSFDDYS SDEDSVAGSSRESRLGSRASLGALSLEYLTTRPSMSGHLHLVLRGREHKKLDLHRDF TVASPAEFVTRFGGDRVIEKVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVVMVT PEDLKANAHEYIKMADHYVPVPGGPNNNNYANVELIVDIAKRIPVQAVWAGWGHAENP</p>

KLPELLCKNGVAFGLPPSEAMWALGDKIASTVVAQTLQVPTLPWSSGLTVEWTEDDL QQGKRISVPEDVYDKGCVKDVEGLEAAERIGFPLMIKASEGGGKGIRKAESAEDFP ILFRQVQSEIPGSPFIPLMKLAQHARHLEVQILADQYGNVSLFGRDCSIQRRHQKIVE EAPATIAPLAIFEFMEQCAIRLAKTVGYVSAGTVEYLYSQDGSFHFLELNPRQLQVEHP CTEMIADVNLPAQQLIAMGVPLHRLKDIRLLYGESPWGVTPISEFETPSNPPLARGHV IAARITSENPDGFKPSSGTVQELNFRSSKNVWGYFSVAATGGLHEFADSQFGHCFSW GENREEAISNMVVALKELSIKRGDFRTTVEYLINLLETESFQNNIDITGWLDDYLIAEKV QAEKPDIMLGVVCGALNVADAMFRTCTMTDFLHSLERGVLPADSLNLDVDELIYGGV KYILKVARQSLTMFVLMNGCHIEIDAHLRLNDGGLLSYNGNSYTYMKKEEVDYSRIT IGNKTCVFEKENDPTVLRSPSAGKLTQYTVEDGGHVEAGSSYAEMEVMKIMTLNVQE RGRVKYIKRPGAVLEAGCVVARLELDDPSKVHPAEPFTGELPAQQTLPILGEKLHQVF HSVLENLTNVMSGFCLPEPVFSIKLKEWVQKLMMLLRHPSLPLLELQEIIMTSVAGRI APVEKSVRRVMAQYASNITSVLCOFPSPQIATILDCHAATLQKADREVFINTQSIV QLVQRYRSRGIRGYMKTIVLDLLRRYLRVESKARDADANTSGMVGVRSLSFTSVWCFV SPESHYDKCVINLREQFKPDMSQVLDICFSHAQVAKKNQVIMLIDELCGPDPPLSDSE LISILNELTQLSKSECHKVALRARQILIASHLPSYELRHQVSEIFLSAIDMYGHQFC PENLKKLILSETTIFDVLPFFYHANKVVMASLEVVYRRGYIAYELNSLQHRQLPDD TCVVEFQFMLPSSHPNRMTPVISITNPDLLRHSTELFMDSGFSPLCQRMGAMVAFRRF EDFTRNFDEVISCFANVPKDTPLFSEARTSLYSEDDCKSLREEPHILNVSICADHL EDEALVPILRTFVQSKNILDVYGLRRITFLIAQEFAEDRIYRHLEPALAFQLELNRM RNFDLTAVPCANHKMHLYLGAAKVKEGVEVTDHRFFIRAIRHSDLTITKEASFYELQN EGERLLEAMDELEVAFNNTSVRTDCNHIFLNFVPTVIMDPFKIEESVRYMVMRYGSR LWKLRVLQAEVKINIRQTTGSAVPIRLFITNESGYLLDISLYKEVTDSDSGNIMFHS FGNKQGPQHGMLINTPYVTKDLLQAKRFQAQTLGTTYIYDFPEMFQASPAQAQTRVHV HNVQALFKLWGSPPDKYPKDILTYTELVLDSQQLVEMNRLPGGNEVGMVAFKMRFKTQ EYPEGRDVIIGNDITFRIGSFPGEDLLYLRASEMARAEIPKIYVAANSGARIGMA EEIKHMFHVAWVDPEDPHKKKKTVAFSAGNWIRSLTKVFFKGFYLYLTPQDYTRISS LNSVHCKHIEEGGESRYMITDIIGKDDGLGVENLRGSGMIAGESLAYEEIVTISLVT CRAIGIGAYLVRGQQRVIQVENSIIILTGASALNKVLGREVYTSNNQLGGVQIMHYNG VSHITVPDDFEGVYTIILEWLSYMPKDNHSPVPIITPTDIDREIEFLPSRAPYDPRWM LAGRPHPTLKGTWQSGFFDHGSFKEIMAPWAQTVVTGRARLGGIPVGVIAVETRTVEV AVPADPANLDSEAKIIQAGQVWFPSAYKTAQAVKDFNREKLPLMIFANWRGFSGGM KDMYDQVLKFGAYIVDGLRQYKQPIIYIPPYAELRGGSWVVIDATINPLCIEMYADK ESRGVLEPEGTVEIKFRKKDLIKSMRRIDPAYKKLMEQLGEPDLSKDRKDLLEGRLK AREDLLLPIYHQVAVQFADFHDTPGRMLEKGVISDILEWKTARTFLYWRLLRLLEDQ VKQEILQASGELSHVHIQSMRLRRWFVETEGAVKAYLWDNNQVVQWLEQHWQAGDGP STIRENITYLKHDSVLKTIIRGLVEENPEVAVDCVIYLSQHSIPAERAQVVHLLSTMD PAST

Further analysis of the NOV76a protein yielded the following properties shown in Table 76B.

Table 76B. Protein Sequence Properties NOV76a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 25 and 26

A search of the NOV76a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 76C.

Table 76C. Geneseq Results for NOV76a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV76a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU32848	Novel human secreted protein #3339 - Homo sapiens, 2486 aa. [WO200179449-A2, 25-OCT- 2001]	26..2498 1..2486	2316/2555 (90%) 2339/2555 (90%)	0.0
AAR05707	Acetyl-CoA-carboxylase - Gallus sp, 2324 aa. [JP02057179-A, 26- FEB-1990]	163..2498 17..2324	1728/2375 (72%) 2003/2375 (83%)	0.0
AAB86033	Bovine acetyl-coenzyme A carboxylase-alpha protein fragment - Bos taurus, 2288 aa. [DE19946173-A1, 05-APR-2001]	204..2497 14..2288	1719/2342 (73%) 1969/2342 (83%)	0.0
AAR98811	Erysiphe graminis acetyl coenzyme A carboxylase - Erysiphe graminis f.sp.hordei, 2273 aa. [FR2727129-A1, 24- MAY-1996]	235..2490 42..2271	1045/2326 (44%) 1432/2326 (60%)	0.0
AAY24150	Candida albicans acetyl CoA carboxylase - Candida albicans, 2270 aa. [WO9932635-A1, 01- JUL-1999]	239..2489 88..2269	1015/2300 (44%) 1396/2300 (60%)	0.0

In a BLAST search of public sequence databases, the NOV76a protein was found to have homology to the proteins shown in the BLASTP data in Table 76D.

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Table 76D. Public BLASTP Results for NOV76a				
Protein Accession Number	Protein/Organism/Length	NOV76a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O00763	Acetyl-CoA carboxylase 2 (EC 6.4.1.2) (ACC-beta) [Includes: Biotin carboxylase (EC 6.3.4.14)] - Homo sapiens (Human), 2483 aa.	1..2498 1..2483	2349/2528 (92%) 2384/2528 (93%)	0.0
O70151	ACETYL-COA CARBOXYLASE - Rattus norvegicus (Rat), 2456 aa.	1..2497 1..2455	2068/2524 (81%) 2224/2524 (87%)	0.0

Table 77A. NOV77 Sequence Analysis			
	SEQ ID NO: 219	1624 bp	
NOV77a, CG59630-01 DNA Sequence	CGCGCGCGCGGGATGGAGCCGAGCCCGGCGGCGCCGGAGCTGCCGGCGCGGGGCC CCGGCGGCGCCTGCGAGCTGGGCCCGGCGGCGGAGGCGGCCATGAGCCTCGCCAT CCACAGCACACGGGCACCCGTACGACCTGGCCGTGCCGCCGACGAGACGGTGGAG GGGCTGCGCAAGCGGTTGTCCAGCGCCTCAAAGTGCCCAAGGAGCGCTGGCTCTTC TCCACAAAGACACGCGGCTCAGTTCGGGGAAGCTGCAGGAGTTTCGGCGTGGGTGATGG CAGCAAGCTGACCTTGGTACCCACCGTGAAGCGGGCTCATGTCTCAGGCCTCAAGG CCGGAACAGTCCGTGATGCAAGCTCTCGAGAGTCTCAGGAGACGAGCCCCAGCGG CGCCCGGGCGGGCGGGCTGGCGGAGGAGGCTTCGGAAATACAGATTCAATTTATT TAAGCGTCCGTGGCACCGACAGGGACCCAGAGCCAGAGAGGGGCGGCGAGAGGCC CAGGTTCAGTGACTTCCTGTGGGCGGTTTCGCCACTGACACTGGCTTCGCTGTGGGCG ACCACATGATGTTCTGTGACGTGACGTTCGCGGCCCAGACCGTCCACTGCAACACCG CCATGTGCTGGCCGTGCGGCCCGCGCGCTGTGCGCGGGGGGACCCAGCATAGCC TCCCCGTGTCTCGCCCTGCGGCGCGGTGTCCAGTGCAGGCGAGTCCCCCGGTGC CCACAGCCCGTCCCCTGCATCTCCCTCGCCCATCACAGCCGGCTCCTTCGGTCCCA CGCAGCCTCCACCACCTGCCCGGAGCAGATGGACTGCTCCCCACGGCCAGCAGCAGT GCCAGTCTGGTGCCAGCACCGTCTACCCAGGGGCCAGCCCTGCCCGCCGTCCC GAAAACCGGCGCGCTCATCGAGAGCTTTGTGAATCACGCCCGGGGGTCTTCTCAGG GACCTTCTTGGCAGCTACACCCAACTGCCAAGACAGCAGCGGGCGGCGCGCGGT GACATCGGCACCATCTGCAGATCCTGAACGACCTCCTGAGCGCCACCGGCACTACC AGGGCATGCCCCCTTCGCTGGCCAGCTCCGCTGCCACGCCCAGTGTCTCCCGGCTC ACCGGCCCCCGACCTGGCCCCCAGAACTACCTCCTGCGAGAAGCTCAGGCTGCCCCC TCAGCTCCTCGTGCAGGGCCAGAGCCAGATCCGATGTGCAAGCCCCGGGTGACC GGCTTCGGCAGACAGAAAACCGGCCACGCGCTGCAAGGTGGAACGGCTGCAGCTGCT TCTGCAGCAGAAACGGCTCCGTAGAAAGGCCCGGCGGGACGCGCGGGGTCCGTACCAC TGGTCACCCAGCGCAAGGCCGCGCCGACGACAGCAGTAGCAGCGGGGGCGGCGCA GCCCCAGCGAGGCTCCGGCTTGGGCTCGACTTCGAGGACTCCGTGTGGAAGCCAGA AGTCAACCTTGACATCAAGTCAGAGTTCGTGGTGGCTTAGGATCTTCGGATCGGCCAC CCTCGCCCTCGCACCCAGCCAGGGCGGGGACTCCGAGAGCCCGGAGAGAAC		
	ORF Start: ATG at 13	ORF Stop: TAG at 1546	
	SEQ ID NO: 220	511 aa	MW at 53949.3kD
NOV77a, CG59630-01 Protein Sequence	MEPQPGGARSCRRGAPGGACELGPAAEAAPMSLAIHSTTGTTRYDLAVPPDETVEGLRK RLSQRLLKVPKERLALLHKDTRLSSGKLQEFVGDGSKLTLVPTVEAGLMSQASRPEQS VMQALESLTETQPPAAPGPGRAGGGGFRKYRFLFKRPWHRQGPSPERGGERRPQVSD FLSGRSPLTLALRVGDHMMFVQLQLAAQHAPLQHRHVLAIAAAGDPSIASPV SPCRPVSSAARVPPVPTSPSPASPSPIAGSFRSHAASSTCPEQMDCSPTASSASPG ASTTSTPGASPAPRSRKPGAVIESFVNHPGVFSGTFSGLHPNCQDSSGRPRRDIGT ILQILNDLLSATRHYQGMPPSLAQLRCHAQCSPASPAPDLAPRTTSCCKLTAAPSASL LQGQSQIRMCKPPGDRLRQENRATRCRVERLQLLLQKRLRRKARRDARGPYHWSPS RKAGRSDDSSSGGGSPSEASGLGLDFEDSVWKPEVNPDIKSEFVVA		

Further analysis of the NOV77a protein yielded the following properties shown in Table 77B.

Table 77B. Protein Sequence Properties NOV77a	
PSort analysis:	0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1526 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV77a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 77C.

Table 77E. Domain Analysis of NOV77a			
Pfam Domain	NOV77a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	31..99	19/79 (24%) 46/79 (58%)	0.00033
PI3_PI4_kinase: domain 1 of 1	411..427	7/18 (39%) 14/18 (78%)	1.5

Example 78.

The NOV78 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 78A.

Table 78A. NOV78 Sequence Analysis			
	SEQ ID NO: 221	1034 bp	
NOV78a, CG59561-01 DNA Sequence	CCACCGCCACAGCTGCCAGCATGTCTGGCCAGACATCAAGACGCCGACCGCCATCCA GATCTGCCGGATTATGCGGGACGCTAATGTGGCCCGCAATGTCTACGGCGGGACCATC CTGAAGATGATCAAAGAGGCGGGCGCCATCATCAGCACCCGGCATTGCAATCCGCAGAG ACGGGGATCGCTGTGTGGCCGCTCTGGCTCGGGTCGAGTGCACCCACTTCTGTGGCC CATGTGCATCGGTGAGGTGGCCACGTCAGCGCGGAGATCACCTACACCTCCAAGCAC TCTGTGGAGGTGCAGGTCAACATGATGTCCGAAAACATCCTCACAGGTGCCAAAAAGC TGACCAATAAGGCCACCCTCTGGTATGCGCCCTGTGCTGACGAACGTGGACAAGGT CCTCGAAGAGCCTCCTGTTGTGTATTTCGGCAGGAGCAGGAGGAGGAGGGGCCAGAAG CGGTACAAAACCCAGAAGCTGGAGCGCATGGAGACCAACTGGAGGAACGGGGACATCG TCCAGCCAGTCTCTCAACCCAGAGCCGAACACTGTGCTACGCTACAGCCAGTCCAGCTTGAT CCACTGGTGGGGCCTTCAGACTGTACCCTGCACAGCTTCGTGCATGAAGGGGTGACC ATGAAGGTCATGGACGAGGTGCGCGGGATCTTGGCTGCACGCCACTGCAAGACCAACC TCGTACAGCCTCCATGGAGGCCATTAATTTTGACAACAAGATCAGAAAAGGCTGCAT CAAGACCATCTCCGGACGCATGACCTTCACGAGCAATAAGTCCGTAGAGATCGAGGTG TTGGTGGATGCCGACTGTGTTGTGGACAGCTCTCAGAAGCGCTACAGGGCCGCCAGTG TCTTACCTATGTGTGCTGAGCCAGGAAGGCAGGTGCGTGCCCATGCCCCAGCTCGT GCCGGAGACCCAGGACGAGAAGGGCTTTGAGGCCCTGGCTCGGTGGCTACGCCCTATAA TCCCAGCACTTTAGGATGCTGAGGCAGGCGGATCACTTGACGTGAGGA		
	ORF Start: ATG at 21	ORF Stop: TAA at 984	
	SEQ ID NO: 222	321 aa	MW at 35738.7kD
NOV78a, CG59561-01 Protein Sequence	MSGPDIKTPTAIQICRIMRDANVARNVYGGTILKMIKEAGAIISTRHCNPQNGDRCA ALARVECTHFLWPMCI GEVAHVSAEITYTSKHSVEVQVNMSENILTGAKKLTKATL WYAPLSLTNVQKLEPPVVYFRQEQQEKGKRYKTQKLERMETNWRNGDIVQPVLPNP EPNTVSYSSQLIHLVGPSDCTLHSPVHEGVTMVKVMEVAGILAAHCKTNLVTASME AINFDNKIRKGCIKTISGRMTFTSNKSVEIEVLVDADCVVDSSQKRYRAASVFTYVSL SQEGRSLPMPQLVPETQDEKGFPAWLGGSR		

- 5 Further analysis of the NOV78a protein yielded the following properties shown in Table 78B.

Table 78D. Public BLASTP Results for NOV78a				
Protein Accession Number	Protein/Organism/Length	NOV78a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O00154	Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase) (BACH) - Homo sapiens (Human), 338 aa.	1..310 1..313	274/313 (87%) 293/313 (93%)	e-154
Q91V12	ACYL-COA HYDROLASE (HYPOTHETICAL 37.6 KDA PROTEIN) - Mus musculus (Mouse), 338 aa.	1..310 1..313	265/313 (84%) 287/313 (91%)	e-150
Q64559	Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase) (BACH) (ACT) (LACH1) (ACH1) - Rattus norvegicus (Rat), 338 aa.	1..310 1..313	263/313 (84%) 286/313 (91%)	e-149
JC5416	palmitoyl-CoA hydrolase (EC 3.1.2.2), hepatic - rat, 343 aa.	12..310 17..318	251/302 (83%) 276/302 (91%)	e-142
Q9Y541	DJ202O8.3.1 (HBACH (BRAIN ACYL-COA HYDROLASE (ACYL COENZYME A THIOESTER HYDROLASE, EC 3.1.2.2)) (ISOFORM 1)) - Homo sapiens (Human), 237 aa (fragment).	1..202 33..236	181/204 (88%) 190/204 (92%)	e-100

PFam analysis predicts that the NOV78a protein contains the domains shown in the Table 78E.

Table 78E. Domain Analysis of NOV78a			
Pfam Domain	NOV78a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Acyl-CoA_hydro: domain 1 of 1	165..305	46/147 (31%) 131/147 (89%)	1.1e-47

Example 79.

The NOV79 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 79A.

Table 79A. NOV79 Sequence Analysis

	SEQ ID NO: 223	4203 bp
NOV79a, CG59452-01 DNA Sequence	<p> AATGTGATGGGATCACTAGCATGTCTGCGGAGAGCGGCCCTGGGACGAGATTGAGAAA TCTGCCAGTAATGGGGGATGGACTAGAAACTTCCCAAATGTCTACAACACAGGCCCCAG GCCAACCCAGCCAGCCAAACGACGACGACCAACCCCGCCCGCCAGAGACCTCCA ACCTTAACAAGCCCAAGAGGACAGCAACCAACTGCAATACCTGCTCAGAGTGGTGTCT CAAGACACTATGGAAACACCAAGTTTGCATGGCCTTTCCAGCAGCCTGTGGATGCCGTC AAGCTGAACCTCCCTGATTACTATAAGATCATTAACCGCTATGGATATGGGAACAA TAAAGAAGCGCTTGGAAAACAACTATTACTGGAATGCTCAGGAATGTATCCAGGACTT CAACACTATGTTTACAAATTGTTACATCTACAACAAGCCTGGAGATGACATAGTCTTA ATGGCAGAAGCTCTGGAAAAGCTCTTCTTGCAAAAATAAATGAGCTACCCACAGAAG AAACCGAGATCATGATAGTCCAGGCAAAAGGAAGAGGACGTGGGAGGAAAGAAACAGG TACAGCAAAACCTGGCGTTTCCACGGTACCAACACAACTCAAGCATCGACTCCTCCG CAGACCCAGACCCCTCAGCCGAATCCTCCTCTGTGCAGGCCAGCCCTACCCCTTCC CTGCCGTACCCCGGACCTCATCGTCCAGACCCCTGTCTATGACAGTGGTGCTCCCA GCCACTGCAGACGCCCCCGCAGTGGCCCCCAGCCACACCCCGCCAGCGCTCCAGCT CCCCAGCCGTAAGAGCCACCCACCATCATCGCGGCCACCCACAGCCTGTGAAGA CAAAGAAGGGAGTGAAGAGGAAAGCAGACACCCACCCACCCACCATGACCCCAT TCACGAGCCACCTCGTGGCCCCGAGGCCAAGACCAACCAAGAGTGGCCAGCGCGG GAGAGCAGCCGCTGTGAAACCTCCAAAGAAGGACGTGCCGACTCTCAGCAGCACC CAGCACCAGAGAAGAGCAGCAAGGTCTCGGAGCAGCTCAAGTGTGCAGCGGCATCTCT CAAGGAGATGTTTGCCAAGAAGCAGCGCCCTACGCTGGCCCTTCTACAAGCCTGTG GACGTGGAGGCACTGGGCCTACACGACTACTGTGACATCATCAAGCACCCTATGGACA TGAGCACAATCAAGTCTAACTGGAGGCCGTGAGTACCGTGATGCTCAGGAGTTTGG TGCTGACGTCCGATTGATGTTCTCAACTGCTATAAGTACAACCCCTCCTGACCATGAG GTGGTGGCCATGGCCCAAGCTCCAGGATGTGTGGAATGGCCTTTGCCAAGATGC CGGACGAGCCTGAGGAGCCAGTGGTGGCCGTGTCTCCCGGCAGTGGCCCTCCAC CAAGGTTGTGGCCCGCCCTCATCCAGCGACAGCAGCAGCATAGTCTCTCGGACATG GACAGTTCGACTGATGACTCTGAGGAGGAGCGAGCCAGCGGTGGCTGAGTTCAGG AGCAGCTCAAAGCCGTGCACGAGCAGCTTGCAGCCCTCTCTCAGCCCCAGAGAACAA ACCAAAGAAAAGGAGAAAGACAAGAAGGAAAAGAAAAGAAAAGCAAAAGCACAAGG GAGGAAGTGAAGAGAATAAAAAAGCAAAGCCAAGGAACCTCTCTAAAAAGACGA AGAAAAATAATAGCAGCAACAGCAATGTGAGCAAGAAGGAGCCAGCGCCCATGAAGAG CAAGCCCCCTCCACAGTATGAGTCCGAGGAAGAGGACAAGTGCAGCGCTATGCTCTAT GAGGAGAAGCGGAGCTCAGCTTGGACATCAACAGCTCCCGGCGAGAAGCTGGGGC GCGTGGTGACATCATCCAGTCAAGGAGCCCTCCCTGAAGAATTCCAACCCGACGA GATTGAATCGACTTTGAGACCCCTGAAGCCGTCCACACTGCGTGAGCTGAGCGCTAT GTCACCTCCTGTTTGGGAAGAAAAGGAAACCTCAAGCTGAGAAAGTTGATGTGATTG CCGGCTCCTCAAGATGAAGGGCTTCTCGTCTCAGAGTCCGAGAGCTCCAGTGAGTC CAGCTCCTGTACAGCGAAGACTCCGAAACAGAGATGGCTCCGAAGTCAAAAAGAAAG GGGCAACCCGGGAGGGAGCAGAAGCAGCACCATCATCACCACATCAGCAGATGCAGC AGGCCCCGGCTCTGTGCCCCAGCAGCCGCCCCCGCCTCCCCAGCAGCCCCACCGCC TCCACCTCCGAGCAGCAACAGCAGCCGCCACCCCGCCTCCACAGCAGCCCCACCGC CAGCAGGAGCCCGCGATGAAGTCTCGCCCCACCTTCTATTGCCACCCAGGTGC CCGTCTGGAGCCCCAGCTCCAGGACGCTTCTTGACCCCATCGGCCACTTCAACCA GCCCATCTGCACCTGCGCAGCCTGAGCTGCCCCCTCACTCGCCGCTGAG CACAGCACTCCACCCATCTCAACAGCAGCAGTGGTCTCTCTCCAGCTTTGCACA ACGCACTACCCAGCAGCCATCACGGCCAGCAACCGAGCCGCTGCCCTGCCCTCCCA GCCCGCCGCCCCCAGCCGTGTCAACAGCCTTGACCAACACCTGCTCCCAAG CCCCCATGGCCCAACCCCCCAAGTGTCTGCTGGAGGATGAAGAGCCACTGCCCCAC CCCTCACTCCATGCAGATGCAGCTGTACCTGCAGCAGTGCAGAAGGTGCAGCCCC TACGCCGCTACTCCCTTCCGTGAAGGTGAGTCCAGCCCCACCCCTGCTGCCGCC CCACCCACCCCTCTGTGCAGCAGCAGTGCAGCAGCAGCCGCCACCCACCCACAC CCAGCCCCAGCCTCCACCCAGCAGCAGCATCAGCCCCCTCCACGGCCCGTGCATT GCAGCCCATGCAGTTTTCACCCACATCCAACAGCCCCCGCCACCCAGGGCCAGCAG CCCCCATCCGCCCCAGGCCAGCAGCCACCCCGCCGAGCCTGCCAAGCCTCAGC AAGTCATCCAGCACCACATTACCCCGGCACCAAGTCCGAGCCCTACTCAACCGG TCACCTCCGGAAGCCCCCTCCCGCTTATGATACATTCCCCCAGATGTACAGTTT CAGAGCCTGACCCACAGTCTCCACCCAGCAAAACGTCCAGCCTAAGAAACAGGTAA CTGGCAGGGCTGGGCCAAGTCTGTGGGCCAGGGCCGGGGTGCCTGCCACCTCACC GGCCGCTGTGCTGTGCCATCCAGGAGCTGCGTGTCTGCTCGCTCGTGGCCAGC CCCCCTCGTGGTGGTGAAGGAGGAGAAGATCCACTCACCATCATCCGAGCAGCCCT TCAGCCCCCTGCTGCGGCCGAGCCCCCAAGCAGCCGAGAGCATCAAGGCCCGCT TTATGTTCCAGGGCCGAAATGAAGCCTGTGGATGTGCGGAGGCCCTGTGATCGGCC CCAGAGCAGAACGCACCGCCACAGGGGCCCTGACAAGGACAAACAGAAACAGGAGC CGAAGACTCCAGTTGGCCCAAAAAGGACCTGAAATCAAGAACATGGGCTCCTGGGC CAGCTAGTGCAAGCATCCGACCAACCCCTCCTCCACAGCAAGTCAAGCAGCAGC AGCTTCGAGCAGTTCCGCCGCGCCGCTCGGGAGAAAGAGGAGCGTGAGAAGGCCCTGA AGGCTCAGGCCGAGCAGCTGAGAAGGAGAAGGAGCGCTGCGGAGGAGCGCATGAG GAGCCGAGAGGACAGGATGCGCTGGAGCAGGCCCGCGGGCCATGAGGAGGACGCT CGGCGCCAGGAGCAGCAGCAGCAGCAGCGCCAGGAGCAACAGCAGCAGCAGCAACAGC AAGCAGTGCCTGGTGGTGGCCGCCACCCCAAGGCCCAGAGCTCCAGGCCCATGTC CATGCTGGACAGCAGAGGGAGTTGGCCCGGAAGCGGAGCAGGAGCAAGACGCGCG GAAGCCATGGCAGCTACCATTTGACATGAATTTCCAGAGTGATCTATTGTCAATATTG AAGAAAATCTTTCTGAGCGCACCTAG </p>	

	ORF Start: ATG at 21	ORF Stop: TGA at 4191	
	SEQ ID NO: 224	1390 aa	MW at 154728.4kD
NOV79a, CG59452-01 Protein Sequence	MSAESGPGTRLRLNLPVMDGLETSQMSTTQAQAQPQANAASTNPPPPETSNNPKPKR QTNQLQYLLRVVLKTLWKHQFAWPFQPPVDAVKLNLPDYKIIKTPMDMGTIKKRLN NYYWNAQECIQDFNTMTNCYIYNKPGDDIVLMAEALFKLFLQKINELPTEETIMIV QAKGRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPPPVQATPHPPPAVTPDL IVQTPVMTVVPQPLQTPPPVPPQPPPPAPAPQPVQSHPIIAATPQPVKTKKGVKR KADTTTPTTIDPIHEPPSLPPEPKTTKLQRRRESSRPVKPKKDVDPDQQHPAPEKSS KVSEQLKCCSGILKEMFAKHAAYAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSK LEAREYRDAQEPGADVRLMFSNCKYNPPDHEVAMARKLDVFEMRFAKMPDEPEEP VVAVSSPAVPPPTKVVAAPSSSDSSSDSSSDSSSDSDSDSDSEEERAQRLAEQLKAVH EQLAALSQPPQNKPKKKEKDKKEKKKEKHKKKEVEENKSKAKEPPPKTKKNNSSN SNVSKKEPAPMKSKPPPTYESEEEDKCKPMSYEEKRQLSLDINKLPGEKLG RVVHI IQ SREPSLKNNSNPDEIEIDFETLKPSTLRELERYVTSLCKRRKPKQAEKVDVIAGSSKMK GFSSESSESSESSESSESSESESEMAPSKKKKGHPGREQKQHSHHHHHQMQQAPAPVP QQPPPPPPQPP PGSVFDPIGHFTQPIHLHPQPELPPHLPQPEHSTPPHILNQHAVVSPPALHNLPPQP SRPSNRAAALPKPARPPAVSPALQTPLLPQPPMAQPPQVLLDEEPPAPPLTSMQM QLYLQQLQKVQPTPLLPVSKVQSQPPPPPLPPPPHPSVQQQLQQPPPPPPPPPPPPPP QQHQPPPPRPVHLQPMQFSTHIQQPPPPQGGQPPHPPPPQPPPPQPAKPPQVVIQHSH SPRHHKSDPYSTGHLREAPSPLMIHSPQMSQFQSLTHQSPPPQNVQPKKQVTGRAGPS PVGGGRGCLPTSPAAPVPVPSQELRAASVVQPQLVVKKEKIHSPIIRSEFPSPSLRP EPPKHPESIKAPVYVPGPEMKPVDVGRPVIRPPEQNAPPPGAPDKDKQKQEPKTPVAP KKDLKIKNMGSWASLVQKHPTTSSSTAKSSSDSFEQFRRAAREKEEREKALKQAQAEHA EKEKERLRQERMRSREDEDALEQARRAHEEARRRQEQQQQQRQEQQQQQQQQAAAVAA AATPQAQSSQPQSMLDQRELARKREQERRRREMAAATIDMNFQSDLLSIFEENLF		

Further analysis of the NOV79a protein yielded the following properties shown in Table 79B.

Table 79B. Protein Sequence Properties NOV79a	
PSort analysis:	0.9800 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV79a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 79C.

Table 79C. Geneseq Results for NOV79a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV79a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAV57898	Human transmembrane protein HTMPN-22 - Homo sapiens, 688 aa. [WO9961471-A2, 02-DEC- 1999]	1..667 1..667	667/667 (100%) 667/667 (100%)	0.0

AAY07027	Breast cancer associated antigen precursor sequence - Homo sapiens, 754 aa. [WO9904265-A2, 28-JAN-1999]	44..724 13..708	407/732 (55%) 487/732 (65%)	0.0
AAY07114	WO9904265 Seq ID No: 685 - Homo sapiens, 947 aa. [WO9904265-A2, 28-JAN-1999]	35..738 4..686	357/761 (46%) 444/761 (57%)	e-170
AAW81168	Transcriptional regulatory factor RING3 - Homo sapiens, 947 aa. [WO9848015-A1, 29-OCT-1998]	35..738 4..686	357/761 (46%) 444/761 (57%)	e-170
AAU16206	Human novel secreted protein, Seq ID 1159 - Homo sapiens, 235 aa. [WO200155322-A2, 02-AUG-2001]	51..255 1..203	118/206 (57%) 137/206 (66%)	2e-59

In a BLAST search of public sequence databases, the NOV79a protein was found to have homology to the proteins shown in the BLASTP data in Table 79D.

Table 79D. Public BLASTP Results for NOV79a				
Protein Accession Number	Protein/Organism/Length	NOV79a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O60885	Bromodomain-containing protein 4 (HUNK1 protein) - Homo sapiens (Human), 1362 aa.	1..1390 1..1362	1357/1391 (97%) 1360/1391 (97%)	0.0
Q9ESU6	CELL PROLIFERATION RELATED PROTEIN CAP - Mus musculus (Mouse), 1400 aa.	1..1390 1..1400	1318/1400 (94%) 1338/1400 (95%)	0.0
AAL67833	BROMODOMAIN-CONTAINING PROTEIN BRD4 LONG VARIANT - Mus musculus (Mouse), 1400 aa.	1..1390 1..1400	1318/1400 (94%) 1338/1400 (95%)	0.0
O60433	R31546_1 - Homo sapiens (Human), 731 aa (fragment).	1..719 12..730	719/719 (100%) 719/719 (100%)	0.0
AAL67834	BROMODOMAIN-CONTAINING PROTEIN BRD4 SHORT VARIANT - Mus musculus (Mouse), 723 aa.	1..719 1..720	694/720 (96%) 700/720 (96%)	0.0

PFam analysis predicts that the NOV79a protein contains the domains shown in the

Table 79E. Domain Analysis of NOV79a

Pfam Domain	NOV79a Match Region	Identities/ Similarities for the Matched Region	Expect Value
bromodomain: domain 1 of 2	63..152	42/92 (46%) 82/92 (89%)	8.6e-45
bromodomain: domain 2 of 2	356..445	40/92 (43%) 81/92 (88%)	3e-40

Example 80.

The NOV80 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 80A.

Table 80A. NOV80 Sequence Analysis

	SEQ ID NO: 225	1776 bp
NOV80a, CG59572-01 DNA Sequence	TGGTTCGTTTATTCCTGGGGTTGTCATATCATGGCTTATAATGACACAGACAGAAACC AGACTGAGAAGCTCCTAAAAAGAGTACGAGAACTGGAGCAAGAGGTGCAAGACTTAA AAAGGAACAGGCCAAAAATAAGGAGGACTCAAACATTAGAGAAAATTCAGCAGGAGCT GGAAAACTAAGCGTGCTTTGATTTAGTGCTCATGGCCGAAGACACGTAGCCCTAA GAATAGCCTATATGGGCTGGGGATACCAGGGCTTTGCTAGTCAGGAAAAACAAATAA TACCATTGAAGAGAACTGTTGAAGCTCTAACCAAGACTCGACTAGTAGAAAGCAGA CAGACATCCAACATATCACCGATGTGGGAGAACAGATAAAGGAGTTAGTGCTTTGGAC AGGTGATCTCACTTGACCTTCGCTCTCAGTTCCAAGGGGCAGGGATTCCGAGGACTT TAATGTAAAGAGGAGGCTAATGCTGCTGCTGAAGAGATCCGTTATACCCACATTCTC AATCGGGTACTCCCTCCAGACATCCGTATATTGGCCTGGGCCCTGTAGAACCAGCT TCAGTGCTAGGTTGAGCTGCTTACCGGACTTACCGCTATTTTTCCCTCGTGCTGA TTTAGATATTGTAACCATGGATTATGCAGCTCAGAAGTATGTTGGCACCATGATTTT AGGAACCTGTGTAAGATGTAGCCAAACGGTGTGATTAAATTTTCAGAGGACTATTC TATCTGCTCAAGTACAGCTAGTGGGCCAGAGCCCAGGTGAGGGGAGATGGCAAGAAC TTTCAGTTATGTCAAGTGAAGTGAAGTGGCCAGGCATTCTTTATCATCAAGTCCGA TGTATGATGGCTATCCTCTTTCTGATTGGCCAAAGGAATGGAGAAGCCAGAGATTATG ATGAGCTGCTGAATATAGAGAAAAATCCCCAAAGCCTCAATATAGTATGGCTGAGA ATTTCTCTAGTCTTATATGACTGTAAGTTTGAAGATGTCAAGTGGATCTATGACCAG GAGGCTCAGGAGTTCAATATTACCCACCTACAACACTGTGGGCTTAATCATGCTGTCA AAATCACATGTTGTATAGTATGCTACAAGGACTGGACACTGTTCCAGTACCCGTGTGG AATAGGACCAAGATGGATGGAATGACAGAATGGGGAATGTTAAGCCCTCTGTGATA AAGCAGACAGTGCCTTTGTAGAAGGAGTGAAGATGCGCACATATAAGCCCTCATGG ACCGTCTAAATGCCAAGGACTGGAATCCCGGATCCAGCATTTTGTACGTAGGGGACG AATTGAGCACCCACATTTATCCATGAGGAAGAAACAAAAGCCAAAAGGACTGTAAT GACACACTAGAGGAAGAGAACTAATTTGGAGACACCAACGAAGAGGGTCTGTGTTG ACACAGAAATTAAGCATCATTTAAACATAGACAATTTGCCAGGATCTAGGAACCAC CTAATGGTAGGTGGACAGAAAAGGAAAAAAAAAAAAATTTACTTGAAGTACTAGGAA TTCAGATGATCAGCTCTTAAAAAAAAAAAAAAAAAGCAAAAGACTAAAGCCCTATTAA GAAGTTATTGCTTTAATAAGAAATTTCAAATATTCTCTATCCCGGTCCAAAAGGATT AAGCGATTAAAGAACGTAAAAATGGAGATGTATTTACATACACCTGGAACCTGTGCCT TGTATTCAAATTCATTAAGCCTAATCCTGCAAGAA	
	ORF Start: ATG at 31	ORF Stop: TAA at 1474
	SEQ ID NO: 226	481 aa MW at 55646.8kD
NOV80a, CG59572-01 Protein Sequence	MAYNDTRNQTEKLLKRVRELEQEVORLKKKEQAKNKEDSNIRENSAGAGKTKRAFDFS AHGRRHVLRVIAIYMGWYQGFASQENTNNTIEEKLFEALTKRLVSRQTSNYHRCGR TDKGVSAPFGQVLSLDLRSQFPRGRDSEDFNVKEEANAEEIIRYTHILNRVLPDIRI LAWAPVEPSFSARFSLERTYRYFFPRADLDIVTMDYAAQKYVGTDFRNLKMDVAN GVINFQRTILSAQVQLVGQSPGEGRWQEPFQLCQFEVTTGAFLYHQVRCMMAILFLIG QGMEKPEIIDEELNIEKNPQKPQYSMAVEFPLVLYDCKFENVKWIYDQEAQEFNITHL QQLWANHAVKTHMLYSMLQGLDTPVPCGIGPKMDGMTWGNVPSVVKQTSFAVEGV KMRITYKPLMDRPKCQGLSRIQHFVRRRIEHPHLFHEEETKAKRDCNDTLEENTNL EPTKRVCDTEIKSI	
	SEQ ID NO: 227	1508 bp

NOV80b, CG59572-02 DNA Sequence	CATGGCTTATAATGACACAGACAGAAACCAGACTGAGAAGCTCCTAAAAAGAGTACGA GAACTGGAGCAAGAGGTGCAAGACTTAAAAAGGAACAGGCCAAAAATAAGGAGGACT CAAACATTAGAGAAAATTCAGCAGGAGCTGGAAAACTAAGCGTGCATTGTATTTCAG TGCTCATGGCCGAAGACAGTAGCCCTAAGAAATAGCCTATATGGGCTGGGGATACCAG GGCTTTGCTAGTCAGGAAAAACAAATAATACCATTGAAGAGAACTGTTTGAAGCTC TAACCAAGACTCGACTAGTAGAAAGCAGACAGACATCCAATATCACCGATGTGGGAG AACAGATAAAGGAGTTAGTGCCTTTGGACAGGTGATCTCACTTGACCTTCGCTCTCAG TTTCCAAGGGGCAGGGATTCCGAGGACTTTAATGTAAAAGAGGAGGCTAATGCTGCTG CTGAAGAGATCCGTTATACCCACATTCTCAATCGGGTACTCCCTCCAGACATCCGTAT ATTGGCTGGGCCCTGTAGAACCAAGCTTCAGTGCTAGGTTCACTGTCCTTGAGCGG ACTTACCGCTATTTTTCCCTCGTGCTGATTAGATATTGTAACCATGGATTATGCAG CTGAGAAGTATGTTGGCACCCATGATTTCAGGAACCTGTGTAAAATGGATGAGCCAA CGGTGTGATTAATTTTCAGAGGACTATCTATCTGCTCAAGTACAGCTAGTGGGCCAG AGCCAGGTGAGGGGAGATGGCAAGAACCTTCCAGTTATGTCAGTTTGAAGTGACTG GCCAGGCATTCCCTTATCATCAAGTCCGATGTATGATGGCTATCCCTCTTCTGATTGG CCAAGGAATGGAGAAGCCAGAGATTATGATGAGCTGCTGAATATAGAGAAAAATCCC CAAAAGCCTCAATATAGTATGGCTGTAGAATTTCTCTAGTCTTATATGACTGTAAGT TTGAAAATGTCAAGTGGATCTATGACCAGGAGGCTCAGGAGTTCAATATTACCACCT ACAACAACGTGGGCTAATCATGCTGTCAAACTCACATGTTGTATAGTATGCTACAA GGACTGGACACTGTTCCAGTACCCTGTGGAATAGGACCAAGATGGATGGAATGACAG AATGGGGAAATGTTAAGCCCTCTGTCATAAAGCAGACCAAGTGCCTTTGTAGAAGGAGT GAAGATGCGCACATATAAGCCCTCATGGACCGTCTAAATGCCAAGGACTGGAATCC CGGATCCAGCATTGTGACGTAGGGGACGAATTGAGCACCACATTTATTCCATGAGG AAGAACAAAAGCCAAAAGGAGCTGTAATGACACACTAGAGGAAGAGAACTAATAATTT GGAGACACCAACGAAGAGGGTCTGTGTTGACACAGAAATAAAAGTATCATTTAAACA TAGACAATTTGCCAGGATCTAGGAACCACCTAATGGTAGGTGGACAGAAAAGGAAAAA		
	ORF Start: ATG at 2	ORF Stop: TAA at 1445	
	SEQ ID NO: 228	481 aa	MW at 55646.8kD
NOV80b, CG59572-02 Protein Sequence	MAYNDTRNQTEKLLKRVRELEQEVQRLKKEQAKNKEDSNIRENSAGAGTKRAFDFS AHGRRHVALRIAYMGWGYQGFASQENTNNTIEEKLFEALT KRLVESRQTSNYHRCGR TDKGVSAGQVILDLRSQFPRGRDSEDFNVKEEANAABEEIRYTHILNRVLPPIRI LAWAPVEPSFSARFSCLERTYRYFFPRADLDIVTMDYAAQKYVGTHTDFRNLCKMDVAN GVINFQRTILSAQVLVGQSPGEGRWQEPFQLCQFEVTFQAFLYHQVRCMMAILFLIG QGMEKPEIIDELLNIEKNPQKPYSMAVEFPLVLYDCKFENVKWIYDQEAQEFNITHL QQLWANHAVKTHMLYSMLQGLDTPVPVPCGIGPKMDGMTWGNVKPSVIEQTSAPVEGV KMRTYKPLMDRPKCQGLSRIQHFRRGRIEHPHLFHEETKAKRDCNDTLEBENTNL ETPTRKVCVDTEIKSII		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 80B.

Table 80B. Comparison of NOV80a against NOV80b.		
Protein Sequence	NOV80a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV80b	1..481 1..481	459/481 (95%) 459/481 (95%)

Further analysis of the NOV80a protein yielded the following properties shown in Table 80C.

Table 80C. Protein Sequence Properties NOV80a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0142 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV80a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 80D.

Table 80D. Geneseq Results for NOV80a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV80a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79457	Human protein SEQ ID NO 3103 - Homo sapiens, 490 aa. [WO200157190-A2, 09-AUG- 2001]	1..481 10..490	478/481 (99%) 480/481 (99%)	0.0
AAM78473	Human protein SEQ ID NO 1135 - Homo sapiens, 481 aa. [WO200157190-A2, 09-AUG- 2001]	1..481 1..481	478/481 (99%) 480/481 (99%)	0.0
AAG64907	Human depressed growth rate protein DEG1 - Homo sapiens, 248 aa. [CN1296014-A, 23-MAY- 2001]	209..431 1..223	223/223 (100%) 223/223 (100%)	e-132
AAG02637	Human secreted protein, SEQ ID NO: 6718 - Homo sapiens, 96 aa. [EP1033401-A2, 06-SEP-2000]	361..456 1..96	96/96 (100%) 96/96 (100%)	5e-53
AAB96592	Putative P. abyssi pseudouridilate synthase I - Pyrococcus abyssi, 263 aa. [FR2792651-A1, 27-OCT- 2000]	65..367 3..261	79/305 (25%) 140/305 (45%)	4e-16

- 5 In a BLAST search of public sequence databases, the NOV80a protein was found to have homology to the proteins shown in the BLASTP data in Table 80E.

Table 80E. Public BLASTP Results for NOV80a				
Protein Accession Number	Protein/Organism/Length	NOV80a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BZE2	FKSG32 - Homo sapiens (Human), 481 aa.	1..481 1..481	481/481 (100%) 481/481 (100%)	0.0
Q96J23	HYPOTHETICAL 55.6 KDA PROTEIN - Homo sapiens (Human), 481 aa.	1..481 1..481	478/481 (99%) 480/481 (99%)	0.0
Q96NB4	CDNA FLJ31140 FIS, CLONE IMR322001218, HIGHLY SIMILAR TO MUS MUSCULUS PSEUDOURIDINE SYNTHASE 3 (PUS3) MRNA - Homo sapiens (Human), 481 aa.	1..481 1..481	478/481 (99%) 479/481 (99%)	0.0
Q9JI38	PSEUDOURIDINE SYNTHASE 3 - Mus musculus (Mouse), 481 aa.	5..480 4..480	407/479 (84%) 434/479 (89%)	0.0
Q9D0F7	2610020J05RIK PROTEIN - Mus musculus (Mouse), 316 aa.	5..314 4..315	276/312 (88%) 291/312 (92%)	e-158

PFam analysis predicts that the NOV80a protein contains the domains shown in the Table 80F.

Table 80F. Domain Analysis of NOV80a			
Pfam Domain	NOV80a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PseudoU_synth_1: domain 1 of 1	88..307	70/249 (28%) 176/249 (71%)	4.7e-57

Example 81.

- 5 The NOV81 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 81A.

Table 81A. NOV81 Sequence Analysis		
	SEQ ID NO: 229	3080 bp
NOV81a, CG59522-01 DNA Sequence	TTCCAGCCGGCAGGATGGAGGACGAGGAAGGCCCTGAGTATGGCAAACCTGACTTTGT GCTTTTGGACCAAGTGACCATGGAGGACTTCATGAGGAACCTGCAGCTCAGGTTTCGAG AAGGGCCGCATCTACACCTACATCGGTGAGGTGCTGGTGTCCGTGAACCCCTACCAGG AGCTGCCCTGTATGGGCTGAGGCCATCGCCAGGTACCAGGGCCGTGAGCTCTATGA GCGGCCACCCATCTCTATGCTGTGGCCAACGCCGCTACAAGGCAATGAAGCACCGG	

	<p>TCCAGGGACACCTGCATCGTCATCTCAGGGGAGAGTGGGGCAGGGAAGACAGAAGCCA GTAAGCACATCATGCAGTACATCGCTGCTGTCACCAATCCAAGCCAGAGGGCTGAGGT GGAGAGGGTCAAGGACGTGCTGCTCAAGTCCACCTGTGTGCTGGAGGCCTTTGGCAAT GCCCCACCAACCGCAATCACAACCTCAGCCGCTTTGGCAAGTACATGGACATCAACT TTGACTTCAAGGGGGACCCGATCGGAGGACACATCCACAGCTACCTACTGGAGAAGTC TCGGGTCTCAAGCAGCACGTGGGTGAAAGAACTTCCACGCCTTCTACCAATTGCTG AGAGGCAGTGAGGACAAGCAGCTGCATGAACTGCACTTGGAGAGAAACCTGCTGTAT ACAATTTACACACCAGGGAGCAGGACTCAACATGACTGTGAGTGATGAGCAGAGCCA CCAGGCAGTGACCGAGGCCATGAGGGTTCATCGGCTTCAGTCTCGAAGAGGTGGAGTCT GTGCATCGCATCTGGCTGCCATATTGCACCTGGGAAACATCGAGTTTGTGGAGACGG AGGAGGGTGGGCTGCAGAAGGAGGGCCTGGCAGTGGCCGAGGAGGCACTGGTGGACCA TGTGGCTGAGCTGACGGCCACACCCGGGACCTCGTGCTCCGCTCCCTGCTGGCTCGC ACAGTTGCTCGGAGGCAGGGAACCTATAGAGAAGGGCCACACTGCAGCTGAGGCCA GCTATGCCCGGGATGCTGTGCCAAGGCAGTGTACCAGCGGCTGTTTGGTGGGTGGT GAACAGGATCAACAGTGTATGGAACCCCGGGGCGGGATCCTCGGCTGTAGTGGCAAG GACACAGTCATTGGCGTGTGGACATCTATGGCTTCGAGGTGTTTCCCGTCAACAGTT TCGAGCAGTTCTGCATCAACTACTGCAACGAGAAGCTGCAGCAGCTATTATCCAGCT CATCTGAAGCAGGAACAGGAAGAGTACGAGCGCGAGGGCATCACTGGCAGAGCGT GAGTATTTCAACAACGCCACCATTTGGATCTGGTGGAGCGGCCACCGTGGCATCC TGGCCGTGCTGGACGAGGCTGCAGCTCTGCTGGCACCATCACTGACCGAATCTTCCT GCAGACCTGGACATGCACACCGCCATCACCTACACTACACAGCCGCCAGCTCTGC CCACAGACAAGACCATGGAGTTTGGCCGAGACTTCCGGATCAAGCACTATGACGGGG ACGTACAGTACTCCGTGGAAGGCTTCATCGACAAGAACAGAGATTTCTCTTCCAGGA CTTCAAGCGTGGCTGTACAAACAGCACGGACCCCACTCTACGGCGTGGGCGCGGAC GGGCAGCAGGACATCACAGAGGTGACCAAGCGCCCTGACGGCTGGCACACTTTCA AGAACTCCATGTTGGCCCTGGTGGAGAACCTTGCCTCCAAGGAGCCCTTCTACGTCCG CTGCATCAAGCCCAATGAGGACAAGGTAGCTGGGAAGCTGGATGAGAACCACTGTCCG CACCAGTTCGCATACCTGGGCTGCTGGAGAATGTGAGGGTCCGAGGGCTGGCTTCG CTTCCCGCCAGCCCTACTCTCGATTCTGCTCAGGTACAAGATGACCTGTGAATACAC ATGGCCCAACCACTGCTGGGCTCCGACAAGGCAGCCGTGAGCGCTCTCTGGAGAGC CACGGGCTGCAGGGGACGTGGCCTTTGGCCACAGCAAGCTGTTTCATCCGCTACCCCC GGACACTGGTCACTGGAGCAGAGCCGAGCCGCTCATCCCCATATTGTGTGCT ATTGCAGAAGGATGGCGGGGCACCTTGGCGAGGTGGCGCTCGCGGAGGTGAGGGCT ATCTACACCATCATGCGCTGGTTCCGGAGACACAAGGTGCGGGCTCACCTGGCTGAGC TGCGAGCGGCGATTCCAGGCTGCAAGGCAGCCGCACTCTACGGGCGTGACCTGTGTG GCCGCTGCCCTCTGCTGCTGCAAGCCTTCCAGGACACCTGCCAGCACTGCTCTGC AGGTGGCGGGCCCGGAGCTGGTGAAGAATCCCCCTTCAGACATGCCCAGATCA AGGCCAAGGTGGCCGCCATGGGGGCCCTGCAAGGGCTTCGTGAGGATGGGGCTGCCG ACGGGCTGGGCGCGAGACTACCTGTCTGCACTGACAATCCACAGCATCAAGC CTGTTTGCTCAGCGACTAAAGACACTTCAGGACAAGATGGCTTCGGGGCTGTGCTCT TTTCAAGCCATGTCCGCAAGGTGAACCGCTTCCACAAGATCCGGAACCGGGCCCTCCT GCTCACAGCAGCACTCTACAAGCTGGACCCTGACCGGAGTACCGGGTGTGCGG GCCGTGCCCTTGAGGCGGTGACGGGGCTGAGCGTGACAGCGGAGGAGACAGCTGG TGGTGTGCACGCCCGCGGCCAGGACGACCTCGTGGTGTGCTGCACCGCTCCCGGCC GCCATTGGACAACCGCGGTGGGGAGCTGGTGGGCGTGCTGGCGCAGCACTGCCCGAG GAGGGCCGACCTGGAGGTTGCGCTCTCCGACTGCATCCACTAAGCCATCGCGGG TCCGGCGCTCATCTCGTGGAGCCAGGCGGAGCAGCCAGAGCCGATTTCGGCTG CGCTCGCGGCTCCTTCAACCTGCTCTGGCCAGCCGCTGAGCGCCCGCACCCGCGCA CCCCGA</p>		
	ORF Start: ATG at 15	ORF Stop: TGA at 3054	
	SEQ ID NO: 230	1013 aa	MW at 116044.5kD
NOV81a, CG59522-01 Protein Sequence	<p>MEDEEGPEYGPDPFVLLDQVTMEDFMRNLQLRFEKGRIYTYIGVELVSVNPNYQELPLY GPEAIARYQGRELYERPPHYAVANAAYKAMKHSRDTCIVISGESGAGKTEASKHIM QYIAAVTNPSQRAEVERVKDVLKSTCVLEAFGNARTNRNHNSSRFKGYMDINDFDKG DPIGGHIHSYLLEKSRVLKQHVGERNFHAFYQLLRGSEDKQLHELHLERNPAVYNFT QGAGLNMVTSDQSHQAVTEAMRVIGFSPPEEVSVHRIILAILHLGNIEFVTEEGGL QKEGLAVAEELVDHVAELTATPRDLVLRSLARTVASGGRELIEKGHTAAEASYARD ACAKAVYQRLFPEWVNINRINSVMEPRGRDPRRDGKDTVIGVLDIYGFVFPVNSFEQFC INYCNEKLQQLFIQLILKQEQEYEREGITWQSVYFNNATIVDLVERPHRGILAVLD EACSSAGTITDRIFLQTLDMHRRHLHYTSRQLCPTDKTMEFGRDRFRIKHYAGDVTYS VEGFIDKNRDLFQDFKRLLYNSTDPTLRAMWPDGQQDITEVTKRPLTAGTLFKNSMV ALVENLASKEPFYVRCIKPNEDKVGAKLDENHCRHQVAYLGLLENVRRRAGFASRQP YSRFLRLRYKMTCEYTPWNHLLGSDKAASVALLQHGLOGDVAFGHSLKFI RSPRTLVT LEQSRARLIP IIVLLQKAWRGTLARWRCRRRLRAIYTIMRWFRRHKVRHAELQRRF QAARQPPLYGRDLVWLPPLPAVLQPFQDTCHALFCRWRARQLVKNIPSPDMPQIKARVA AMGALQGLRQDWGCRRAWARDYLSSATDNPTASSLFAQLRLTKLDKDGFAVLFSHV RKVNRFHKIRNRALLTDQHLKLPDRQYRVMRAVPLEAVTGLSVTSGGDLVLVLA RGODDLVVCVLRSRPFLDNRVGLVGLAAHCRREGRTLVRVSDCIPLSHRGVRRRI SVEPRPEQPEPDFRCARGSFLLWPSR</p>		

Further analysis of the NOV81a protein yielded the following properties shown in Table 81B.

Table 81B. Protein Sequence Properties NOV81a	
PSort analysis:	0.8800 probability located in nucleus; 0.3902 probability located in microbody (peroxisome); 0.2210 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV81a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded 5 several homologous proteins shown in Table 81C.

Table 81C. Geneseq Results for NOV81a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV81a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU23125	Novel human enzyme polypeptide #211 - Homo sapiens, 1026 aa. [WO200155301-A2, 02-AUG-2001]	1..1013 9..1026	1009/1018 (99%) 1011/1018 (99%)	0.0
AAU23128	Novel human enzyme polypeptide #214 - Homo sapiens, 909 aa. [WO200155301-A2, 02-AUG-2001]	1..853 9..866	851/858 (99%) 851/858 (99%)	0.0
AAM80123	Human protein SEQ ID NO 3769 - Homo sapiens, 764 aa. [WO200157190-A2, 09-AUG-2001]	243..1011 1..762	438/769 (56%) 570/769 (73%)	0.0
AAM79139	Human protein SEQ ID NO 1801 - Homo sapiens, 753 aa. [WO200157190-A2, 09-AUG-2001]	254..1011 1..751	434/758 (57%) 564/758 (74%)	0.0
AAM39991	Human polypeptide SEQ ID NO 3136 - Homo sapiens, 1063 aa. [WO200153312-A1, 26-JUL-2001]	10..933 47..986	410/966 (42%) 556/966 (57%)	0.0

In a BLAST search of public sequence databases, the NOV81a protein was found to have homology to the proteins shown in the BLASTP data in Table 81D.

Table 81D. Public BLASTP Results for NOV81a				
Protein Accession Number	Protein/Organism/Length	NOV81a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q63357	MYOSIN I - Rattus norvegicus (Rat), 1006 aa.	1..1011 1..1004	606/1011 (59%) 780/1011 (76%)	0.0
A53933	myosin I myr 4 - rat, 1006 aa.	1..1011 1..1004	604/1011 (59%) 778/1011 (76%)	0.0
Q96R16	UNCONVENTIONAL MYOSIN 1G VALINE FORM - Homo sapiens (Human), 633 aa (fragment).	33..646 1..619	612/619 (98%) 612/619 (98%)	0.0
Q96R15	UNCONVENTIONAL MYOSIN 1G METHONINE FORM - Homo sapiens (Human), 633 aa (fragment).	33..646 1..619	611/619 (98%) 612/619 (98%)	0.0
Q23978	Myosin 1A (M1A) (Brush border myosin 1A) (BBM1A) - Drosophila melanogaster (Fruit fly), 1011 aa.	8..1012 6..1007	503/1017 (49%) 686/1017 (66%)	0.0

PFam analysis predicts that the NOV81a protein contains the domains shown in the Table 81E.

Table 81E. Domain Analysis of NOV81a			
Pfam Domain	NOV81a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PRK: domain 1 of 1	97..109	8/13 (62%) 10/13 (77%)	3.7
Vir_DNA_binding: domain 1 of 1	575..592	5/18 (28%) 14/18 (78%)	8.2
myosin_head: domain 1 of 1	11..689	305/747 (41%) 531/747 (71%)	8.1e-288

Example 82.

The NOV82 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 82A.

Table 82A. NOV82 Sequence Analysis			
	SEQ ID NO: 231		1066 bp
NOV82a, CG59520-01 DNA Sequence	GAACGAATGGGAAACAGAAATCAGATATTTATGCCCAAGCAAAGCAGGATTTCTGTT AGCACTACTCCCAGATCGTTAGGGTGCTGACTGAGGATGAGATGGGGCACCCAGAGAC AGGAGATGCTACTGCCCGGCTCAAGGAGGTCTGGAGTACAATGCCATTGGAGGCAAG TATCACCGAGGTTTGATGGTGCTAGTAGCGTTCCGGGAGCTGGTGGAGCCGAGGAAAC TGGATGCTGATAGTCTCCAGTGGGCACCGACTGTGGGCTGGTATGCGCAACTGCTGCA AGCTTTCTTCTGGTGGCAGATGACATTATGGATTATCCCTTACCTGCCAGGGACAG ATCTCCTGGTATCAGAAGCTGGGCATGGGTTTGGATGCCATCAATGATGCTATCCTTC TGAAGCATGTATCTACTGCTGCTGAAGCTGTATTGCCGGGAGCAGCCCTATTACCT GAACCTGATGGAGCTCTTCCAGCAGAATTCTTATCAGACTGAGATTGGGCAGACCCCT GACCTCATCACAAACCCAGGGCAATGTGGATCTTCGAGATGCACCGAAAAAGGC ACAAATCTGTTGTCAAGTACAAGACAGCTTTCTACTCCTTCTACCTTCTGTAGCTGC AGCCATGTACATGTCAAGAATGGATGACAAGAAGGAGCACACCAGTGCCAAGAAGATC CTGCTGGAGATTCAAGAGTTCTTTCAGATTTCAGGATGATTACCTTGACTTCTCTGGG ACCCAGTGTGACTGGCAGAGTTGGCAATGACTTCCAGGACAACAAATGCAGCTGGCT GGTGGTTTCAGTGTCTGTACAGGCCACTCCAGAACAGTACCAGATCCTGAAGGAAAAT TACAGGCAGAAGGAGGCCGAGAAGGTGGCCCGGGTGAAGGCACTATACGAGGAGCTGG ATCTGCCAGCCGTGTTCTTGCAAGTATGAGAAAGACAGTTACAGCCACGTTATGGGTCT CATCGAACAGTACGAGAGCCCTGCCCCAGCCATCTTTCTGGGGCTTGTGCACAA ATCTACAAGTGGAAAAAGTGAC		
	ORF Start: ATG at 7		ORF Stop: TGA at 1063
	SEQ ID NO: 232		352 aa MW at 40740.3kD
NOV82a, CG59520-01 Protein Sequence	MGNQKSDIYAQAKQDFVQHYSQIVRVLTEDEMGHPETGDATARLKEVLEYNAIGGKYH RGLMVLVAFRELVEPRKLDADSLQWAPTGVGWAQLLQAFLLVADDIMDSSLTCQGQIS WYQKLGMLDAINDAILLEACIYCLLKLYCREQPYLNLMEFLQNSYQTEIGQTLDEL ITTPQGNVDLRRCTEKRHSVVKYKTAFFSYFLPVAAAMYSRMDKKEHTSAKKILL EIQEFFQIQDDYLDLDFSGDPSVTGRVGNDFQDNKCSWLNVQCLLQATPEQYQILKENYR QKEAEKVARVKALYEELDLPVFLQYEKDSYSHVMGLIEQYAEPLPPAIFLGLVHKIY KWKK		

Further analysis of the NOV82a protein yielded the following properties shown in
 5 Table 82B.

Table 82B. Protein Sequence Properties NOV82a	
PSort analysis:	0.4066 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV82a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 82C.

Table 82C. Geneseq Results for NOV82a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV82a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG29733	Arabidopsis thaliana protein fragment SEQ ID NO: 35427 - Arabidopsis thaliana, 342 aa. [EP1033405-A2, 06-SEP-2000]	10..352 2..342	147/343 (42%) 219/343 (62%)	7e-75
AAG29732	Arabidopsis thaliana protein fragment SEQ ID NO: 35426 - Arabidopsis thaliana, 349 aa. [EP1033405-A2, 06-SEP-2000]	10..352 9..349	147/343 (42%) 219/343 (62%)	7e-75
AAG29734	Arabidopsis thaliana protein fragment SEQ ID NO: 35428 - Arabidopsis thaliana, 305 aa. [EP1033405-A2, 06-SEP-2000]	47..352 1..305	138/306 (45%) 204/306 (66%)	4e-73
AAY43635	Amino acid sequence of the farnesyl pyrophosphate synthase enzyme - Phaffia rhodozyma, 355 aa. [EP955363-A2, 10-NOV-1999]	12..352 11..355	145/346 (41%) 208/346 (59%)	4e-69
AAB48971	Sunflower seedling farnesyl pyrophosphate synthase (FPS) - Helianthus annuus, 341 aa. [EP1063297-A1, 27-DEC-2000]	13..352 6..341	138/343 (40%) 204/343 (59%)	3e-64

In a BLAST search of public sequence databases, the NOV82a protein was found to have homology to the proteins shown in the BLASTP data in Table 82D.

PFam analysis predicts that the NOV82a protein contains the domains shown in the Table 82E.

Table 82E. Domain Analysis of NOV82a			
Pfam Domain	NOV82a Match Region	Identities/ Similarities for the Matched Region	Expect Value
polyprenyl_synt: domain 1 of 1	43..315	82/285 (29%) 237/285 (83%)	6.3e-91

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Table 83C. Protein Sequence Properties NOV83a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV83a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 83D.

Table 83D. Geneseq Results for NOV83a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV83a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79976	Human protein SEQ ID NO 3622 - Homo sapiens, 125 aa. [WO200157190-A2, 09-AUG- 2001]	1..101 25..125	100/101 (99%) 100/101 (99%)	1e-52
AAM78992	Human protein SEQ ID NO 1654 - Homo sapiens, 101 aa. [WO200157190-A2, 09-AUG- 2001]	1..101 1..101	100/101 (99%) 100/101 (99%)	1e-52
AA Y49967	Human sentrin protein sequence - Homo sapiens, 101 aa. [US5985664-A, 16-NOV-1999]	1..101 1..101	89/101 (88%) 94/101 (92%)	2e-45
AA W87984	Ubiquitin-like domain of the protein SUMO1 - Mammalia, 101 aa. [WO9857978-A1, 23-DEC- 1998]	1..101 1..101	89/101 (88%) 94/101 (92%)	2e-45
AA W60079	Homo sapiens sentrin-1 polypeptide - Homo sapiens, 101 aa. [WO9820038-A1, 14-MAY- 1998]	1..101 1..101	89/101 (88%) 94/101 (92%)	2e-45

- 5 In a BLAST search of public sequence databases, the NOV83a protein was found to have homology to the proteins shown in the BLASTP data in Table 83E.

Table 83F. Domain Analysis of NOV83a			
Pfam Domain	NOV83a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	20..95	14/83 (17%) 66/83 (80%)	4.7e-18

5 The NOV84 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 84A.

Table 84E. Domain Analysis of NOV84a			
Pfam Domain	NOV84a Match Region	Identities/ Similarities for the Matched Region	Expect Value
SKI: domain 1 of 1	9..182	37/206 (18%) 114/206 (55%)	1.1

Example 85.

The NOV85 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 85A.

Table 85A. NOV85 Sequence Analysis		
	SEQ ID NO: 239	4332 bp
NOV85a, CG59704-01 DNA Sequence	GGCGTATTAAACGCGCGGGTGCACACCCCCACGGGCGCGCAATGAACAACATATGTGCTT AATGACGAGATCGGCCAGGGTGCCTTCAGCACTATTTACAAGGGCCGCTATCGCACCA CCACCGAGTTCTACGCGATTGCTTCCATCGACAAGAAGCGACGGAGCGCGTCGTGAA CTGCGTTTCAGCTGTTACGCTCCATGCACCACTCAAACGTCATAGAGTTCCACAACCTGG TATGAGACCAACAATCACTTGTGGATCATACGGAGTACTGCACCGGGCGAGACATGA GCACGATCCTCCGCTCGAACATTAATCTCACCCTCAGGCGGTCCAGGCGTTCGGCCG TGATGTGGCGATGGGCTCATGTACATCCACAGTAAGGGTGTGCTGTATAACGACTTG CAGACTCGCAATCTGCTGATGGACTCCGACGCAATGCTGCGCTTCCACGACTTAGCT TGGCCTGTCTCTTCCAAGACGCGCGACGCGGCACTGGTGGGACGCCACTGTACAT GGCCCCGAGTTGTTTCATGGCGGATCGCCCGCTGACTCGATGGCATCAGACCTGTGG TCCTTCGTTGTGTGCTGACGAGCTGGCGACAGGCAAGCCGCTTTCGCCATCCG ACCTCGAGACGCTGCTGGGCGACATACTACGAGTCCGACGCGAGCGGTGCCGTGGTGC GCCGGAGTCTTTCAAACGCTCCTGTGCGGCTGCTGGAAAAGGACCGTTGAAGCGC TACGCGTGGGTGATGTTGTCCGACGAGTTCTGGGATGAGCCCTTTCGCCGTGCCGA GCAACGCTTTCCATCTCAGGTGGCGTGGGAGGACTACAAGCGTTTCGGTTCTGGACG CGGTGCGAGTCAGTATAATTGGACGGACTCCGATGTGCGTGTGGCAGTGGCTCACGCC GTGGGGGCGAGCAAAATCAAACGCTTCTACGCACAACGTTGGAGGAGAGGGAGCGAGCG CTGCGACGTTGAACGTCGCGAAGGAGCTGGACTTCACTGCAAGCGCGCGATGTTGCT GGAACGGTTACCGGAGCGGACACAGGAGCGTGTGCGCAGCAACAGGCCATGTCCGG ACCGCGCACGGCAGCGCTGGTGCACGGCTGCCATCCACGGCTCAGCGGCGACCTCCG CAAGACGTTCAAGGACAAGGCGGCTGCTCAAGATTGTGGAAGAGGTCAAACCGCT GTGAGGGCTTCAAGCGTGGGTGCTTCCACGTCGCTGCGCCACCGGGCATGAGG GAGCGCACTGGACCGCTTGTCTCAGAAGCTCGGGATGAAGCTGTTGCCGTGGCGAG CACTGATGCTTTCGAGGACTGCGAACCGCTGCTAGCGCACCGGACACCATATCAG CTACTGCGAGGTGGCCGCGAAGGAGTTCGAGATCGAGATGACGCTCAAGGACATCGCT GCCAAGTGGGAGACCAATGCTTTCATCATCGAGGCATACAAGGACAGGACAGTACA TCCTCAAGGACACCTCGAGGTGGTGGAGCTCCTCGACGAGCACTCAACGTCGTCCA GCAGTGCAGTTCTTCCATTCAAGGGCTACTTCGAGGAGTCCATCAGGACTGGGAG CGCTCCCTCAACCTCATCTCCGACATACTCGAACAATGGCTGAGTCCGAGCGAGCT GGCGTTATCTGGAGCCGATCCTCAACTCGGAGGACATCGCATGCAGTACCGGACT GTCCACGCTGTTGAGAAGGTGGACCGCACATGGAGACGTGTATGGGCAACCGCGAC GCGCAGCCAAACGCACTCGAGTACTGCATTGGCACAAACAAGCTCTTGGACCACTGC GCGAGGCGAACCGCTCCTCGAAGTGTGTCAGCACTTGTATGGCGCAGAAGTCAACGT TGCCGCTGTTGGTCCGACTGGCACCGCAAGTCCATCTCACTCGCGCGTCTCGTGCT GGCGGCGCATGCGGCCAACTTTCTGGCCTCAACTTCACTTCTCGGCGCAGACAA AGTGCACAGTGTGAGAATTCACTGATGGCCAAGTTCGATAAGCGCGCTCGCACGT CTACGGCGCCCTGCGCGTAAGCACTTTCTCATCTTCAATTGACGACGCAACCTGCGC CAGCCAGAGAAGTACGGCGCGCAGCCCCGGTGGAGCTTCTCGGCGAGATGCTCGCCC AAGGCGGCTTCTACAACCTTACAGGTGGCATCAAGTGGTCTCCATCATCGACTGCTC GTTTGGCTGCGATGGGGCGCTGGCGGGGGCGCAGCCGGTTTCGAACCGCTTT ATGCGCTAATTCAATTACCTTGCTTCCCGAGATGTCGGAATGCGGAGATGCTGATGC TCTTGACGGCCATCCTCGTGGCGGCTCGCGCAGAGCGGCTCGTGCACCGCTCGC GAACGTGCGCTCCGCGGTGGTCGATAGCAGTTGCGGGTGTTCGCAAGTGCACCCAG GTCTTTTGGCGGACCGGCGCAGTGCATACTCTTCAACATGCGGATGCGGATGTGATGC GTGTTTTTCCCTCTTGTACACAGCAGACAAGTCGGTGTGTCAGTTCGGAGGAATCCAT CGTGGCGCTGTGGATGCACGAGATGCAGCGCTTCTACGATCGCTCGTGCAGCGC ACAGACAAGGTGTTTCATCGAGTACCTCAATGCCGAGCTGCCGTCATGGGGTGG ACAAGTCTACAACGAGGTAGTGAAGGCTGACCGCTCATCTTGGCGACGTAAGTGCAG CGACAAGGGCGTGTACGAGCAGATTACCGACATGAACGCCCTCACGACACCGCATGAAT GAGCTGTGAGGGCTACAATGACGAGAATGAAGTGAAGATGAACCTCGTCTCTTCC TCGACGCCATCGAGCATGTCTGCGGTATCTCGCGGTGCTGCGACTGCCGAACGGGCA CTGCCCTCTCTCGCGTGGCGGGTGGGACGCAAGTCACTACCGCGCTGGCTTGT	

	<p>TCTCTGATTGCCGAGATGGAGGTGTTACGATTGAGCTGTGAAGAAGCTTCGGTGTCA AGGAATGGCAGAGAGCCTCGCGAAGTTGCTGCTCGAGTGTGGCAAGGACGAGAAGAA GCGGACGTTTCTTTCGCCGACACCCAGCTGGCGCATCCGACGTTTCTGGAGGATGTG GCGGGCCTGCTCACATCGGGTGATGTGCCGAACCTCTTTGAGGACCAAGATATCGAGC TCATCAACGACAAGTTTCGCGGCGTCTGCCCTAAGCGAGAACCTGCCAACGACGAAGGT GTCGGGTACGCGCGCTTTGTGAAGGAGGCGCGAGCCAACCTGCACCTTGTGCTCGCC TTCTCTCCCATCGGAGAGGCGTTTCGCGAGCGCTGCGTATGTTCCCATCGCTCATTG CGTGCTGCACAATCGACTGGTTTGTCTGAGTGGCCATCCGAGGCGCTACTGTCGGTAGC CGCAGTGCAGCTGAACGCCGCGACGTTACTGACGTGATGGGGGCGGCAAGCCATGCC GACTTGC CGGGTGTCTCCAGGCAGTGCACCGCGCGGCGGCGGAGGTGACGGAGCGCT TCTTCACGGAACGCGTCTGCTGCTGACGTGACGCCGACGCTCTATCTGTCGCTCCT CTCCAAGTTCAAAGTGATGGCGGCGGCAAAACGCCGCTTCGTTGCGGAGCAGCGCGG CGCTCGAGAAGGGGCTGGAGAAGCTGCGGCACACCGAGGTGAAGTGGCGGAGCTGG AGGCCAGCTCAAGGCGCAGCAGCCGTTCTGGTGCAGAAAAAGGCGAGATTACGTG GATGATGGAGCGGCTGACGGTGGACCGAAAGGAGGCGCGGTGAAGGAGGCGGACGCG CGCAGGAGGGCCAGCTTCCCGGTGGCCGTGCTGCATACGGCGGTGAAGATGACGAAT GAGCCGCGGATGGGGCTGCGGGCGAACGTGATGCGCTCCTACTACGGCTTCACTCCCG AGGACCTCGAGCAGGAGGAGAAGCCCGCGAGTTCAAAGAGTGTGATGGCATCCGC ATGCTGTGCTCCATACCGAGCACTGAAGAGCAGGCTCTCTGGAGCCTGGCATCGTGG GGTGGCCCTCAGCTTCCCCACTCACTGTGGGAAGTTTCTTAGTGTCTCTGAGCCGTGT TTCTCATCCGTGCGTGAAGATAAACCTGCTTCAAGGATGTGTTGGTGAAGAGCTTCC CTACCTAGCTTCTGTAACGCCACTGCATGCCACCACTGCTGAGTACTGTTTGTGTC TAGGTTGGTGTCACTTCTCATTTTACCAGAAAGTGAAGCTC</p>		
	ORF Start: ATG at 41	ORF Stop: TGA at 3944	
	SEQ ID NO: 240	1301 aa	MW at 146115.7kD
NOV85a, CG59704-01 Protein Sequence	<p>MNNYVLNDEIGQAFSTIYKGRYRTTEFYAIAASIDKKRRERVVNCVQLLRSMHHSNV IEFHNWYETNNHLWIIIEYCTGGDMSTILRSNINLTQAVQAFGRDVMGLMYIHSKG VYNDLQTRNLLMDSAAMLRFHDFSLACLFQDAATRPLVGTPLYMAPELFMADRPLYS MASDLWSFGCVLHELATGKPPFAASDLETLGDLTSPTPAVPGAPESFQTLTLCGLLE KDPLKRYAWVDVVRSEFWDEPLPLPSNGFPSQVWEDYKRSRSGRGASQYNWTDSDVR VAVAHAVGAASNAETHNVEERERAAATLNVAKELDFTASAAMLLERLPERTQERAAH ATGHVATAHGLVHGCPSTASAATSPRRSRTRRRCSRLWKRKPLSRASSRGCPSTSL RHPGMRERHWTGLSQKLGMLVPGDTLMLEDCEPLLARDTIIISYCEVAAKESQIEM TLKDMRAKWKTCFIIIEAYKETGTYLKDTSEVVELLDEHLNVVQQLQFSPFKGYFEE SITDWERSLNLISDILEQWLECRARWYLEPIILNSEDIAQLPRLSTLFKVDRTWRR VMGNAHAQPNALCYCIGTNKLLDHLREANRLLEVLQHLMAQKVNVAAGVPTGTGKSIS LARLVLGGMPPANFLGLNFTFSAQTKCTVLQNSLMAKFDKRSHVYGAPAGKHLFIPI DDANLPQPEKYGAQPPVELLRQMLAQGGFYNTGGIKWSSIIDCSLALAMGPPGGGRS RVSNRFMRYFNILAFPEMSDMSKRTILQAILVGGLAQSLADRLANVASAVVDSTLRV FRKCTQVFLPTPAHVHYSFNMRDVMRVFPLLYTADKSVLQSEESIVRLWMHEMQRVFY DRLVDATDKGLFIEYLNALFPMGVDSYNEVVKADRLIFADVLSDKGVYEQITDMNA LTRMNELLEAYNDENEVKMNLVFLDAIEHVCRISRVLRPLNGHCLLLGVGSGSRKS LTRLACSLIAEMEVFTIELSKNFGVKWHESLAKLLLECGKDEKRTFLFADTQLAHP TFLEDVAGLLTSGDVPNLFEDQDIELINDKFRGVCLSENLPKTVSVYARFVKEARAN LHLVLAFSPIGAFRSRLRMFPSLIACCTIDWFAEWPSEALLSVAAVQLNAGDVTDM GAASHADLPQCFAVHRAAAEVTERFFTETRRSYVTPSYLSLLSNFKVMAAAKRRF VREQRGRLEKGLKLRHTEVQVAELEAQLKAQPPVLVQKKAIEIQSMERLTVDRKEAA VKEADARREAQLPGGRAAYGGEDDE</p>		

Further analysis of the NOV85a protein yielded the following properties shown in Table 85B.

Table 85B. Protein Sequence Properties NOV85a	
PSort analysis:	0.8800 probability located in nucleus; 0.3562 probability located in microbody (peroxisome); 0.1671 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV85a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 85C.

Table 85C. Geneseq Results for NOV85a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV85a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79863	Human protein SEQ ID NO 3509 - Homo sapiens, 2127 aa. [WO200157190-A2, 09-AUG- 2001]	602..1287 168..847	218/692 (31%) 347/692 (49%)	1e-89
AAM79862	Human protein SEQ ID NO 3508 - Homo sapiens, 2127 aa. [WO200157190-A2, 09-AUG- 2001]	602..1287 168..847	218/692 (31%) 347/692 (49%)	1e-89
AAM78879	Human protein SEQ ID NO 1541 - Homo sapiens, 2143 aa. [WO200157190-A2, 09-AUG- 2001]	602..1287 108..787	218/692 (31%) 347/692 (49%)	1e-89
AAM78878	Human protein SEQ ID NO 1540 - Homo sapiens, 2067 aa. [WO200157190-A2, 09-AUG- 2001]	602..1287 108..787	218/692 (31%) 347/692 (49%)	1e-89
AAM80293	Human protein SEQ ID NO 3945 - Homo sapiens, 1774 aa. [WO200157190-A2, 09-AUG- 2001]	910..1293 33..405	153/393 (38%) 227/393 (56%)	5e-70

- 5 In a BLAST search of public sequence databases, the NOV85a protein was found to have homology to the proteins shown in the BLASTP data in Table 85D.

Table 85D. Public BLASTP Results for NOV85a				
Protein Accession Number	Protein/Organism/Length	NOV85a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL37427	CILIARY DYNEIN HEAVY CHAIN 7 - Homo sapiens (Human), 4024 aa.	628..1293 1975..2655	271/692 (39%) 395/692 (56%)	e-132
Q27812	DYNEIN HEAVY CHAIN ISOTYPE 7B (EC 3.6.1.3) - Tripneustes gratilla (Hawaian sea urchin), 1314 aa (fragment).	601..1247 654..1310	264/667 (39%) 389/667 (57%)	e-127
Q9MBF8	1 BETA DYNEIN HEAVY CHAIN - Chlamydomonas reinhardtii, 4513 aa.	611..1293 2486..3159	257/693 (37%) 377/693 (54%)	e-117
Q9VJC6	DHC36C PROTEIN - Drosophila melanogaster (Fruit fly), 4010 aa.	596..1275 1913..2604	249/699 (35%) 383/699 (54%)	e-116
Q9VWZ3	DHC16F PROTEIN - Drosophila melanogaster (Fruit fly), 4081 aa.	618..1301 2022..2709	248/704 (35%) 380/704 (53%)	e-108

PFam analysis predicts that the NOV85a protein contains the domains shown in the Table 85E.

Table 85E. Domain Analysis of NOV85a			
Pfam Domain	NOV85a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pkinase: domain 1 of 1	4..250	80/286 (28%) 190/286 (66%)	6.8e-62
DEAD: domain 1 of 1	613..637	7/25 (28%) 22/25 (88%)	0.83
dNK: domain 1 of 1	865..1020	32/179 (18%) 101/179 (56%)	6.8

Example 86.

- 5 The NOV86 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 86A.

Table 86A. NOV86 Sequence Analysis			
	SEQ ID.NO: 241	1420 bp	
NOV86a, CG59628-01 DNA Sequence	GTCCAGCTTTAGCTCTCTGCTCGCCGCCGCCGCTGTGCGCCGCCACCTCCTCTGATCTA CGAAAGTCATGTTACCCCAACACCGGGAGGCTGGCAGGATGTACAGTTTTATCACAGG TGC AAGCCGTGGCATTGGCAAAGCTATTGCATTGAAAGCAGCAAAGGATGGAGCAAAT ATTGTTATTGCTGCAAAGACCGCCAGCCACATCCAAAACCTTCTAGGCACAATCTATA CTGCTGCTGAAGAAATTGAAGCAGTTGGAGGAAAGGCCTTGCCATGTATTGTTGATGT GAGAGATGAACAGCAGATCAGTGCTGCAGTGGAGAAAGCCATCAAGAAATTTGGAGGA ATTGATATTCTGGTAAATAATGCCAGTGCCATTAGTTTGACCAATACATTGGACACAC CTACCAAGAGATTGGATCTGATGATGAACGTGAACACCAGAGGCCACCTACCTTGCATC TAAAGCATGTATTCTCTTATTTGAAAAAGAGCAAAGTTGCTCATATCCTCAATATCAGT CCACCAGTGAACCTAAATCCAGTTTGGTTCAAACAGCACTGTGCTTATACCATTGCTA AGTATGGTATGTCTATGTATGTGCTTGGAAATGGCAGAAGAATTTAAAGGTGAAATTGC AGTCAATGCATTATGGCCTAAACAGCCATACACACTGCTGCTATGGATATGCTGGGA GGACCTGGTATCGAAAGCCAGTGTAGAAAAGTTGATATCATTGCAGATGCAGCATATT CCATTTTCCAAAAGCCAAAAAGTTTTACTGGCAACTTTGTCAATTGATGAAAATATCTTT AAAAGAAGAAGGAATAGAAAAATTTGACGTTTATGCAATTAACGAGTGCATCCTTTG CAACCAGATTTCTTCTTAGATGAATACCCAGAAGCAGTTAGCAAGAAAGTGAATCAA CTGGTGCTGTTCCAGAATTCAAAGAAGAGAAACTGCAGCTGCAACCAACCAACCGTTT TGGAGCTGTGGAAGAAACATTTAGAATTGTTAAGGACTCTCTCAGTGATGATGTTGTT AAAGCCACTCAAGCAATCTATCTGTTTGAACCTCTCCGTGAAGATGGTGGCACGTGGT TTCTTGATCTGAAAAGCAAGGGTGGGAATGTCGGATATGGAGAGCCTTCTGATCAGGC AGATGTGGTGATGAGTATGACTACTGATGACTTTGTAAAAATGTTTTCAGGTAAACTA AAACCAACAATGGCATTATGTCTCAGGGAAATTGAAGATTAAAGGTAACATGGCCCTAG CAATCAAATTGGAGAAGCTAATGAATCAGATGAATGCCAGACTGTGAAGGAAAAATATA AAAAAAAAGTCGACTGCTATGCTCAAAAAGTAAAAAAGCTCAACAGTTAAAAATCTAA TGTTTGTTTTCTTCTCTGTTATATTATA		
	ORF Start: ATG at 67	ORF Stop: TGA at 1321	
	SEQ ID NO: 242	418 aa	MW at 45394.2kD
NOV86a, CG59628-01 Protein Sequence	MLPNTGRLAGCTVFITGASRGIGKATALKAAKDGANIVIAAKTAQPHPKLLGTIYTAA EETIEAVGGKALPCIVDVRDEQQISA AVEKAIKKFGGIDILVNNASATSLNTLDTPTK RLDLMMNVNTRGYLASKACIPYLKKS KVAHILNISPLNLPVWFKQHCAYYTIKAYG MSMYVLGMAEEFKGEIAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDI IADAAYSIF QKPKSFTGNFVIDENILKEEGIENFDVYAIKPGHPLQPDFLDEYPEAVSKKVESTGA VPEFKEEKLQLQPKPRSGAVEETFRI VKDSLSDDVVKATQAIYLFELSGEDGGTWFLD LKS KGGNVGYGEPDQADVVMSTTDDFVKMFSGLKPTMAFMSGKLKIKGNMALAIK LEKLMMNQMNARL		

Further analysis of the NOV86a protein yielded the following properties shown in Table 86B.

Table 86B. Protein Sequence Properties NOV86a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.5000 probability located in microbody (peroxisome); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV86a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 86C.

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV86a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81260	Human AFP protein sequence SEQ ID NO:38 - Homo sapiens, 418 aa. [WO200129221-A2, 26-APR-2001]	1..418 1..418	418/418 (100%) 418/418 (100%)	0.0
AAB84367	Amino acid sequence of human alcohol dehydrogenase 21612 - Homo sapiens, 418 aa. [WO200144446-A2, 21-JUN-2001]	1..418 1..418	418/418 (100%) 418/418 (100%)	0.0
AAG81258	Human AFP protein sequence SEQ ID NO:34 - Homo sapiens, 383 aa. [WO200129221-A2, 26-APR-2001]	1..382 1..382	382/382 (100%) 382/382 (100%)	0.0
ABB10251	Human cDNA SEQ ID NO: 559 - Homo sapiens, 278 aa. [WO200154474-A2, 02-AUG-2001]	141..418 1..278	271/278 (97%) 274/278 (98%)	e-156
AAU23020	Novel human enzyme polypeptide #106 - Homo sapiens, 278 aa. [WO200155301-A2, 02-AUG-2001]	141..418 1..278	271/278 (97%) 274/278 (98%)	e-156

Table 86D. Public BLASTP Results for NOV86a				
Protein Accession Number	Protein/Organism/Length	NOV86a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC38510	SEQUENCE 37 FROM PATENT WO0129221 - Homo sapiens (Human), 418 aa.	1..418 1..418	418/418 (100%) 418/418 (100%)	0.0
CAC38508	SEQUENCE 33 FROM PATENT WO0129221 - Homo sapiens (Human), 383 aa.	1..382 1..382	382/382 (100%) 382/382 (100%)	0.0

Q99LV2	HYPOTHETICAL 54.9 KDA PROTEIN - Mus musculus (Mouse), 496 aa.	1..418 1..496	355/496 (71%) 390/496 (78%)	0.0
Q9BT58	SIMILAR TO RIKEN CDNA 2610207I16 GENE - Homo sapiens (Human), 345 aa.	163..418 90..345	253/256 (98%) 254/256 (98%)	e-143
Q9VB10	CG5590 PROTEIN (GH01709P) - Drosophila melanogaster (Fruit fly), 412 aa.	4..418 3..412	238/422 (56%) 300/422 (70%)	e-128

PFam analysis predicts that the NOV86a protein contains the domains shown in the Table 86E.

Table 86E. Domain Analysis of NOV86a			
Pfam Domain	NOV86a Match Region	Identities/ Similarities for the Matched Region	Expect Value
beta-lactamase: domain 1 of 1	222..236	4/15 (27%) 14/15 (93%)	6.5
adh_short: domain 1 of 1	9..321	74/339 (22%) 211/339 (62%)	2.4e-29
SCP2: domain 1 of 1	306..415	41/114 (36%) 87/114 (76%)	1.5e-25

Example 87.

The NOV87 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 87A.

Table 87A. NOV87 Sequence Analysis		
	SEQ ID NO: 243	888 bp
NOV87a, CG59516-01 DNA Sequence	TTCAACAAGGGCCCTCTACAGGCTCTTGGCGGACGTCCAGAACAGGCTTCTGTTC AATATGACTCCCAGAAGGAGGCAGAGCTCCGCAGCTGGATCAAGGGATTCAGTGGCCT CTCCATCCGCCCCGACTTCCAGAAGGCCTGAAGGACGGGATTATTTTATGCACATC GTGAACAACTGCAGCCGGGCTCAGTCCCCAAGATCAACGGCTTCCGTGTAGAACTGG CACCAGCTAGAAAACTCTCCAACATCCTCAAGGCAATGGTCAGTACGGCATGATCC CGTGGACCTATTGAGGCCAACGACCTGTTTGAGAGTGGGAACAATATGCAGGTGCGG GTGTCTCTCTCGCCCTGGCAGGGAAGGCCAAGACTAAGGGGCTGCAGAGCGGGTGG ACATCCGTGACAAGTACTCAGAGAAGCAGAACTTCAACGACACCACCATGAAGGCCAG GCTGTGCGTCATCCGGCTGCAGATTACCAACAAATGTGCCAGCCAGTCAGGCATGACC GCATACGTACAGAGGAGGCATCTCTACGACCCCAAGAACCCGATCCTGCCCCCATGG ACAACCTCGACCATCAGCCTCCGGATGGGTACAAACAAGTGCAGCCAGCCAGGTGGCAT GACGGCTCCCGGGAACAGTGGCACATCTATGACACCAAGTTGGGAATCGACAAGTGT GAGAACTCTCCTATGTCCCTGAAGATGGGCTACACGCAGGTCGCCAATCACAGCAGAC AGGTCTTTGGCCTAGGCCGGCAAATATATGAACCAAGTACCAGCCGGGTGGCCAGT GGCCACGGGCTCCCTCCGCGGCAACTGCCAGGGCCAGGGGAGGCCCTTAGTAC CAGGAGGAGACCAGCTAC	
	ORF Start: TTC at 1	ORF Stop: TAG at 865

	SEQ ID NO: 244	288 aa	MW at 31831.2kD
NOV87a, CG59516-01 Protein Sequence	FNKGPSPYRLADVQNRLLFKYDSQKEAELRSWIKGFTGLSIRPDFQKGLKDGIILCTLVNKLQPGSVPKINGFRVELAPARKPLQHPQNGQLRHPDVLDFEANDLFESGNNMQVFLVSLALAGKAKTKGLQSGVDIRDKYSEKQNFNDTTMKARLCVIRLQITNKCASQSGMAYVTRRHLYDPKPNRILPMPDNSTISLRMGNTNKCASQVGMTAPGNQWHIYDTKLGIIDKGENSSMSLKMGYTQVANHSRQVFLGRQIYEPKYQPGGPVAHGAPSAAGNCPGPGGEAP		
	SEQ ID NO: 245	888 bp	
NOV87b, CG59516-02 DNA Sequence	TTCACAAGGGCCCTCTACAGGCTCTTGGCGGACGTCAGAACAGGCTTCTGTTCATAATATGACTCCCAGAGGAGGCAGAGCTCCGCACTGGATCAAGGATTCACTGGCCCTCTCCATCCGCGCCGACTTCCAGAAGGGCCTGAAGGACGGGATTATTTTATGCACACTGTGAACAACTGCAGCCGGGCTCAGTCCCCAAGATCAACGGCTTCCTGTGTAGAACTGCACCCAGCTAGAAAACTCTCCAACATCCTCAAGGCAATGGTCAGCTACGGCATGATCCGTGGACCTATTTTGAGGCCAACGACCTGTTTGAAGTGGGAACAAATATGCAGGTGCGCGTGTCTCTTCTCGCCCTGGCAGGGAAGGCCAAGACTAAGGGGCTGCAGACGCGGGTGCACATCCGTGACAAGTACTCAGAGAAGCAGAACTTCAACGACACCACCATGAAGGCCACGCTGTGCGCTCCGCTGCAGATTACCAACAAATGTGCCAGCCAGTCAGGCATGACGTCATACGTACAGGAGGCATCTCTACGACCCCAAGAACCGCATCCTGCCCCCATGCACAACCTCGACCATCAGCCTCCGGATGGGTACAACAAGTGCAGCAGGTCAGGTGGGCATGACGGCTCCGCGGAACAGTGGCACATCTATGACACCAAGTTGGGAATCGACAAGTGTGAGAACTCCTCCATGTCCCTGAAGATGGGCTACACGCAGGTTCGCAATCACAGCAGAGAGGTCTTTGGCCTAGGCCGGCAAATATATGAGCCCAAGTACCAGCCGGGTGGCCAGTGGCCCCAGGGGCTCCCTCCGCGCAACTGAGCAGGGCCAGGGGAGGCCCTTAGTAGACAGGAGAGACCAGCTAC		
	ORF Start: TTC at 1	ORF Stop: TAG at 865	
	SEQ ID NO: 246	288 aa	MW at 31831.2kD
NOV87b, CG59516-02 Protein Sequence	FNKGPSPYRLADVQNRLLFKYDSQKEAELRSWIKGFTGLSIRPDFQKGLKDGIILCTLVNKLQPGSVPKINGFRVELAPARKPLQHPQNGQLRHPDVLDFEANDLFESGNNMQVFLVSLALAGKAKTKGLQSGVDIRDKYSEKQNFNDTTMKARLCVIRLQITNKCASQSGMAYVTRRHLYDPKPNRILPMPDNSTISLRMGNTNKCASQVGMTAPGNQWHIYDTKLGIIDKGENSSMSLKMGYTQVANHSRQVFLGRQIYEPKYQPGGPVAHGAPSAAGNCPGPGGEAP		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 87B.

Table 87B. Comparison of NOV87a against NOV87b.

Protein Sequence	NOV87a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV87b	1..288	288/288 (100%)
	1..288	288/288 (100%)

Further analysis of the NOV87a protein yielded the following properties shown in Table 87C.

Table 87C. Protein Sequence Properties NOV87a

PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.2110 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV87a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 87D.

Table 87D. Geneseq Results for NOV87a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV87a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR94888	Carponin - Homo sapiens, 297 aa. [JP08073380-A, 19-MAR-1996]	1..265 6..272	136/269 (50%) 176/269 (64%)	7e-63
AAR72588	Carponin protein - Homo sapiens, 297 aa. [WO9509010-A, 06-APR-1995]	1..265 6..272	136/269 (50%) 176/269 (64%)	7e-63
AAB43807	Human cancer associated protein sequence SEQ ID NO:1252 - Homo sapiens, 163 aa. [WO200055350-A1, 21-SEP-2000]	164..273 4..116	67/113 (59%) 82/113 (72%)	6e-30
AAM73074	Human bone marrow expressed probe encoded protein SEQ ID NO: 33380 - Homo sapiens, 71 aa. [WO200157276-A2, 09-AUG-2001]	157..225 2..71	49/70 (70%) 55/70 (78%)	4e-21
AAM60434	Human brain expressed single exon probe encoded protein SEQ ID NO: 32539 - Homo sapiens, 71 aa. [WO200157275-A2, 09-AUG-2001]	157..225 2..71	49/70 (70%) 55/70 (78%)	4e-21

- 5 In a BLAST search of public sequence databases, the NOV87a protein was found to have homology to the proteins shown in the BLASTP data in Table 87E.

Table 87E. Public BLASTP Results for NOV87a				
Protein Accession Number	Protein/Organism/Length	NOV87a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q08094	Calponin H2, smooth muscle - Sus scrofa (Pig), 296 aa (fragment).	1..287 6..296	219/291 (75%) 237/291 (81%)	e-116
Q99439	Calponin H2, smooth muscle (Neutral calponin) - Homo sapiens (Human), 309 aa.	1..288 6..297	218/292 (74%) 235/292 (79%)	e-115

20200909 00626007

Q08093	Calponin H2, smooth muscle - Mus musculus (Mouse), 305 aa.	1..288 6..293	214/291 (73%) 231/291 (78%)	e-112
O93547	CALPONIN H3 - Xenopus laevis (African clawed frog), 295 aa.	1..269 5..276	179/273 (65%) 208/273 (75%)	6e-91
Q922F8	UNKNOWN (PROTEIN FOR MGC:8135) - Mus musculus (Mouse), 242 aa.	59..288 1..230	166/233 (71%) 179/233 (76%)	8e-83

PFam analysis predicts that the NOV87a protein contains the domains shown in the Table 87F.

Table 87F. Domain Analysis of NOV87a			
Pfam Domain	NOV87a Match Region	Identities/ Similarities for the Matched Region	Expect Value
CH: domain 1 of 1	23..123	27/124 (22%) 65/124 (52%)	0.068
calponin: domain 1 of 2	159..183	17/26 (65%) 21/26 (81%)	3.8e-07
calponin: domain 2 of 2	198..223	15/26 (58%) 19/26 (73%)	3e-08

Example 88.

The NOV88 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 88A.

Table 88A. NOV88 Sequence Analysis		
	SEQ ID NO: 247	2213 bp
NOV88a, CG59671-02 DNA Sequence	CGTGAGGCACCCACTCTGGGAGCACAGAGAGCTCAGGTAGCCTGCCTAGATGGCGGGC CGCACCTGGGCCGCGCGCTCGGGAGGCTGCTGGGCAGCCTGCCAGGGCTCTCGGGGC AGCCCGCGCGGCCGCGTGC GG GGTGAGCGCGCCGCGCAGGGCGGCCTCGGGACCTC GGGCAGCGCTCCCGCAGTTG CAGCAGCAGCAGCAGCAGCCAGGCTCGTATCCCGCGCTG AGTG CACAGGCAGCCCGGAGCCGCGCGCTTCTGGGGCCTCTGGCGCGGGACATC TCGTGTGGGACACCCCTAC CACACCGTCTGGGACTGCGACTTCAGCACTGGCAAGAT CGGCTGGTTCCTGGGAGGCCAGTTAAATGTCTCTGTCAACTGCTGGACCAGCATGTT TGAGGATCACCTACAGGGA CTA C TGGAGACCACGTGCCGCTGGCCAAACACGCTGAA GAGGCATGGAGTCCACCGTGGGACCGTGTGCCATCTACATGCCCGTGTCCCATTTG GCTGTGGCAGCAATGCTGGCCTGTGCCAGGATCGGAGCTGTCCACACAGTCACTTTG CTGGCTTCAGTG CAGAGTCTTGGCTGGGAGGATCAATGATGCCAAGTGCAAGTGGT TATCACCTTCAACCAAGGACTCCGGGGTGGGCGCGTGGTGGAGCTGAAGAAATAGTG GATGAGGCTGTGAAGCACTGCCCCACCGTG CAGCATGTCTGGTGGCTCACAGGACAG ACAACAAGGTCCACATGGGGGATCTGGACGTCCCGCTGGAGCAGGAAATGGCCAAGGA GGACCCTGTTTGCGCC CAGAGAGCATGGGCAGTGAGGACATGCTCTTCATGCTGTAC ACCTCAGGGAGCACCGGAATGCCCAAGGGCATCGTCCATACCCAGGCAGGCTACCTGC TCTATGCCGCCCTGACTCACAAGCTTGTGTTTGACCACCAAGCCAGGTGACATCTTTGG CTGTGTGGCCGACATCGGTTGGATTACAGGACACAGCTACGTGGTGTATGGGCCTCTC TGCAATGGTGCCACAGCGTCTTTTGGAGACACCCAGTTTATCCCAATGCTGGTC GGTACTGGGAGACAGTAGAGAGGTTGAAGATCAATCAGTTCATGGCGCCCAACGGC TGTCCGGCTGTTGCTGAAATACGGTGATGCCTGGGTGAAGAAGTATGATCGCTCCTCC	

	CTGCGGACCTGGGGTCACTGGGAGAGCCCATCAACTGTGAGGCCTGGGAGTGGCTTC ACAGGGTGGTGGGGACAGCAGGTGCACGCTGGTGGACACCTGGTGGCAGACAGAAAC AGGTGGCATCTGCATCGCACCACGGCCCTCGGAAGAAGGGGCGGAAATCCTCCCTGCC ATGGCGATGAGGCCCTTCTTTGGCATCGTCCCCGTCTCATGGATGAGAAGGGCAGCG TCGTGGAGGGCAGCAACGTCTCCGGGGCCCTGTGCATCTCCAGGCCTGGCCGGGCAT GGCCAGGACCATCTATGGCGACCACCAGCGATTGTGGACGCCTACTTCAAGGCCTAC CCAGGCTATTACTTCACTGGAGACGGGGCTTACCGAAGTGGGGCGGCTATTACAGAG TCACAGGGCGGATGGATGATGTCATCAACATCAGTGGCCACCGGCTGGGGACCCGAGA GATTGAGGACGCCATCGCCGACCACCTGCAGTACCAGAAAGTGTGTCTATTGGCTAC CCCCACGACATCAAAGGAGAAGCTGCCTTTGCCTTCATTGTGGTGAAAGATAGTGGCG GTGACTCAGATGTGGTGGTGCAGGAGCTCAAGTCCATGGTGGCCACCAAGATCGCCAA ATATGCTGTGCCTGATGAGATCCTGGTGGTGAAACGTCTTCCAAAACAGGTCTGGG AAGGTCATGCGGGCGCTCCTGAGGAAGATCATCACTAGTGAAGGCCAGGAGCTGGGAG ACACTACCACCTTGGAGGACCCAGCATCATCGCAGAGATCCTGAGTGTCTACCAGAA GTGCAAGGACAAGCAGGCTGCTGCTAAGTGAGCTGGCACCTGTGGGGCTCTTGGGAT GGGCGGGCACCAAGCCCTGGCTGTCTCTCCAGAAAGTACCCCTGAGGTTGGCGTC TTCCTACGT		
	ORF Start: ATG at 50		ORF Stop: TGA at 2117
	SEQ ID NO: 248	689 aa	MW at 74855.9kD
NOV88a, CG59671-02 Protein Sequence	MAARTLGRGVRLGLSLRGLSGQPAPPCGVSAAPRAASGPSGAPAVAAAAAQPFSY PALSQAAREPAAFWGPLARDTLVWDTPTYHTVWDCDFSTGKIGWFLGGQLNVSNCLD QHVRSKSPESVALIWERDEPGTEVRITYRELLETTCLRLANTLKRHGVRHGRDRAIYMPV SPLAVALACARIGAVHTVIFAGFSAESLAGRINDAKCKVITFNQGLRGGRVVELK KIVDEAVKHCPTQHVLAHRTDNKVHMGDLVPLEQEMAKEDPVCAPESMGSEDMLF MLYTSGSTGMPKGI VHTQAGYLLYALHKLKLVFDHQPGDIFGCVADIGWITGHSYVVY GPLCNGATSVLFESTPVYPNAGRYWETVERLKNQFYGAPTAVRLLLKYGDWVKKYD RSSRLTLGSVGEPI NCEAWEWLHRVVGDSRCTLVDTWWTETGGICIAAPRSEGEAEI LPAMAMRPFFGIVPVLMEDEKGSVVEGSNVSGALCISQAWPGMARTIYGDHQRFDVAYF KAYPGYYFTGDGAYRTEGGYYQITGRMDDVINISGHRGLGTAEIEDAIADHPAVPESAV IGYPHDIKGEAAFAFIVVKDSAGDSVVVQELKSMVATKIAKYAVPDEILVVKRLPKT RSGKVMRRLLRKIITSEAQELGDTTTLLEDPISIAEILSVYQKCKDKQAAAK		

Further analysis of the NOV88a protein yielded the following properties shown in Table 88B.

Table 88B. Protein Sequence Properties NOV88a	
PSort analysis:	0.6500 probability located in plasma membrane; 0.6000 probability located in nucleus; 0.4340 probability located in mitochondrial inner membrane; 0.3000 probability located in Golgi body
SignalP analysis:	Likely cleavage site between residues 23 and 24

A search of the NOV88a protein against the Geneseq database, a proprietary
5 database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 88C.

Table 88C. Geneseq Results for NOV88a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV88a, Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU23058	Novel human enzyme polypeptide #144 - Homo sapiens, 664 aa. [WO200155301-A2, 02-AUG-2001]	26..689 1..664	663/664 (99%) 663/664 (99%)	0.0
AAB34712	Human secreted protein encoded by DNA clone vo9 1 - Homo sapiens, 518 aa. [WO200055375-A1, 21-SEP-2000]	172..689 1..518	518/518 (100%) 518/518 (100%)	0.0
AAU23050	Novel human enzyme polypeptide #136 - Homo sapiens, 479 aa. [WO200155301-A2, 02-AUG-2001]	224..689 18..479	459/466 (98%) 461/466 (98%)	0.0
ABB12253	Human acetate-coA ligase homologue, SEQ ID NO:2623 - Homo sapiens, 446 aa. [WO200157188-A2, 09-AUG-2001]	1..446 1..446	446/446 (100%) 446/446 (100%)	0.0
AAR23968	facA gene product - Penicillium chrysogenum, 669 aa. [WO9207079-A, 30-APR-1992]	58..684 45..669	305/629 (48%) 407/629 (64%)	e-175

In a BLAST search of public sequence databases, the NOV88a protein was found to have homology to the proteins shown in the BLASTP data in Table 88D.

Table 88D. Public BLASTP Results for NOV88a				
Protein Accession Number	Protein/Organism/Length	NOV88a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q99NB1	ACETYL-COA SYNTHETASE 2 - Mus musculus (Mouse), 682 aa.	1..687 1..680	599/687 (87%) 638/687 (92%)	0.0
Q9BEA3	ACETYL-COA SYNTHETASE 2 - Bos taurus (Bovine), 675 aa.	1..689 1..675	575/689 (83%) 625/689 (90%)	0.0
Q9NUB1	DJ568C11.3 (NOVEL AMP-BINDING ENZYME SIMILAR TO ACETYL-COENZYME A	212..689 1..478	478/478 (100%) 478/478 (100%)	0.0

	ASKLSGLTTNVVDI ILAHHFGQEEELQANLDLIQTYRMHIAQDINQDNLQFLNSYNGR RDLEIERPILGQNDNKSRTLKCSTLLVVGDNSPAUEAVVECNRLNPIINTLLKMDAC GGLPQVVQPGKLTEAFKYFLQGMGYVPSASMTLRARSRTHSTSSSLGSGESPFSRVS TNQSDGTQESCESPDVDRHQTMVSC	
	SEQ ID NO: 251	1175 bp
NOV89b, CG56870-02 DNA Sequence	TCGTTATCTGACCTCATGGATGAACCTCAGGATGTTGAGCTCACAGAGATCAAACCA TCTCAATAGTAAAGATGGTACAAGAACTTCCAGGACTTTGACTGTGAGGAACATGA TATAGAAACAACCTCATGGTGTGGTCCACGTCCTATAAGAGGCTTACCCAAAGGAAAC AGACAGTTTATACTAAACATATCATGACATTTGGCCTCAACCATAAATCTGTTTCAATG CATTCTTTAACTTTGAGGATATGCAAGAGATCACCAGCACTTTGCTGTCTGTATGTT GGATGCCCCAGGCCAGCAGGAAGGTGCACCTCTTTCCCAACAGGGTATCAGTACCC ACAATGGATGAGCTGGCTGAAGTGTGCTGCTCTGTTCTTACCCACCTAAGCTGAAAC GCATCATTGGAATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTTGCATCAA CCATCCAGAGCTTTGTGGAAGGCCTTTGTGCTCATTAAATGTTGACCTTTGCGCTAAAGGC TGGATTGACTGGGCAGCTTCCAAACTCTCTGGCCTGACAACCAATGTTGTGGACATTA TTTTGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAAC CTACAGAAATGCATATTGCCAAGACATCAACCAAGACAACTGCAGCTCTTCTTGAAT TCCTACAATGGACGCGAGAGACCTGGAGATCGAAAGACCCATACTGGGCCAAATGATA ACAAATCAAAAACATTAAAGTGTCTACTTTTACTGGTGGTAGGGACAATTCGCTGCG AGTTGAGGCTGTGGTCAATGCAATCCCGCTGAACCTATAAATACTGTTTGTCTGA AAGATGGCGGACTGTGGGGGACTGCCCCAGGTAGTTACGCTGGGAAGCTCACCAGG CCTTCAAGTACTTTTTCAGGGAATGGGCTACATACCTATGCCACATGACTCGCT CGCCCAAGTACGAACCTCAACCTCGAGTAGCCTCGGCTGTGGAGAAAGTCCCTTC AGCCGGTCTGTACCAGCAATCAGTCAGATGGAACCTCAAGAATCCTGTGAGTCCCTG ATGCTCTGGACAGACACGACCATGGAGGTGCTCTGCTAAGCAGATGCTCCTCCCT GGACCATGCAAGTC	
	ORF Start: ATG at 16	ORF Stop: TAA at 1141
	SEQ ID NO: 252	375 aa MW at 41376.2kD
NOV89b, CG56870-02 Protein Sequence	MDELQDVQLTEIKPLLNDKNGTRNFQDFDCEHDIETHGVVHVITIRGLPKGNRPVIL TYHIDIGLNHKSCFNFAFNFDQMGEITQHFVAVCHVDAPGQGEAPSFPTGYQYPTMDEL AEVLPPVLTHLSKSIIGIGVGAGAYILSRFALNHPELVEGLVLINVDPAKGVWDWA ASKLSGLTTNVVDI ILAHHFGQEEELQANLDLIQTYRMHIAQDINQDNLQFLNSYNGR RDLEIERPILGQNDNKSRTLKCSTLLVVGDNSPAUEAVVECNRLNPIINTLLKMDAC GGLPQVVQPGKLTEAFKYFLQGMGYVPSASMTLRARSRTHSTSSSLGSGESPFSRVS TNQSDGTQESCESPDVDRHQTMVSC	
	SEQ ID NO: 253	1232 bp
NOV89c, CG56870-03 DNA Sequence	ACTTCTTTCTTTTCTGTTTCAGAGTTACTGATTTATTCTTGAGATTCTCTACTCTCG TTATCTGACCTCATGGATGAACCTCAGGATGTTGAGCTCACAGAGATCAAACCACTTC TAAATGATAAGGAACATGATATAGAAACAACCTCATGGTGTGGTCCACGTCCTACTAAG AGGCTTACCAAGGAACAGACCACTTATACTAACATATCATGACATTTGGCCTCAAC CATAAATCCTGTTTCAATGCATTCTTAACTTTGAGGATATGCAAGAGATCACCAGC ACTTTGCTGTCTGTATGTGGATGCCCCAGGCCAGCAGGAAGGTGCACTCTTTCCC AACCGGTTATCAGTACCCCAATGGATGAGCTGGCTGAAATGCTGCTCTGCTTCTT ACCCACCTAAGCCTGAAAGCATCATTGGAATTGGAGTTGGAGCTGGAGCTTACATCC TCAGCAGATTTGCACTCAACCATCCAGAGCTTGTGGAAGGCCTTGTGCTCATTAAATG TGACCTTGGCCTAAGGCCTGGATTGACTGGGCAGCTTCCAACCTCTCTGGCCTGACA ACCAATGTTGTGGACATTAATTTGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCA ACCTGGACCTGATCAAACCTACAGAATGCATATTGCCAAGACATCAACCAAGACAA CCTGACGCTCTTCTGAATTCTTACAATGGCGCAGAGACCTGGAGATCGAAAGACCC ATACTGGGCCAAATGATAACAAATCAAAAACATTAAAGTGTCTACTTTTACTGGTGG TAGGGGACAATTCGCTGCACTTGGAGCTGTGGTCAATGCAATTCGCCGTGAACCC TATAAATACAACCTTTGCTAAGATGGCGGACTGTGGGGGACTGCCCGAGGTAGTTCAG CCTGGGAAGCTCACCAGGCCCTTCAAGTACTTTTTCAGGGAATGGGCTACGTCCCGT CTGCAGCATGATCGGCTCGCCGATCACGAACCACTCAACCTCGAGTAGCACTCGG CTCTGGAGAAAGTCCCTTCAGCCGCTCTGTCCACAGCAATCAGTCAGTAGGAACCTAA GAATCCTGTGAGTCCCTGTAGTCTGACAGACACCAAGCATGGAGGTGCTCCTGCT AAGCAGATGCTCCTCCCTGGACCATTGCAAGTCCATCCTTCAATGACCACTCCATA ATATAACATTTTCAAT	
	ORF Start: ATG at 71	ORF Stop: TAA at 1160
	SEQ ID NO: 254	363 aa MW at 39967.8kD
NOV89c, CG56870-03 Protein Sequence	MDELQDVQLTEIKPLLNDKEHDIETHGVVHVITIRGLPKGNRPVILTYHIDIGLNHKSC FNFAFNFDQMGEITQHFVAVCHVDAPGQGEAPSFPTGYQYPTMDELAEMLPVLTHLS LKSIIIGIGVGAGAYILSRFALNHPELVEGLVLINVDPAKGVWDWAASKLSGLTTNV VDI ILAHHFGQEEELQANLDLIQTYRMHIAQDINQDNLQFLNSYNGRRDLEIERPILGQ NDNKSRTLKCSTLLVVGDNSPAUEAVVECNRLNPIINTLLKMDACGGLPQVVQPGKL TEAFKYFLQGMGYVPSASMTLRARSRTHSTSSSLGSGESPFSRVSNTNQSDGTQESCE SPDVDRHQTMVSC	
	SEQ ID NO: 255	1220 bp

NOV89d, CG56870-04 DNA Sequence	ACTTCTTTCTTTCTGTTTCAGAGTTACTGATTATTCTTGAGATTCTCTACTCTCG TTATCTGACCTCATGGATGAACCTCAGGATGTTTTCAGCTCACAGAGATCAAACCACTTC TAAATGATAGAATGGTACAAGAACTTCAGGACTTTGACTGTGAGGAACATGATAT AGAAACAACACTCATGGTGTGGTCCACGTCACTATAAGAGGCTTACCCAAAGGAAACAGA CCAGTTATACTAACATATCATGACATTGGCCTCAACCGTAAATCCTGTTTCAATGCAT TCTTTAACTTTGAGGATATGCAAGAGATCACCCAGCACTTTGCTGTCTGTATGTGGA TGCCCCAGGCCAGCAGGAAGGTGCACCCTCTTTCCCAACAGGGTATCAGTACCCACA ATGGATGAGCTGGCTGAAATGCTGCCTCCTGTTCTTACCCACCTAAGCCTGAAAAGCA TCATTGGAATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTGCACTCAACCA TCCAGAGCTTGTGGAAGGCCTTGTGCTCATTAAATGTTGACCTTGCGCTAAAGGCTGG ATTGACTGGGCAGCTTCCAAACTCTCTGGCCTGACAACCAATGTTGTGGACATTATTT TGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAACCTA CAGAAATGCATATTGCCCAAGACATCAACCAAGACAACCTGCAGCTCTTCTGAATTCC TACAATGGACGCAGAGACCTGGAGATCGAAAGACCCATACTGGGCCAAAATGATAACA AATCAAAAACATTAAAGTGTCTACTTTACTGGTGGTAGGGGACAATTGCGCTGCAGT TGAGGCTGTGATGGCGGACTGTGGGGACTGCCCCAGGTAGTTGAGCCTGGGAAGTTC ACCGAGGCCTTCAAGTACTTTTTCAGGGAATGGGCTACACACCATCTGCCAGCATGA CTCGGCTCGCCCGATCACGAACCCACTCAACCTCGAGTAGCTCGGCTCTGGAGAAAG TCCCTTCAGCCGGTCTGTCAACAGCAATCAGTCAGATGGAATCAAGAATCCTGTGAG TCCCTGTATGTCCTGGACAGACACCAGACCATGGAGGTGTCTGCTAAGCAGATGCTC CTCCCTGGACCATTGCAAGTCCATCCTTCAAATGACCACCTCCATAATATAACATTTCC AT		
	ORF Start: ATG at 71		ORF Stop: TAA at 1148
	SEQ ID NO: 256	359 aa	MW at 39652.2kD
NOV89d, CG56870-04 Protein Sequence	MDELQDVQLTEIKPLLNKNGTRNFQDFDCQEHDIETTHGVVHVITIRGLPKGNRPVIL TYHDI GLNRKSCFNFAFFNFEDMQEITQHFAVCHVDAPGQOEGAPSPFTGYQYPTMDEL AEMLPPVLTHLSLKSIIIGIGVGAGAYILSRFALNHPPELVEGLVLINVDPCAKGWIDWA ASKLSGLTNNVVDIILAHHFQGEELQANLDLIQTYRMHIAQDINQDNLQFLNSYNGR RDLEIERPILGQNDNKSRTLKCSTLLVVGDNSPAUEAVMADCGGLPQVVQPGKFTAEAF KYFLQMGYTPSASMTLRARSRTHSTSSSLGSGESPFSSRVTSNQSDGTQESCESPDV LDRHQTMEVSC		
	SEQ ID NO: 257	970 bp	
NOV89e, CG56870-05 DNA Sequence	ATGGATGAACCTCAGGATGTTGAGCTCACAGAGATCAAACCACTTCTAAATGATAAGA ATGGTACAAGAACTTCCAGGACTTTGACTGTGAGTATCAGTACCCACAATGGATGA GCTGGCTGAAATGCTGCCTCCTGTTCTTACCACCTAAGCCTGAAAAGCATCATTTGGA ATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTGCACTCAACCATCCAGAGC TTGTGGAAGGCCTTGTGCTCATTAAATGTTGACCTTGCGCTAAAGGCTGGATTGACTG GGCAGCTTCCAAACTCTCTGGCCTGACAACCAATGTTGTGGACATTATTTGGCTCAT CACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAACCTACAGAATGC ATATTGCCCAAGACATCAACCAAGACAACCTGCAGCTCTTCTTGAATTCCTACAAATGG GCGCAGAGACCTGGAGATCGAAAGACCCATACTGGGCCAAAATGATAACAAATCAAAA ACATTAAAGTGTCTACTTTACTGGTGGTAGGGGACAATTGCGCTGCAGTTGAGGCTG TGGTGCAATGCAATTCCTGCCTGAACCTTATAAATACAATTTGCTAAAGATGGCGGA CTGTGGGGGACTGCCCCAGGTAGTTGAGCCTGGGAAGCTCACCGAGGCTTCAAGTAC TTTTTGCAGGGAATGGGCTACGTCCCGTCTGCCAGCATGACTCGGCTCGCCGATCAC GAACCACTCAACCTCGAGTAGCCTCGGCTCTGGAGAAAGTCCCTTCAGCCGGTCTGT CACCAGCAATCAGTCAGATGGAATCAAGAATCCTGTGAGTCCCTGATGTCTCTGGAC AGACACCAGACCATGGAGGTGTCTGCTAAGCAGATGCTCTCCCTGGACCATTGCA AGTCCATCCTTCAAATGACCACCTCCATAATATAACATTTTCAT		
	ORF Start: ATG at 1		ORF Stop: TAA at 898
	SEQ ID NO: 258	299 aa	MW at 32956.9kD
NOV89e, CG56870-05 Protein Sequence	MDELQDVQLTEIKPLLNKNGTRNFQDFDCQYQYPTMDELAEMLPVLTHLSLKSIIIG IGVGAGAYILSRFALNHPPELVEGLVLINVDPCAKGWIDWAASKLSGLTNNVVDIILAH HFGQEEELQANLDLIQTYRMHIAQDINQDNLQFLNSYNGRRDLEIERPILGQNDNKS TLKCSLLVVGDNSPAUEAVVECNRLNPINTLLKMDACGGLPQVVQPGKLTAEAFKY FLQMGYVPSASMTLRARSRTHSTSSSLGSGESPFSSRVTSNQSDGTQESCESPDVLD RHQTMEVSC		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 89B.

AAB94494	Human protein sequence SEQ ID NO:15186 - Homo sapiens, 363 aa. [EP1074617-A2, 07-FEB-2001]	1..375 1..363	360/375 (96%) 361/375 (96%)	0.0
AAU31598	Novel human secreted protein #2089 - Homo sapiens, 395 aa. [WO200179449-A2, 25-OCT-2001]	68..374 1..307	282/323 (87%) 286/323 (88%)	e-154
AAB95462	Human protein sequence SEQ ID NO:17944 - Homo sapiens, 286 aa. [EP1074617-A2, 07-FEB-2001]	133..375 44..286	240/243 (98%) 242/243 (98%)	e-138

In a BLAST search of public sequence databases, the NOV89a protein was found to have homology to the proteins shown in the BLASTP data in Table 89E.

Table 89E. Public BLASTP Results for NOV89a				
Protein Accession Number	Protein/Organism/Length	NOV89a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UGV2	NDRG3 protein - Homo sapiens (Human), 375 aa.	1..375 1..375	373/375 (99%) 374/375 (99%)	0.0
Q96PL8	NDR1-RELATED DEVELOPMENT PROTEIN NDR3 - Homo sapiens (Human), 375 aa.	1..375 1..375	372/375 (99%) 373/375 (99%)	0.0
Q9QYF9	NDRG3 protein (Ndr3 protein) - Mus musculus (Mouse), 375 aa.	1..375 1..375	358/375 (95%) 368/375 (97%)	0.0
AAH18504	SIMILAR TO N-MYC DOWNSTREAM REGULATED 3 - Mus musculus (Mouse), 388 aa.	1..375 1..388	359/388 (92%) 368/388 (94%)	0.0
Q96SM2	CDNA FLJ14759 FIS, CLONE NT2RP3003290, MODERATELY SIMILAR TO MUS MUSCULUS NDR1 RELATED PROTEIN NDR3 - Homo sapiens (Human), 363 aa.	1..375 1..363	360/375 (96%) 361/375 (96%)	0.0

PFam analysis predicts that the NOV89a protein contains the domains shown in the Table 89F.

Table 89F. Domain Analysis of NOV89a

Pfam Domain	NOV89a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Orn_Arg_deC_N: domain 1 of 1	62..89	7/33 (21%) 24/33 (73%)	1.9
abhydrolase: domain 1 of 1	87..310	48/239 (20%) 142/239 (59%)	0.0066
Ndr: domain 1 of 1	22..346	210/340 (62%) 311/340 (91%)	3.7e-211

Example 90.

The NOV90 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 90A.

Table 90A. NOV90 Sequence Analysis

Table 90A. NOV90 Sequence Analysis			
	SEQ ID NO: 259	632 bp	
NOV90a, CG59764-01 DNA Sequence	GAAACTATAAAGGGTCCGAACCTCTTTTAAAGGATCCCAATGCATTCTTTGATCCC TCGCCGGTGCACGGTACCACCATCCCAGCTGTGAGGCTGCCATCAACACCCACATCA GCCTGGAGCTCCACGCATCCTATGTGTACCTGTCCATGGCCTTCTACTTCGACCAGGA CGACGCGGCCCTGGAGCACTTTGACCGCTACTTCTGCGCCAGTCGCAAGGAGAAAAGG GAGCACGCCAGGAGCTGATGAGCCTGCAGAACCTGCGCGGTGGCCGCATCTGCCTTC ATGACATCAGGAAGCCAGAGGCCAAGGCTGGGAGAGCGGGCTCAAGGCCATGGAGTG CACCTTCCACCTGGAGAAGAATCAACCAGAGCCTCCTGGAGCTGCACCACTGGCC AGGGAGAACGGCGACCCCCAGCTCTGCGACTTCTTGGAGAACGACTTCTTGAACCAGC AGGCCAAGACCATCAAAGAGCTGGGTGGCTACCTGAGCAACCTGCACAAGATGGGGGC CCCGGAAGCAGGCTGGCAGAGTACCTCTTTAACAAGCTCACCTGGGCGCGACGCAA CCACTTCCTTGAACCAGCAGGCCAAGACCATCAAAGAGATTGGTGGCTACCT		
	ORF Start: ATG at 41	ORF Stop: TGA at 590	
	SEQ ID NO: 260	183 aa	MW at 21159.6kD
NOV90a, CG59764-01 Protein Sequence	MHFFDPSPVRRYHHPSCEAAINTHISLELHASVYVLSMAFYFDQDDAALEHFDYFLR QSQEKREHAQELMSLQNLRRGRI CLHDIRKPEGQGWESGLKAMECTFHLEKNINQSL ELHQLARENGDPQLCDFLENDFLNQAKTIKELGGYLSNLHKMGAPEAGLAEYLFNKL TLGRSEPLP		

Further analysis of the NOV90a protein yielded the following properties shown in

5 Table 90B.

Table 90B. Protein Sequence Properties NOV90a

PSort analysis:	0.4500 probability located in cytoplasm; 0.1400 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV90a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 90C.

Table 90C. Geneseq Results for NOV90a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV90a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU07889	Polypeptide sequence for human hspG34a - Homo sapiens, 221 aa. [WO200166752-A2, 13-SEP-2001]	7..180 45..218	159/174 (91%) 164/174 (93%)	4e-91
AAU07890	Polypeptide sequence for human hspG34b - Homo sapiens, 183 aa. [WO200166752-A2, 13-SEP-2001]	6..177 6..177	125/172 (72%) 149/172 (85%)	6e-70
AAB90804	Human shear stress-response protein SEQ ID NO: 108 - Homo sapiens, 183 aa. [WO200125427-A1, 12-APR-2001]	7..180 7..180	114/174 (65%) 141/174 (80%)	6e-64
AAR71567	Human monocyte growth factor - Homo sapiens, 183 aa. [JP07031482-A, 03-FEB-1995]	7..180 7..180	114/174 (65%) 141/174 (80%)	6e-64
AAU27741	Mouse full-length polypeptide sequence #66 - Mus musculus, 182 aa. [WO200164834-A2, 07-SEP-2001]	6..180 6..180	112/175 (64%) 141/175 (80%)	5e-63

- 5 In a BLAST search of public sequence databases, the NOV90a protein was found to have homology to the proteins shown in the BLASTP data in Table 90D.

Table 90D. Public BLASTP Results for NOV90a				
Protein Accession Number	Protein/Organism/Length	NOV90a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BXU8	Ferritin heavy polypeptide-like 17 - Homo sapiens (Human), 183 aa.	6..177 6..177	125/172 (72%) 149/172 (85%)	2e-69
P29389	Ferritin heavy chain (Ferritin H subunit) - Cricetulus griseus (Chinese hamster), 185 aa.	6..180 10..184	115/175 (65%) 142/175 (80%)	6e-64

A26886	ferritin heavy chain - chicken, 180 aa.	6..180 5..179	112/175 (64%) 142/175 (81%)	1e-63
P08267	Ferritin heavy chain (Ferritin H subunit) - Gallus gallus (Chicken), 179 aa.	6..180 4..178	112/175 (64%) 142/175 (81%)	1e-63
Q95MP7	FERRITIN - Canis familiaris (Dog), 183 aa.	6..180 6..180	112/175 (64%) 143/175 (81%)	2e-63

PFam analysis predicts that the NOV90a protein contains the domains shown in the Table 90E.

Table 90E. Domain Analysis of NOV90a			
Pfam Domain	NOV90a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Bacteriofer: domain 1 of 1	14..159	35/172 (20%) 76/172 (44%)	6.7
ferritin: domain 1 of 1	17..173	92/161 (57%) 138/161 (86%)	4.7e-87

Example 91.

The NOV91 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 91A.

Table 91A. NOV91 Sequence Analysis			
	SEQ ID NO: 261	487 bp	
NOV91a, CG59710-01 DNA Sequence	TGCTGTGCGTTGTCTTTCTTCTCACTCAAGCCTGTGAAATCTCTCTTTCAAGGTTGACAGACTAATGGAGTTGCATTTTAAATATCTGGGTGCAATGCAGGTGGCGGACAAGAAGATTGAAGGGGAAAAACACGACATGGTCCGGCGAGGAGAGATCATCGACAATGACACCGAAGGAGGAGTTCTACCTCCGGCGCCTGGATGCGGGGCTCTTGTCTCCAGCACATCTGCTACATCATGGCCGAGATCTGCAATGCCAATGTCCCCAGATTCCGCAGAGGGTTCAACAGATCCTAAACATGCGAGGAAGCTCCATCAAAATTGTCAAGGCATATCATCAAGGAGTATGTCAGAGAACATCGGGACGGCCGGAGCCCGAGTTCGGGAGAACGAGCAAAAGCCGATCCTGGGCTTGCTGGAGAACTTCTAGAGGCACCTTGGCCCTGCGCATCATGGACTCTCTCAGCTTCCCTCCAGGATCAG		
	ORF Start: ATG at 65	ORF Stop: TAG at 431	
	SEQ ID NO: 262	122 aa	MW at 14385.4kD
NOV91a, CG59710-01 Protein Sequence	MELHFKYLGAMQVADKKIEGEKHDVRRGEIIDNDTEEEFYLRRLDAGLFVLQHICYIMAEICNANVPQIRQVRHQILNMRGSSIKIVRHIIKEYAENIGDGRSPFRENEQKRILGLENF		

Further analysis of the NOV91a protein yielded the following properties shown in Table 91B.

Table 91B. Protein Sequence Properties NOV91a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV91a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 91C.

Table 91C. Geneseq Results for NOV91a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV91a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU28058	Novel human secretory protein, Seq ID No 227 - Homo sapiens, 518 aa. [WO200166689-A2, 13-SEP-2001]	1..122 397..518	122/122 (100%) 122/122 (100%)	1e-66
AAM93729	Human polypeptide, SEQ ID NO: 3689 - Homo sapiens, 563 aa. [EP1130094-A2, 05-SEP-2001]	1..122 442..563	122/122 (100%) 122/122 (100%)	1e-66
AAB63116	Human secreted protein sequence encoded by gene 39 SEQ ID NO:126 - Homo sapiens, 401 aa. [WO200061748-A1, 19-OCT-2000]	1..119 283..401	119/119 (100%) 119/119 (100%)	1e-64
AAU28246	Novel human secretory protein, Seq ID No 603 - Homo sapiens, 360 aa. [WO200166689-A2, 13-SEP-2001]	1..118 197..316	104/120 (86%) 106/120 (87%)	2e-51
ABB21673	Protein #3672 encoded by probe for measuring heart cell gene expression - Homo sapiens, 32 aa. [WO200157274-A2, 09-AUG-2001]	24..55 1..32	32/32 (100%) 32/32 (100%)	1e-11

- 5 In a BLAST search of public sequence databases, the NOV91a protein was found to have homology to the proteins shown in the BLASTP data in Table 91D.

Table 91D. Public BLASTP Results for NOV91a				
Protein Accession Number	Protein/Organism/Length	NOV91a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96KD2	TESTES DEVELOPMENT-RELATED NYD-SP19 - Homo sapiens (Human), 376 aa.	1..122 255..376	122/122 (100%) 122/122 (100%)	5e-66
Q9H7A5	CDNA: FLJ21108 FIS, CLONE CAS05257 - Homo sapiens (Human), 225 aa.	1..122 104..225	121/122 (99%) 121/122 (99%)	5e-65
O62703	P14 - Bos taurus (Bovine), 122 aa.	1..122 1..122	116/122 (95%) 119/122 (97%)	2e-62
Q9CWL8	5730471K09RIK PROTEIN - Mus musculus (Mouse), 563 aa.	1..122 442..563	115/122 (94%) 118/122 (96%)	3e-62
Q9Y3M7	DJ633020.1 (P14L, SIMILAR TO BOS TAURUS P14) - Homo sapiens (Human), 284 aa (fragment).	1..93 192..284	93/93 (100%) 93/93 (100%)	3e-48

PFam analysis predicts that the NOV91a protein contains the domains shown in the Table 91E.

Table 91E. Domain Analysis of NOV91a			
Pfam Domain	NOV91a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 92.

- 5 The NOV92 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 92A.

Table 92A. NOV92 Sequence Analysis		
	SEQ ID NO: 263	6527 bp
NOV92a, CG59754-02 DNA Sequence	<p>CCACAGAGGGGAAATGCCAGCTTCCCTCTCCCTGGGGCTCCGTGCCCCCTCTGATCCA GCCCTTCGAATCCACCCGCTCCATCGGCCAGCTGCTCTACATTCCCTGTGTGGTG TCCTCGGGGGACATGCCCATCCGTATCACCTGGAGGAAGGACGGACAGGTGATCATCT CAGGCTCGGGCGTGACCATCGAGAGCAAGGAATTCATGAGCTCCCTGCAGATCTCTAG CGTCTCCCTCAAGCACAAACGGCAACTATACATGCATCGCCAGCAACGCAGCCGCCACC GTGAGCATTGTGTCTCCAGAACACAGGTTTTTTATTACCTACCACGGCGGGCTGTACA TCTCTGACGTACAGAAGGAGGACGCCCTCTCCACCTATCGCTGCATCACCAAGCACAA GTATAGCGGGGAGACCCGGCAGAGCAATGGGGCACGCCTCTCTGTGACAGACCTGCT GAGTCGATCCCCACCATCTGGATGGCTTCCACTCCAGGAAGTGTGGGCCGGCCACA</p>	

CCGTGGAGCTGCCCTGCACCGCCTCGGGCTACCTATCCCCGCCATCCGCTGGCTCAA
 GGATGGCCGGCCCCCTCCCGGCTGACAGCCGCTGGACCAAGCGCATCACAGGGCTGACC
 ATCAGCGACTTGCGGACCGAGGACAGCGGCACCTACATTTGTAGAGTCAACCAACCT
 TCGGTTCGGCAGAGGCCACAGGCATCCTCATGGTCATGATCCCCCTCATGTGACCT
 GACACCAAAGAAGCTGAAGACCGGCATTGGCAGCACGGTCATCCTCTCTGTGCCCTG
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	ORF Start: ATG at 129	ORF Stop: TAG at 5958	
	SEQ ID NO: 264	1943 aa	MW at 211904.3kD
NOV92a, CG59754-02 Protein Sequence	MPIRITWRKDGQVVISGSGVTIESKEFMSSLISSVSLKHNGNYTCIASNAAATVSIV SPEHRFFITYHGGLYISDVQKEDALSTYRCITKHKYSGETRQSNARLSVTDPAESIP TILDGFHSQEVWAGHTVLEPCTASGYPIPAIRWLKDGRLPLADSRWTKRITGLTISDL RTEDSGTYICEVNTNFGSAEATGILMVIDPLHVTLPKCLKTGIGSTVILSCALTGSP EFTIRWYRNTELVLPEDAISIRGLSNETLLITSAQKSHSGAYQCFATRKQAQDFAI IALEDGTPRIVSSFSSEKVVNPGEQFSLMCAAKGAPPTVTWALDEDEPIVRDQSHRTN YTMSDGTTIISHMNVTPQPIRDGGVYRCTARNLVGSAEYQARINVRGPPSIRAMRNITA VAGRDTLINCRVIGYPYYSIKWYKDALLLPDNRQVVFENGLTKLTDVQKMGDEGEYL CSVLIQPOLSISQSVHVAVKVPLIQPFEPFPASIGQLLYPCVVSSGDMPIRITWRK DGQVVISGSGVTIESKEFMSSLISSVSLKHNGNYTCIASNAAATVSRERQLIVRVPP RFVVPQPNQDGIYGKAGVLNCSVDGYPPPKVMWKHAKGSGNPQQYHPVPLTGRQILP NSSLLIRHVELEDIGYYLCQASNGVGTDISKSMFLTVKIPAMITSHPNNTIAIKGHAK ELNCTARGERPIIRWEKGDVTIDPDRVMRYAIATKDNNGDEVVSTLKLKPADRGDSVF FSCHAINS YGEDRLIQLTVQEPDPPELEIREVKARSMNLRWTRQFDGNSIITGFDI EYKNKSDSWDFKQSTRNISPTINQANIVDLHPASVYSIRMYSFNKIIGRSEPSKLTIS TEEAAPDPGPPMDVTLQPVTSQSIIQVTKAPKKELOQNGVIRGYQIGYRENSPGSNGQYS IVEMKATGDSSEVYTLNLLKFAQYGVVQAFNRAGTGPSSSEINATTLLEVDPSPQPPEN VRALSIITSDVAVISWSEPPRSTLNGVLKGYRVI FWSLYVDGEWGMQNIITTRERVEL RGMKFTNYSVQVLAYTQAGDVRSSVLYIQTKEDVPGPPAGIKAVPSSASSVVVSWL PPTKPNQVIRKYTIFCSPSGSQGPAPSEYETSPQLFYRIAHNLNRQQYLLWVAAVTS AGRNSSEKVTIEPAGKAPAKIISFGGTVTT PPMKDVRLPCNSVGDPAAPVKKWTKDSE DSAI PVSM DGHRLIHTNGTLLLRVKAEDSGYTTCTATNTGGFDTIIVNLLVQVPPDQ PRLTVSKTSASSITLTWIPGDNNGSSIRGFVLQYSVDNSEEWKDFV ISSERSFKLDS LKCGTWYKVLAAKNVSGSGRISEIEAKTHGREPSFSKDQHLFTHINSTHARLNLQ WNNGGCPITAIVLEYRPGKTWAWQGLRANSSGEVFLTELREATWYELMRACNSAGCG NETAQFATLDYDGSTIPPIKSAQGEQDDVKLFTIGCPVILATLGVALLFIVRKKRKE KRLKRLDAKSLAEMLISKNNRSFDTVPKGPPOGPRLHIDI PRVQLLIEDKEGIKQLG DDKATIPVTDAEFSQAVNPQSFTGVSLLHPTLIQSTGPLIDMSDIRPGTNPVSRKNV KSAHSTRNRYSSQWTLTKCAQSTPARTLTSWRTVSGHGVTVTESDSYSASLSQDTD KGRNSMVSTESASSTYELARAYEHAKLEEQLQHAKEITECFISDSSSDQMTGTGNE NADSMTSMSTPSEPGICRFTASPPKPDADRGNVAVPIPHRANKSDYCNLPYAKSE AFFRKADGREPCVVPVPPREASIRNLARTYHTQARHLTLDPAKSLGLPHGPAPAAAST ATLPQRTLAMPAPPAGTAPPAGPTPAEPPTAPSAAPPAPSTEP PRAGGPHTKMGSSR DSLLEMSTSGVGRSQKQAGAGYSKSYTLV		
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NOV92b, CG59754-01 DNA Sequence	CCACAGAGGGGAAATGCCAGCTTCCCTCTCCCTGGGGCTCCGTGCCCCCTCTGATCCA GCCCTTCGAATCCCACCCGCCTCCATCGGCCAGCTGCTCTACATTCCCTGTGTGGTG TCCTCGGGGGACATGCCCATCCGTATCACCTGGAGGAAGGACGGACAGGTGATCATCT CAGGCTCGGGCGTGACCATCGAGAGCAAGGAATCATGAGTCCCTGCGAGATCTCTAG CGTCTCCCTCAAGCACAAACGGCAACTATACATGCATCGCCAGCAACGCAGCCGCCACC GTGAGCATTGTGTCTCCAGAACACAGGTTTTTTATTACCTACCACCGCGGGCTGTACA TCTCTGACGTACAGAAGGAGGACGCCCTCTCCACCTATCGCTGCATCACCAAGCACAA		

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	ORF Start: ATG at 129	ORF Stop: TAA at 5853	
	SEQ ID NO: 266	1908 aa	MW at 208575.3kd
NOV92b, CG59754-01 Protein Sequence	MPIRITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCIASNAAATVSIV SPEHRFFITYHGGLYISDVQKEDALSTYRCITKHKYSGETRQSNARLSVTDPAESIP TILDGFHSQEVWAGHTVLPCTASGYPIPAIRWLKDRPLPADSRWTKRITGLTISDL RTEDSGTYICEVTNTFGSAEATGILMVIDPLHVTLPKKLKTGIGSTVILSCALTGSP EFTIRWYRNTLVLPDEAISIIRGLSNETLLITSAQKSHSGAYQCFATRKQAQDFAI IALEDGTPRIVSSFSSEKVNPGEQFSLMCAAGAPPTVTWALDDEPIVRDGSHTNR YTMSDGTTIISHMNVTPQPIRDGGVYRCTARNLVGSAEYQARINVRGPPSIRAMRNITA VAGRDTLINCRVIGYPYYSIKWYKDALLLPDNRQVVFENGTLKLTVDVQKMGDEGEYL CSVLIQPOLSISQSVHVAVKVPPLIQPFEPFASIGQLLYIPCVS SSGDMPIRITWRK DGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCIASNAAATVSRERQLIVRVP RFVVPNNQDGIYKAGVLNCSVDGYPPPKVMWKHAKGSGNPQQYHPVPLTGRIQLP NSSLLIRHVLEEDIGYYLQASNGVGTDISKSMFLT VKIPTILDGFHSQEVWAGHTVE LPCTASGYPIPAIRWLKDRPLPADSRWTKRITGLTISDLRTEDSGTYICEVTNTFGE ATGILMVIIEPPDPELEIREVKARSMNLRWTRQRPDGNISITGFDIEYKNKSDSWDF KQSTRNISPTINQANIVDLHPASVYSIRMYSFNKIGRSEPSKELTISTEEASAPDGGP MDVTLQPVTSQSIQVTWKQAPKKEQLQNGVIRGYQIGYRENSPGSNGQYSIVEMKATGD SEVYTLNLLKFAQYGVVQAFNRAGTGPSSSEINATTLVDVPSQPPENVRALSITSD VAVISWSEPPRSTLNGVLKGYRVI FWSLYVDGEWGMQNIITTRERVELRGMKFTNY SVQVLAYTQAGDVRSSVLYIQTKEDVPGPPAGIKAVPSSASSVVVSWLPPTKPNVGI RKYTIFCSSPAPQAPSEYETSPEQLFYRIAHNRGQQYLLWVAAVTSAGRGNSSSEKVT IEPAGKAPAKIISFGGTVTPWMKDVRLPCNSVGDPAVAVKWTKDSEDSAPVSMGDH RLIHTNGTLLLRVKAEDSGYYTCTATNTGGFDTIIVNLLVQVPPDQPRLTVSKTSAS SITLTIWIPGDNNGSSIRGFVLQYSVDNSEEWDVFISSSERSFKLDSLKCGTWYKVKL AAKNSVSGRISEIEAKTHGREPSFKDQHLFTHINSTHARLNQGWNNGGCPITAI VLEYRPGKTAWQGLRANSSGEVFLTELREATWYELRMACNSAGCNETAQFATLDY DGSTIPPIKSAQGEQDDVKLFTIGCPVILATLGVALLFIVRKKRKEKRLKRLRDAKS LAEMLISKNNRSFDTPVKGPPQGPRLHIDI PRVQLLIEDKEGIKQLGEDKATIPVTD EFSQAVNPQSFCQVSLHHPTLIQSTGPLIDMSDIRPGTDPVSRKNVKSASHSTRNYS SQWTLTKCQASTPARTLSDWRTVGSQHGVTVESDSYSASLSQDQDKGRNSMVSTES ASSTYEELARAYEHAKLEEQLQAKFEITECFISDSSDQMTGTNENADSMSTSMSTES SEPGICRFTASPPKPDADRLMLVPGAHLPPQSIHVAVYVRISFLLNKGGGDLASDL SSGRACSEPRSRGTRPPTLVALTPSSSTCEAGDPRWGQGRKGRDSIMREGHRMEEAK PRERQTSGETEVHMEGEAGELGSGSGSEGVGEPAPSRHGGTPHTPSQGPPPLC		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 92B.

Table 92B. Comparison of NOV92a against NOV92b.		
Protein Sequence	NOV92a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV92b	1..1771 1..1760	1663/1773 (93%) 1681/1773 (94%)

Further analysis of the NOV92a protein yielded the following properties shown in Table 92C.

Table 92C. Protein Sequence Properties NOV92a	
PSort analysis:	0.7000 probability located in plasma membrane; 0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.2000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV92a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 92D.

Table 92D. Geneseq Results for NOV92a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV92a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU28091	Novel human secretory protein, Seq ID No 260 - Homo sapiens, 1744 aa. [WO200166689-A2, 13-SEP-2001]	200..1943 1..1744	1744/1744 (100%) 1744/1744 (100%)	0.0
AAM78713	Human protein SEQ ID NO 1375 - Homo sapiens, 1744 aa. [WO200157190-A2, 09-AUG-2001]	200..1943 1..1744	1744/1744 (100%) 1744/1744 (100%)	0.0
AAM39040	Human polypeptide SEQ ID NO 2185 - Homo sapiens, 1744 aa. [WO200153312-A1, 26-JUL-2001]	200..1943 1..1744	1744/1744 (100%) 1744/1744 (100%)	0.0
AAW42086	Human Down syndrome-cell adhesion molecule DS-CAM1 -	44..1778 154..1890	1085/1745 (62%) 1357/1745 (77%)	0.0

	[WO9817795-A1, 30-APR-1998]			
AAW42087	Human Down syndrome-cell adhesion molecule DS-CAM2 - Homo sapiens, 1571 aa. [WO9817795-A1, 30-APR-1998]	44..1457 154..1564	890/1416 (62%) 1109/1416 (77%)	0.0

In a BLAST search of public sequence databases, the NOV92a protein was found to have homology to the proteins shown in the BLASTP data in Table 92E.

Table 92E. Public BLASTP Results for NOV92a				
Protein Accession Number	Protein/Organism/Length	NOV92a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL57166	DOWN SYNDROME CELL ADHESION MOLECULE DSCAML1 - Homo sapiens (Human), 2053 aa.	44..1943 155..2053	1889/1900 (99%) 1892/1900 (99%)	0.0
Q9ULT7	KIAA1132 PROTEIN - Homo sapiens (Human), 1822 aa (fragment).	122..1943 1..1822	1822/1822 (100%) 1822/1822 (100%)	0.0
O60469	Down syndrome cell adhesion molecule precursor (CHD2) - Homo sapiens (Human), 2012 aa.	44..1943 154..2012	1123/1920 (58%) 1410/1920 (72%)	0.0
Q9ERC8	DOWN SYNDROME CELL ADHESION MOLECULE - Mus musculus (Mouse), 2013 aa.	44..1943 154..2013	1119/1921 (58%) 1405/1921 (72%)	0.0
AAL57167	DOWN SYNDROME CELL ADHESION MOLECULE DSCAM - Rattus norvegicus (Rat), 2013 aa.	44..1943 154..2013	1119/1921 (58%) 1405/1921 (72%)	0.0

5 PFam analysis predicts that the NOV92a protein contains the domains shown in the Table 92F.

Table 92F. Domain Analysis of NOV92a			
Pfam Domain	NOV92a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ig: domain 1 of 10	1..48	12/49 (24%) 38/49 (78%)	2.7e-05
ig: domain 2 of 10	72..90	8/19 (42%) 14/19 (74%)	85
ig: domain 3 of 10	130..186	22/60 (37%) 46/60 (77%)	2.1e-14
ig: domain 4 of 10	219..278	16/63 (25%) 44/63 (70%)	4.9e-09
ig: domain 5 of 10	312..377	14/69 (20%) 50/69 (72%)	1.5e-07
ig: domain 6 of 10	409..467	12/61 (20%) 41/61 (67%)	4.8e-05
ig: domain 7 of 10	500..561	17/64 (27%) 49/64 (77%)	3.2e-11
ig: domain 8 of 10	594..659	19/69 (28%) 47/69 (68%)	9.4e-07
ig: domain 9 of 10	693..759	9/70 (13%) 47/70 (67%)	7.9e-06
fn3: domain 1 of 6	777..864	22/89 (25%) 65/89 (73%)	3e-16
fn3: domain 2 of 6	876..968	33/93 (35%) 68/93 (73%)	3.1e-16
fn3: domain 3 of 6	980..1069	26/93 (28%) 69/93 (74%)	2.9e-16
fn3: domain 4 of 6	1081..1167	24/88 (27%) 64/88 (73%)	3.7e-17
ig: domain 10 of 10	1194..1255	17/65 (26%) 46/65 (71%)	4.3e-09
fn3: domain 5 of 6	1274..1357	30/86 (35%) 67/86 (78%)	1.2e-18
fn3: domain 6 of 6	1371..1453	27/86 (31%) 53/86 (62%)	0.045

Example 93.

The NOV93 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 93A.

Table 93A. NOV93 Sequence Analysis			
	SEQ ID NO: 267	1272 bp	
NOV93a, CG59800-01 DNA Sequence	AGAGCCTGGTATGCAGGAGGTGCTCTGTAATACCTGCCCATACATACCCGCCCCAT ACATACCCACCCCATACATACCCACCCCATACATACCTGCCCTGTCCATACCTGCCCC CTACATACCTGCCCGCTCCATACCTGCCCCCTACATACCTGCCCGCTCCATACCTGCC CCCTACATACCTGCTCTGTCTATACCTGTGGCTAGGACTGTGGCCTTGCTTCTTAGCC GCTCAGAGGCTGCCCTCCTCCTCTGCAGAGTGGCGGTGGTAGCAGGGCTTCCCGCGCG CGATGCTGCTCGTGGCCCTGGTGTCTCGCGCCTACTGCCTCTGCGCCCTCCCGCGCG CTGCCCGCGCGGCCCGCGCCCGCGCGCGCCCGCGCCCTCCGAGCCGTCCAGC TCCGTCCACCGCCCGGAGCACCCGGCCTGCCTTTGGCCAGCGGTCCCGGCCGCGCGG GCTTCCCGCAAGCGCTCATCGTTGGCGTGAAGAAGGGCGGCACGCGCCCTGTGGAG GTTTCTGCGGCTGCACCCGACCTCCGCGCGCTGGGCTCTGAGCCCCACTTCTTCGAG AGGTGCCCCGACCGCGGCTCGCTGGTCCCGGAGTCTGATGCCCGAACCCCTGGATG GGCAGATCACCATGGAGACGACCCGGGCTACTTCGTGACGCGAGAGGCCCGCCGCG CATCCACGCCATGTCCCGGACACGAAGCTGATCGTGGTGGTGCAGAACCCCGTGACC CGGGCCATCTCCGACTAGGCCAGACGCTCTCCAAGACCCCGGCTGCCAGCTTCC GCGCCCTGGCCTTCCGCCACGGCCTGGGCCCCGTGGACACAGCCTGGAGCGCCGTCCG CATCGGCCTGTACGCCAGCACCTGGACCACTGGCTGCGCTACTTCCCCCTGTCCCA TTCCTGTTCTGTACGCGGGAGCGTCTGGTCAGCGACCCGCGCGGAGAGGTCCGCGCG TGCAGGACTTCTGGGCTGAAACGGGTCTGTACGGACAAGCACTTCTACTTCAACGC CACCAAGGGCTTCCCCTGCCTCAAGAAGGCCAGGGCGGACGCGTCCCCGTGCCTG GGCAAGTCCAAGGGCGGCCACACCCACGCGTGCCCCAGGCCGTGGTCCGCGCCTGC AGGAGTTCTACCGGCCCTTCAACCGCAGGTTCTACCAGATGACGGGCCAGGACTTCGG CTGGGGCTGAGCGGCACCTGGGGATGCTCAGCACCTTGATTGACACCCGCTCG		
	ORF Start: GAG at 2	ORF Stop: GGC at 1217	
	SEQ ID NO: 268	405 aa	MW at 43994.8kD
NOV93a, CG59800-01 Protein Sequence	MQEVLCKYLPHTYPPHTYPPHTYLPHTYLPHTYLPHTYLPHTYLPHTYLPHTYLPHTY LLCLYLWLGLWPCFLAAQSLPPLQSGGSRASAPMLLVALVLGAYCLCALPGRCP AARAPAPAPAPSEPPSSVHRPAPGLPLASGPGRRRFPQALIVGVKKGTRALLEFLR LHPDXRALGSEXHFFDRXXXXGLXWXRSLMPRTLQDQITMEXTPYFVTRAPRIHA MSPDTKLIIVVRNPVTRAISDXXQTLSTKPLPSFRALAFRHGLGPDVTAWSAVRIGL YQHLHDWLRYPPLSHFLFVSGERLVSDDPAGEVGRVQDFLGLKRVVTDKHFYFNATKG FPCCLKAQQGSRPRCLGKSKGRPHRVPQAXVRRLLQEFYRPFNRRFYQMTGQDFGWG		

Further analysis of the NOV93a protein yielded the following properties shown in Table 93B.

Table 93B. Protein Sequence Properties NOV93a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 7 and 8

A search of the NOV93a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 93C.

Table 93C. Geneseq Results for NOV93a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV93a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB95507	Human protein sequence SEQ ID NO:18067 - Homo sapiens, 390 aa. [EP1074617-A2, 07-FEB-2001]	31..253 11..237	121/229 (52%) 146/229 (62%)	4e-55
AAY17066	Human 3-OST-3B protein - Homo sapiens, 390 aa. [WO9922005-A2, 06-MAY-1999]	31..253 11..237	121/229 (52%) 146/229 (62%)	4e-55
AAB70115	Human 3-OST-3B - Homo sapiens, 391 aa. [WO200113910-A2, 01- MAR-2001]	31..253 11..238	121/230 (52%) 146/230 (62%)	9e-54
AAB70114	Murine 3-OST-3B - Mus sp, 391 aa. [WO200113910-A2, 01-MAR- 2001]	31..253 11..238	119/231 (51%) 147/231 (63%)	2e-51
AAU12275	Human PRO5004 polypeptide sequence - Homo sapiens, 367 aa. [WO200140466-A2, 07-JUN- 2001]	86..253 45..214	102/170 (60%) 117/170 (68%)	9e-48

In a BLAST search of public sequence databases, the NOV93a protein was found to have homology to the proteins shown in the BLASTP data in Table 93D.

Table 93D. Public BLASTP Results for NOV93a

Protein Accession Number	Protein/Organism/Length	NOV93a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96QI5	C439A6.1 (NOVEL PROTEIN SIMILAR TO HEPARAN SULFATE (GLUCOSAMINE) 3-O- SULFOTRANSFERASES) - Homo sapiens (Human), 381 aa (fragment).	85..253 61..229	160/169 (94%) 162/169 (95%)	2e-89
Q96RX7	HEPARAN SULPHATE D- GLUCOSAMINYL 3-O- SULFOTRANSFERASE-3B LIKE - Homo sapiens (Human), 311 aa.	95..253 1..159	153/159 (96%) 155/159 (97%)	1e-85
Q9Y662	HEPARAN SULFATE D- GLUCOSAMINYL 3-O-	31..253 11..237	121/229 (52%) 146/229 (62%)	1e-54

	2.8.2.23) - Homo sapiens (Human), 390 aa.			
Q9QZS6	D-GLYCOSAMINYL 3-O-SULFOTRANSFERASE-3B - Mus musculus (Mouse), 390 aa.	31..253 11..237	119/230 (51%) 147/230 (63%)	3e-52
Q9Y278	HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-2 (EC 2.8.2.23) - Homo sapiens (Human), 367 aa.	86..253 45..214	102/170 (60%) 117/170 (68%)	3e-47

PFam analysis predicts that the NOV93a protein contains the domains shown in the Table 93E.

Table 93E. Domain Analysis of NOV93a			
Pfam Domain	NOV93a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 94.

The NOV94 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 94A.

Table 94A. NOV94 Sequence Analysis		
	SEQ ID NO: 269	2949 bp
NOV94a, CG59761-01 DNA Sequence	<p> <u>GTCCGCTCCGGGCGCGGAGCCGAGCCGCGGAGATGGGGGCGGCGCGCGCGCGC</u> <u>CCCCGCCGGGTCCCGCCCGCGCGCTGCCGCTGAGCGCATGGGCGCGGACCGCGCGC</u> <u>GCCGCTCCGGGAGCCGGGCGGGGTCCCGCACCAACCGCGCGCGGACAGATTGATT</u> <u>CACCTTGAGCTGTAAGTACTGATGTATTAGGGTGACGCTCATTGTTTCATTGACGC</u> <u>AGAGTCCCAAAATGAATATCCAAGAGCAGGGTTTCCCCTGGACCTCGGAGCAAGTTT</u> <u>CACCGAAGATGCTCCCGACCCCACTGCTGGTGAGGAGGAGAACTGGTGTCACA</u> <u>GACCGAGGCGCGCCAGCTACAGTTTCTGCTCCGGGAAAGGTGTTGGCATTAAAGGTG</u> <u>AGACTTCGACGGCCACTCCGAGGCGCTCGGATCTGGACCTGGGGTATGAGCCTGAGGG</u> <u>CAGTGCTCCCCACCCACCATACTGAAGTGGGCTGAGTCACTGCATTCCCTGCTG</u> <u>GATGACCAAGATGGGATAAGCCTGTTCCAGGACTTTCCTGAAGCAGGAGGGCTGTGCCG</u> <u>ACTTGCTGGACTTCTGGTTTGCTGCACTGGCTTCAGGAAGCTGGAGCCCTTGACTC</u> <u>GAACGAGGAGAAGAGGCTGAAGCTGGCGAGAGCCATCTACCGAAAGTACATTCTTGAT</u> <u>AACAATGGCATCGTGTCCCGGAGACCAAGCCAGCCACCAAGAGCTTCATAAAGGGCT</u> <u>GCATCATGAAGCAGCTGATCGATCCTGCCATGTTTGACCAAGCCAGACCGAAATCCA</u> <u>GGCCACTATGGAGGAAAACCTATCCCTCCTTCTTAAGTCTGATATTTATTGGAA</u> <u>TATACGAGGACAGGCTCGGAGAGCCCAAGTCTGTAGTGACAGAGCTCTGGGTCAG</u> <u>GGACAGGGAAGGCATATCTGGATACTGCCGACCTTAATGAAGATGAGGAATGGAA</u> <u>GTGTGACCAAGGATGGATGAGGACGATGGCAGAGACGCTGCTCCCCCGGAAGACTC</u> <u>CCTCAGAAGCTGCTCCTGGAGACAGCTGCCCCGAGGGTCTCCTCCAGTAGACGGTACA</u> <u>GCGAAGGCAGAGAGTTAGGTATGGATCCTGGCGGAGCCAGTCAACCCCTATTATGT</u> <u>CAATGCCGGCTATGCCCTGGCCCCAGCCACCAAGTCCCAACGACGAGCAGCAGAGC</u> <u>CTGTCCAGCATGCAGACACCTGTCCCTCACGGACAGCAGCGTGGATGGGATCCCCC</u> <u>CATACAGGATCCGTAAGCAGCACCGCAGGAGATGCAGGAGAGCGTGCAAGTCAATGG</u> <u>GCGGGTGCCCCCTACCTCACATTCCCCGCACGTACCGGGTGCCGAAGGAGGTCGCGTG</u> <u>GAGCCTCAGAAGTTCGCGGAGGAGCTCATCCACCGCTGGAGGCTGTGCAGCGCACGC</u> <u>GGGAGGCCGAGGAGAAGCTGGAGGAGCGGCTGAAGCGCGTGCGCATGGAGGAGGAAGG</u> <u>TGAGGACGGCGATCCATCATCAGGGCCCCAGGGCCGTGTACAAGTGCCTCCCGCC</u> <u>CCCGCTTGGCACCACTTCCCGCCCCCGCTGTGTTGGACATGGGCTGTGCCGGGCTCC</u> </p>	

	GGGATGCACACGAGGAGAACCCTGAGAGCATCCTGGACGAGCACGTACAGCGTGTGCT GAGGACACCTGGCCGCCAGTCCGCTGGGCTGGCCATCGCTCCCCGACAGTGGGCAC GTGGCCAAGATGCCAGTGGCACTGGGGGGTGGCGCTCGGGGCACGGGAAGCACGTAC CCAAGTCAGGGGGCAAGCTGGACGCGGCCGGCTGCACCACCAACGACAGCTCCACCA CCAGTCCACACAGCACAGCCCGGCCAAGGAGCAGGTGGAGGCCGAGGCCACCCGC AGGGCCAGAGCAGCTTCGCCTGGGGCTGGAACCACACAGCCATGGGGCAAGGTCCC GAGGCTACTCAGAGAGTGTGGCGCTGCCCCCAACGCCAGTGTATGGCCTCGCCACAG TGGGAAGGTGGGCGTGGCGTGCAAAAGAAATGCCAAGAAGGCCGAGTCGGGGAAGAGC GCCAGCACGAGGTGCCAGGTGCCTCGGAGGATGCGGAGAAGAACCAGAAATCATGC AGTGGATCATTGAGGGGAAAGGAGATCAGCAGGCACCGCAGGACCGGCCACGGGTC TTCGGGACGAGGAAGCCACAGCCCCATGAGAACTCCAGACCCTTGTCCCTTGAGCAC CCCTGGGCGGGCCCTCAGCTCCGGACCTCGGTGCAGCCCTCCCACCTCTTCATCCAG ACCCACCATGCCACCCACCCAGCTCCCAACCCCTAACCAGCTGGAGGAGGCGCG CCGACGTCTGGAGGAGGAAGAAAGAGAGCCAGCCGAGCACCCCTCCAAGCAGAGGTAT GTGCAGGAGGTTATGCGCGGGGACGCGCTGCGTCAAGGCGCGCTGCGCGCCGCTGC TGACGTGTACACGCGGTGTCGGACATGGAGCTCTCCGAGACAGAGACAGATCGCA GAGGAAGGTGGGCGGCGGAGTGCCAGCCGTGTGACAGCATCGTTGTGGCGTACTAC TTCTGCGGGGAACCCATCCCTACCGCACCTGGTGAGGGCGCGCTGTACACCTGG GCCAGTTCAAGGAGCTGTGACCAAAAGGGCAGCTACAGATACTACTTCAAGAAAGT GAGCGACGAGTTTACTGTGGGTGGTGTGTTGAGGAGGTTTCAGAGGACGAGGCCGTC CTGCCGCTCTTTGAGGAAGAATCATCGGCAAGTGAGAGGTTGAGTATAGGCTG GTGGGCTGCGCGCTGTGCCAGGCGAGGCCCTTGGCGGGCACGGGTGTACGGCCAGGC AGATGACCTCGTACTCAGGAGCCCGATGGGGAACAGTGTGGGTGTACC		
	ORF Start: ATG at 97		ORF Stop: TGA at 2833
	SEQ ID NO: 270	912 aa	MW at 101118.1kD
NOV94a, CG59761-01 Protein Sequence	MGPDRAPLREPGPSRHHRRARDRLIHFGAVSTDVLGCSAHCSLTQSPKMNIQEQGFP LDLGASFTEDAPRPVPVPEEGELVSTDPRPASYSFCSGKGVGIGKETSTATPRRSDLD LGYEPESASPTPPYLKWAESLHSLDDQDQISLFRFTLKQEGCADLLDFWFACTGFR KLEPCDSNEEKRLKLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIKQLIDPAMFD QAQTEIQATMEENTYPSFLKSDIYLEYTRTGSSEPKVCSQSSSGGTGKGISGYLPTL NEDEEWKCDQDMDDEDDGRDAAPPGRLPQKLLLETAAPRVSSRRYSEGREFFRYGSWRE PVNPIYVYVAGYALAPATSANDSEQQLSSDADTLSTDSVDGI PPYRIRKQHRREM ESVQVNGRVPLPHIPRTYRVPKEVRVFPQFAEELIHRLEAVQRTREAEKLEERLKR VRMEEEGEDGDPSSGPPGPKHLPPAPAWHHFPPRLCWTWACAGLRDAHEENPESILD EHVQRLVLRTPGRQSPGPGHRS PDSGHVAKMPVALGGAASGHGKHPKSGAKLDAAGLH HHRHVHHVHHSTARPKQVEAEATTRAQSSFAWGLEPHSHGARSRGYSESVAAPNA SDGLAHSGKVGAVACKRNKAESGKSASTEVPGASEDAEKNQKIMQWIEGEKEISR RRTGHGSSGTRKPKPHNSRPLSLEHPWAGPQLRTSVQPSHLFIQDPTMPHPAPNPL TQLEEARRRLEEEKRA SRAPSKQRYVQVMRRGRACVRPACAPLVHVPVAVSDMELS ETETRSQRKVGGSQAQPCDSIVVAYYFCGEP I PYRTLVRGRAVTLGQFKELLTKKGSY RYYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVERVD		

Further analysis of the NOV94a protein yielded the following properties shown in Table 94B.

Table 94B. Protein Sequence Properties NOV94a	
PSort analysis:	0.6000 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV94a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 94C.

Table 94C. Geneseq Results for NOV94a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV94a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG68175	Wnt signaling protein SEQ ID NO:91 - Homo sapiens, 900 aa. [WO200177327-A1, 18-OCT-2001]	13..912 1..900	898/900 (99%) 898/900 (99%)	0.0
AAW96264	Human axin - Homo sapiens, 900 aa. [WO9902179-A1, 21-JAN-1999]	13..912 1..900	898/900 (99%) 898/900 (99%)	0.0
AAW96265	Murine axin - Mus musculus, 992 aa. [WO9902179-A1, 21-JAN-1999]	6..912 84..992	781/914 (85%) 820/914 (89%)	0.0
AAW93569	Human conductin protein - Homo sapiens, 840 aa. [WO9911780-A2, 11-MAR-1999]	60..912 12..840	378/892 (42%) 506/892 (56%)	e-171
AAW93570	Human conductin protein - Homo sapiens, 840 aa. [WO9911780-A2, 11-MAR-1999]	60..912 12..840	378/892 (42%) 506/892 (56%)	e-171

In a BLAST search of public sequence databases, the NOV94a protein was found to have homology to the proteins shown in the BLASTP data in Table 94D.

Table 94D. Public BLASTP Results for NOV94a

Protein Accession Number	Protein/Organism/Length	NOV94a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O15169	Axin 1 (Axis inhibition protein 1) (hAxin) - Homo sapiens (Human), 900 aa (fragment).	13..912 1..900	898/900 (99%) 898/900 (99%)	0.0
Q96S28	AXIN - Homo sapiens (Human), 862 aa.	50..912 1..862	858/863 (99%) 858/863 (99%)	0.0
O35625	Axin 1 (Axis inhibition protein 1) (Fused protein) - Mus musculus (Mouse), 992 aa (fragment).	6..912 84..992	781/914 (85%) 820/914 (89%)	0.0
O70239	Axin 1 protein (Axis inhibition protein 1) (rAxin) - Rattus norvegicus (Rat), 893 aa (fragment).	6..912 21..893	756/914 (82%) 793/914 (86%)	0.0

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T08422	negative regulator axin [imported] - rat, 832 aa.	46..912 2..832	726/872 (83%) 760/872 (86%)	0.0
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PFam analysis predicts that the NOV94a protein contains the domains shown in the Table 94E.

Table 94E. Domain Analysis of NOV94a			
Pfam Domain	NOV94a Match Region	Identities/ Similarities for the Matched Region	Expect Value
RGS: domain 1 of 2	137..198	23/75 (31%) 44/75 (59%)	5.6e-06
RGS: domain 2 of 2	231..260	13/30 (43%) 21/30 (70%)	0.12
TP2: domain 1 of 1	585..709	33/147 (22%) 52/147 (35%)	9.6
DIX: domain 1 of 1	830..912	40/86 (47%) 83/86 (97%)	5.6e-44

Example 95.

The NOV95 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 95A.

Table 95A. NOV95 Sequence Analysis		
	SEQ ID NO: 271	2223 bp
NOV95a, CG59756-01 DNA Sequence	TTGCAGGCATCACCCACGCCCTCTGCACCCACGCTGGAGGACGGGGAGGTTGTCAGGG GCTATGATGAGATGAGTGGGGGCCGCTTCGACTTTGATGATGGAGGGCGTACTGCGG GGGCTGGGAGGGGGAAAGGCCATGGGCATGGACTGTGCACAGGCCCAAGGGCCAG GGCGAATACTCTGGCTCTCTGGAACCTTTGGCTTTGAGGTGGCAGGTGTCTACACCTGGC CCAGCGGAAACACCTTTGAGGGATACTGGAGCCAGGGCAAACGGCATGGGCTGGGCAT AGAGACCAAGGGGCGCTGGCTCTACAAGGGCGAGTGGACACATGGCTTCAAGGGACGC TACGGAATCCGGCAGAGCTCAAGCAGCGGTGCCAAGTATGAGGGACACCTGGAACAATG GCCTGCAAGACGGCTATGGCACCAGACCTATGCTGATGGAGGGACGTACCAAGGCCA GTTACCAACGGCATGCGCCATGGCTACGGAGTACGCCAGAGCGTGCCTACGGGATG GCCGTGGTGGTGCCTCGCCGCTGCGCACGTGCTGCTCCCTGCGCAGCGAGCACA GCAACGGCAGCGTGGCCCCGGACTCTCCCGCTCGCCGGCTCCGACGCGCCCGCGCT GCCCTCGCCGCCATCCCGCTGGCGGCTTCGCGCTCAGCTCCTGGCCAATGCCGAG GCGGCCGCGCGGGCGCCCAAGGGCGCGGCTCTTCCAGCGGGGCGCGCTGCTGGGCA AGCTGCGCGCGCAGAGTTCGCGCACGTCCGTGGGTAGCCAGCGCAGCGGTGTGAGCTT CCTTAAGAGCGACCTCAGCTCGGGCGCCAGCGACGCGCGTCCACCGCCAGCCTGGGA GAGGCCGCGCAGGGCGCGCAGGAGCGCACCTTCGAGGCGGATATCGGACGCAACCA CCACCGAGACCTACATGGGCGAGTGAAGAACGACAAACGCTCGGGCTTCGGCGTGAG CGAACGCTCCAGTGGCTCCGCTACGAGGGCGAGTGGCTGGACAACCTGCGCCACGGC TATGGCTGCACACGCTGCGCGACGCCACCGCGAGGAGGGCAAGTACCGCCACAACG TGCTGGTCAAGGACACCAAGCGCCGATGTGACAGCTCAAGAGCAACAGGTCCGCCA GAAAGTGGAGCACAGTGTGGAGGGTCCCCAGCGCGCGCTGTATCGCGCGCCAGAAG GCCGAGATTGCCGCTCCAGGACAAAGCCACGCCAAGGCCAAAGCTGAGGCAGCGGAAC AGGCCGCGCTGGCTGCCAACAGGAGTCCAACATTGCTCGACTTTGGCCAGGGAGCT GGCTCCGACTTCTACAGCCAGGTCCGGAATATCAGAAGCGCGCGCTGTGACGAGG ATCTGGAGAACTCGGAGAGCTGTGGAGCCCCCGACCGGGGCGCGCGCGCAGCGG GCCTCCACAGCGCGCCGCGAGAGCCCGAGCTGCACGAGCGTGAGACCCCTCGGGC CGAGGGTGGCTCCCCGTACCGGCCGGGACGCCCCCGCAGCCCAAGCGGCCAGGCCG GGGTGTCAAGGACGCGCTGTGAGCCAGGCGCTGGAACGCGCAGCCAGCGCGGTG AGGCGAGCGGTGAGTCACTCCGTCCGAGGGCGGGCGCGCGCAGCCCGCGCGCTCC	

	AGCCACCGAGCGCATGGCCATCGAGGCTCTGCAGGCACCGCTGCGCCGTCGCGGGAG CCGGAGGTGGCGCTTACCAGGGCTACCACAGCTATGCTGTGCGCACACGCGCGCCG AGCCCCACCTTTGAGGACCAGCCGAGCCGAGGTCTCCGGTCCGAGTCCGCGCC CTCGTCCCGGCCACCGCCCGCTGCAGGCCCCACGCTCCGAGGCCCCGAGCCTGCA CGCGAGACCCCGCCAAGCTGGAGCCCAAGCCATCATCCCCAAGCCGAGCCAGGG CCAAGGCCCGCAAGACTGAGGCTCGAGGGCTGACCAAGGCGGGGCCAAGAAGAAGGC GCGGAAGGAGGCCGACTGGCGGCAGAGGCGGAGGTGGAGGTGGAGAGGTCCCCAAC ACCATCCTCATCTGCATGGTGTATCCTGCTGAACATCGGCCTGGCCATCCTCTTTGTT ACCTCCTGACCTGACCGTTCGCTTACCAGGTGCAGCCAGCTGGCTGGAGGAGGGGTTGG GGGCGAGGAGCCCTGGGG		
	ORF Start: ATG at 70		ORF Stop: TGA at 2158
	SEQ ID NO: 272	696 aa	MW at 74220.7kD
NOV95a, CG59756-01 Protein Sequence	MSGGRFDDGGAYCGWEGGKAHGHGLCTGPKGQGEYSGSWNFGEVAGVYTWPSGN TFEGYWSQGRHGLGIETKGRWLYKGEWTHGFKGRYGIHQSSSGAKYEGTWNGLQD GYGTETYADGGTYQGQFTNGMRHGYGVRSVPYGMVVRSPRLTSLSSLRSEHSNGT VAPDSPASPASDGPALPSPAIPRGGFALSLLANAEAAARAPKGGGLFQRGALLGKLRR AESRTSVGQSRVSVFLKSDLSSGASDAASTASLGEAAEGADEAAPFEADIDATTET YMGWKNDRKRSFGVSRSSGLRYEGEWLDNLRHGYGCTTLPDGHREEGKYRHNVLVK DTKRRLQLKSNKVRQKVEHSVEGAQRAAAIARQKAEIAASRTSHAKAKAEAAEQAL AANQESNIARTLARELAPDFYQPGPEYQKRLLQEI LENSESLLEPPDRGAGAAGLPQ PPRESPQLHERETPRPEGGSPSPAGTTPQPKRPRPGVSKDGLLSPGAWNGEPSGEGSR SVTPSEGAGRSPARPATERMAIEALQAPPAPSREPEVALYQGYHSYAVRTTPPEPPP FEDQPEPEVSGSESAPSPATAPLQAPTLRGPEPAETPAKLEPKPIIPKAEPRAKAR KTEARGLTKAGAKKARKEAALAAEAEEVEVEVPNTILICMVLINIGLAILFVHLLT		

Further analysis of the NOV95a protein yielded the following properties shown in Table 95B.

Table 95B. Protein Sequence Properties NOV95a	
PSort analysis:	0.8000 probability located in nucleus; 0.7000 probability located in plasma membrane; 0.3133 probability located in microbody (peroxisome); 0.2000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV95a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 95C.

Table 95C. Geneseq Results for NOV95a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV95a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79123	Human protein SEQ ID NO 1785 - Homo sapiens, 628 aa. [WO200157190-A2, 09-AUG-2001]	3..696 4..628	293/704 (41%) 377/704 (52%)	e-127
AAM80107	Human protein SEQ ID NO 3753 - Homo sapiens, 378 aa. [WO200157190-A2, 09-AUG-2001]	283..696 24..378	146/421 (34%) 194/421 (45%)	2e-43

Table 95E. Domain Analysis of NOV95a

Pfam Domain	NOV95a Match Region	Identities/ Similarities for the Matched Region	Expect Value
MORN: domain 1 of 7	14..36	10/23 (43%) 13/23 (57%)	1.1
MORN: domain 2 of 7	38..59	9/23 (39%) 15/23 (65%)	0.31
MORN: domain 3 of 7	60..77	8/23 (35%) 15/23 (65%)	3
MORN: domain 4 of 7	106..128	11/23 (48%) 20/23 (87%)	3.7e-06
MORN: domain 5 of 7	129..151	8/23 (35%) 15/23 (65%)	0.027
MORN: domain 6 of 7	291..313	12/23 (52%) 19/23 (83%)	0.00056
MORN: domain 7 of 7	314..336	11/23 (48%) 19/23 (83%)	0.00022

Example 96.

The NOV96 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 96A.

Table 96A. NOV96 Sequence Analysis

	SEQ ID NO: 273	3257 bp
NOV96a, CG59708-01 DNA Sequence	CGTAGGCGCTTCGGCCATGACTGCGGAGCTGCAGCAGGACGACGCGGCCGCGCGGCA GACGGCCACGGCTCGAGCTGCCAATGCTGTTAAATCAACTGAGAGAAATCACAGGCA TTCAGGACCCCTTCCTTCCATGAAGCTCTGAAGGCCAGTAATGGTGACATTACTCA GGCAGTCAGCCTTCTCACTGATGAGAGAGTTAAGGAGCCAGTCAAGACACTGTTGCT ACAGAACCATCTGAAGTAGAGGGAGTGCTGCCAACAGGAAGTATTAGCAAAAGTTA TAGACCTTACTCATGATAACAAAGATGATCTTCAGGCTGCCATTGCTTTGAGTCTACT GGAGTCTCCCAAAATCAAGCTGATGGAAGAGATCTTAACAGGATGCATGAAGCAACC TCTGCAGAACTAAACGCTCAAAGAGAAAACGCTGTGAAGTCTGGGAGAAAACCCCA ATCCCAATGACTGGAGGAGAGTTGATGGTTGGCCAGTTGGGCTGAAAAATGTTGGCAA TACATGTTGGTTAGTGCTGTTATTCACTCTCTCTTCAATTGCCTGAATTCGAAGA CTTGTTCTCAGTTATAGTCTGCCCAAAATGTACTTGAATTTGTCGAAGTCATACAG AAAAGAGAAATATCATGTTTATGCAAGAGCTTCAGTATTTGTTTGCTCTAATGATGGG ATCAAAATAGAAAATTTGTAGACCCGCTGCAGCCCTGGATCTATTAAAGGAGCATTC CGATCATCTGAGGAACAGCAGCAAGATGTGAGTGAATTCACACACAAGCTCCTGGATT GGCTAGAGGACGCATTCCAGCTAGCTGTTAATGTTAACAGTCCCAGGAACAAATCTGA AAATCCAATGGTGACGCTGTTCTATGGTACTTTCCTGACTGAAGGGGTTCTGGAAGGA AAACCCCTTTGTAACAATGAGACCTTCGGCCAGTATCCTCTTCAGGTAACCGGTTATC GCAACTTAGACGAGTGTGTTGGAAGGGGCCATGGTGGAGGGTGATGTTGAGCTTCTTCC CTCCGATCACTCGGTGAAGTATGGACAAGAGCGTTGGTTTACAAAGTACCTCCAGTG TTGACCTTTGAACTCTCAAGATTTGAGTTAATCAGTCCCTTGGGCGCCAGAGAAAA TTCACAATAAGCTGGAATTTCTCAGATTATTTATATGGACAGGTACATGTACAGGAG CAAGGAGCTTATTGAAATAAGAGAGAGTGTATTGAAAGTTGAAGGAGGAAATAAAA ATTCTGCAGCAAAATTTGAAAGGTATGTAAATATGGCTCAGGCCAGCTCGGTTCC CGCTCCCGGACATGCTGAAATATGTTATTGAATTTGCTAGTACAAAACCTGCCTCAGA AAGCTGTCCACCTGAAAGTGACACACATATGACATTACCACTTTCTTCAGTGCACTGC TCGGTTCTGACCAGACATCCAAGGAAAGTACAAGTACAGAAAGCTCTTCTCAGGATG	

	<p>TTGAAAGTACCTTTTCTTCTCTCTGAAAGATTCTTTACCAAGCTCTAAACCAACTGACATC TTCTCGGTCTTCCATGGAATGCCTTCACAGCCAGCTCCACGAACAGTCACAGATGAG GAGATAAAATTTGTAAAGACCTGTCTTCAGAGATGGAGGAGTGAGATTGAACAAGATA TACAAGATTAAAGACTTGTATTGCAAGTACTACTCAGACTTGTGAACAGATGTACTG CGATCCTCTCCTTCGTGAGGTGCCTTATCGCTTGCATGCAGTTCTTGTTCATGAAGGA CAAGCAAATGCTGGACACTATTGGGCTTATATCTATAATCAACCCGACAGAGCTGGC TCAAGTACAATGACATCTCTGTTACTGAATCTTCTGGGAAGAAGTTGAAAGAGATTCT CTATGGAGGCTGAGAAATGTTAGTGCTTACTGTCTGATGTACATTAATGCCAACTA CCCTACTTCAATGCAGAGGCAGCCCCAAGTGAATCAGATCAAAATGCTCAGAAAGTGAAG CCCTATCTGTGGAACCTCAAGCATTACATTCAGGAGGATAAATGGCGGTTTGAGCAGGA AGTAGAGGAGTGGGAAGAAGAGCAGTCTTGCAAAATCCCTCAAATGGAGTCTCCCCC AAGTCTCATCACAGGGCTACTCTACATCACAAGAGCCTTCAGTAGCCTCTTCTCATG GGGTTTCGCTGCTTGTCTGCTGAGCATGCTGTGATTGTAAAGGAGCAAACTGCCAGGC TATTGCAACACAGCCCGTGCCTATGAGAAGAGCGGTGTAGAAGCGGCACTGAGTGAG GCATTCCATGAAGAATACTCCAGGCTCTATCAGCTTGGCAAAGAGACCCCACTCTC ACAGTGTACTCTGACTTCAGCATGTGCTTGTCTACTTTTCCAAAATGAAGCAACCCA AAGGGTAGTAGAACGAACCCCTTCTGGAACAGTTTGCAGATAAAAAATCTTAGCTATGAT GAAAGATCAATCAGCATTATGAAGGTGGCTCAAGCGAAACTGAAGGAAATTTGGTCCAG ATGACATGAATATGGAAGAGTACAAGAGGTGGCATGAAGATTGATGTTTTCGAAA AGTGTCTGTGTATCTCCTAACAGGCTTAGAAGTCTATCAAAAAGGAAAGTACCAAGAG GCATTTCTACTACCTGGTATATGCTTACAGAGCAATGCTGCCCTGCTGATGAAGGGGC CCCGCGGGGGGTCAAAGAATCCGTGATTGCTTTATACCGAAGAAATGCTTCTTGA CTTGAATGCCAAAGCAGCTTCTCTTTTGAACAAATGATGATCATCCGTAAGTCTGAG GGCATTAAATGTGATGAATGAATGATCATCCCTGCATTACCTTATCATTAAATATG ACATTTCCAAGGATGATCTGGATGCCATTGAGGTGATGAGAAACATTGGTGCTCTTA CCTTGGGCAAGATATTGCAGAAAATCTGCAGCTGTGCTTGGGGGATCTTACCAGAG CTTCTAGATCCTTCTGCAGAAATCATCGTCTTGAAAGAGCCTCCAACATATCGACCCA ATTTCCCTTATGACCTATGTAGCCGATTGTCAGCTGTGATGGAGTCAATTGAGGAGT TTCAACTGTGACAGTGAATAAGCTCCCAATGTTCAAGGCCATTCTGGTCTCTGGC TGCTGCTCTTGCACAGAAGTTCGTTGTCTAGTGCTCACCTTGGGAAAAGGATTAG GTGGGCACA</p>			
	<table border="1"> <tr> <td data-bbox="672 945 959 1018">ORF Start: ATG at 17</td><td data-bbox="959 945 1430 1018">ORF Stop: TAA at 3152</td></tr> </table>	ORF Start: ATG at 17	ORF Stop: TAA at 3152	
ORF Start: ATG at 17	ORF Stop: TAA at 3152			
	<table border="1"> <tr> <td data-bbox="672 1018 959 1068">SEQ ID NO: 274</td><td data-bbox="959 1018 1097 1068">1045 aa</td><td data-bbox="1097 1018 1430 1068">MW at 119041.7kD</td></tr> </table>	SEQ ID NO: 274	1045 aa	MW at 119041.7kD
SEQ ID NO: 274	1045 aa	MW at 119041.7kD		
<p>NOV96a, CG59708-01 Protein Sequence</p>	<p>MTAELQDDAAGAADGHSSCQMLLNQLREITGIQDPSFLHEALKASNGDITQAVSL TDERVKEPSQDVTATEPSEVEGSAANKEVLAKVIDLTHDNKDDLQAAIALSLLES QADGRDLNRMHEATSAETKRKRKRCEVWGENPNPNDRWRVWGVGLKNVNGTWC FSAVQSLFQLPEFRRLVLSYSLPNVLENCRSHTTEKRNIMFMQELQYLFALMMGS NRKFVDPASALDLLKGAFRSSEEQQDVSEFTHKLLDWLEDAFQLAVNVNSPRNKSE NPMVQLFYGTFLTEGVREGKPFNNETFGQYPLQVNGYRNLDECLEGAMVEGDVLL PSDHSVKYQGERWFTKLPPVLTFLSRFEFNQSLGQPEKIHNKLEFPQIIYMDRMYR SKELIRNKRECIRKLKEEIKILQQLERYVVKYGSGBPFPPLPDMCLKVIEFASTK PASESCPPESDTHMTLLPLSSVHCSVDQTSKESTSTESSQDVESTFSSPEDSLPKS KPLTSSRSSMEMPSQAPARTVTDEIEINFVKTLQWRSEIEQDIQDLKTCIASTTQ IEQMCDPLLRQVRYRLHAVLVHEGQANAGHYWAYIYNQPRQSWLKYNDISVTESS WEEVERDSYGLLRNVSAVCLMYINAKLPYFNAEAAPTESDQMSVEALSVELKHYI QEDNWRFEQVEEWEEOQSKIPQMESSPNSSSQGYSTSQEPSVASSHGVRLSSEHA VIVKEQTAQAIAANTARAYEKSGVEAALSEAFHEEYSLRYQLAKETPTSHSDPRL QHVLVYVFQNEAPKRVRERTLEQFADKNLSYDERSISIMKVAQAKLKEIGPDDMN MEBYKRWHEDEYSLFRKVSVYLLTGLELYQKGKYQEALESYLVYAYQSNAAALLMK GPRRGVKESVIALYRRKCLLELNAKAASLFETNDDHVSVEGINVMNELIIPCIH LIINNDISKDDLDIAIEVMRNHWCSYLGQDIAENLQLCLGEFLPRLLDPSAEI IVLKEPPTIRPNSPYDLCSRFAAVMESIQGVSTVTVK</p>			
	<table border="1"> <tr> <td data-bbox="672 1478 959 1528">SEQ ID NO: 275</td><td data-bbox="959 1478 1430 1528">3044 bp</td></tr> </table>	SEQ ID NO: 275	3044 bp	
SEQ ID NO: 275	3044 bp			
<p>NOV96b, CG59708-02 DNA Sequence</p>	<p>CGTAGGCGCTTCGCCATGACTGCGGAGCTGCAGCAGGACGACGCGCGCGCGG CAGCGCCACGGCTCGAGCTGCCAAATGCTGTTAAATCAACTGAGAGAAATCAGAG CATTTCAGGACCCCTTCTCTTCTCCATGAAGCTCTGAAGGCCAGTAAGGTGACAT TACTCAGGAGCTCCTCTACTGATGAGAGAGTTAAGGAGCCGATCAAGACACTGT GTGCTACAGAACCATCTGAAGTAGAGGGAGTGCTGCCAACAGGAAGTTATAGCA AAAGTTATAGACCTTACTCATGATAACAAAGATGATCTTCAGGCTGCCATTGCT TTGAGTCTACTGGAGTCTCCCAAATCAAGCTGATGGAAGAGATCTTAACAGGAT GCATGAAGCAACCTCTGTCAGAACTAAACGCTCAAAGAGAAATATCATGTTTAT GCAAGAGCTTCAGTATTGTTGCTCTAATGATGGGATCAAATAGAAAAATTTGT AGACCCGCTTCAGGCTTCTGATCTATTAACAGCTGATGAGTGAATTCACACAA GCTCCTGGATTGGCTAGAGGACGCATTCCAGCTAGCTGTGTTAATGTTAACA ATCCCAGGAACAAATCTGAAAATCCAATGGTGCAGCTGTCTATGTTGATCTT CTGACGTAAGGGGTTCTGTAAGGAAACCCCTTTTGAACAATGAGACCTTCG GCCAGTATCCTCTTCAGGTAAACGGTTATCGCAACTTAGACGAGTGTGTTGAAG GGGCGCATGTTGGAGGCTGATGTTGAGCTTCTCCCTCCGATCACTCGGTGAAG TAGGACAAGAGCTGTTGTTACAAAGCTACTCCAGTGTGACCTTTGAACTCTCA AGATTTGAGTTAATCAGTCCCTTGGGCAGCCAGAGAAAATCACAAATAGCTG GAATTTATATGACAGGTACATGTACAGGACGAGGACTTATTCGAAATAGAGAG GATGTTATTCGAAA</p>			

	GTTGAAGGAGGAAATAAAATTTCTGCAGCAAAATTTGGAAAGGTATGTGAAATATGGC TCAGGCCAGCTCGGTTCCCGCTCCCGACATGCTGAAATATGTTATTGAATTTGCTA GTACAAAACCTGCCTCAGAAAGCTGTCCACCTGAAAGTGACACACATATGACATTACC ACTTTCTTCAGTGCACTGCTCGGTTTCTGACCAGACATCCAAGGAAAGTACAAGTACA GAAAGCTCTTCTCAGGATGTTGAAAGTACCTTTTCTTCTCCTGAAGATTCTTTACCCA AGTCTAAACCACTGACATCTTCTCGGTCTTCCATGGAATGCCTTCACAGCCAGCTCC ACGAACAGTCACAGATGAGGAGATAAAATTTTGTAAAGACTGTTCTTCAGAGATGGAGG AGTGAGATTGAACAAGATATACAAGATTTAAAGACTTGTATTGCAAGTACTACTCAGA CTATTGAACAGATGTACTGCGATCCTCTCCTTCGTCAGGTGCCTTATCGCTTGCATGC AGTTCTTGTTCATGAAGGACAAGCAAATGCTGGACACTATTGGGCTATATCTATAAT CAACCCCGACAGAGCTGGCTCAAGTACAATGACATCTCTGTTACTGAATCTTCTCTGGG AAGAAGTTGAAAGAGATTCCATATGGAGGCCTGAGAAATGTTAGTGCTTACTGTCTGAT GTACATTAATGCCAACTACCCTACTTCAATGCAGAGGCAGCCCAACTGAATCAGAT CAAATGTCAGAAGTGAAGCCCTATCTGTGGAACCTCAAGCATTACATTGAGGAGGATA ACTGGCGGTTTGAGCAGGAAGTAGAGGAGTGGGAAGAAGAGCAGCTTTCGAAAATCCC TCAAATGGAGTCTCCCCCAACTCCTCATCACAGGGCTACTCCAGGTCTATCAGTGGCT TCAGTAGCCTCTTCTCATGGGGTTCGCTGCTTGTCTATCTGAGCATGCTGTGATTGTAA AGGAGCAAACCTGCCCAGGCTATTGCAACACAGCCCGTGCTATGAGAAGAGCGGTGT AGAAGCGCACTGAGTGAGGCATTCCATGAAGAATACTCCAGGTCTATCAGTCTGGCC AAAGAGACCCCCACCTCTCACAGTGATCCTCGACTTCAGCATGTCCTTGTCTACTTTT TCCAAAATGAAGCACCACAAAGGGTAGTAGAACGAACCCCTTCTGGAACAGTTTGCAGA TAAAAATCTTAGCTATGATGAAAGATCAATCAGCATTATGAAGTGGCTCAAGCGAAA CTGAAGGAAATTTGGTCCAGATGACATGAATATGGAAGAGTACAAGAGGTGGCATGAAG ATTATAGTTTGTTCGAAAAGTGTCTGTGTATCTCCTAACAGGCCTAGAACTCTATCA AAAAGGAAAGTACCAAGAGGCACCTTCTACCTGGTATATGCCTACCAAGCAATGCT GCCCTGCTGATGAAGGGGCCCGCGGGGGGTCAAAGAATCCGTGATTGCTTATACC GAAGAAAATGCCCTTCTGGAGCTGAATGCCAAAGCAGCTTCTCTTTTGAACAAATGA TGATCACTCCGTAACCTGAGGGCATTAAATGTGATGAATGAACATGATCATCCCCGTCATT CACCTTATCATTAATAATGACATTTCCAAGGATGATCTGGATGCCATTGAGGTGATGA GAAACCATTTGGTGTCTTACCTTGGGCAAGATATTGCAGAAAAATCTGCAGCTGTGCCT AGGGGAGGATTTTACCCAGACTTCTAGATCCTTCTGCAGAAATCATCGTCTTGAAGAG CCTTCAACTATTCGACCAATTTCTCCCTATGACCTATGTAGCCGATTGAGCTGTGTCA TGGAGTCAATTGAGGGAGTTTCAACTGTGACAGTGAAATAGACTCCACATGTTTCAAG GCCCATCTGGTTCCTGGCTGCCTGCCTCTTGCACAGAAGTTCGTTGTCTATAGTGCTC ACCTTGGGAAAAGGATTAGGTGGGCACA		
	ORF Start: ATG at 17	ORF Stop: TAA at 2939	
	SEQ ID NO: 276	974 aa	MW at 110687.3kD
NOV96b, CG59708-02 Protein Sequence	MTAELQQDDAAGAADGHSSCQMLLNQLREITGIQDPSFLHEALKASNGDITQAVSLL TDERVKEPSQDVTATEPSEVEGSAANKEVLAKVIDLTHDNKDDLQAAIALSLLESPI QADGRDLNRMHEATSATKRSKRINIMFMQELQYLFALMMGSNRKFVDPSPALDLLKGA FRSSEEQQQDVSEFTHKLLDWLEDAFQLAVNVNSPRNKSENPMVQLFYGTFLTGVRE GKPCFNNETFGQYPLQVNGYRNLDCELEGAMVEGDVELLPDSDHVSVKYQGERWFTKLPP VLTFELSRFEFNQSLGQPEKIHNLKLEFPQIIYMDRYMYRSKELIRNKRECIRKLKEEI KILQQLERYVKYGGSPARFPLPDLMLKYVIEFASTKPASESCPPESDTHMTPLSSVH CSVSDQTSKESTSTESSQDVESTFPSSPEDSLPKSKPLTSSRSSMEMPSQAPARTVTD EEINFVKTCQRWRSEIEQDIQDLKTCIASTTQTIEQMYCDPLLRQVPYRLHAVLVHE GQANAGHYWAYIYNQPRQSWLKYNDISVTESSWEEVERDSYGLLRNVQSAYCLMYINAK LPYFNAEAAPTESDQMSVEALSVELKHYIQEDNWRFEQEVEEWEQESCKIPQMESS PNSSSQYSTSQEPSVASSHGVRCLSSSEHAVIVKEQTAQAIAANTARAYEKSGVEAALS EAFHEEYSRLYQLAKETPTSHSDPRLQHVLYVFFQNEAPKRUVVERTLLEQFADKNLSY DERSISIMKVAQAKLKEIGPDDMNMEYKRWHEDEYSLFRKVSVYLLTGLELYQKGKYQ EALSYLVYAYQSNALLMKGPRRGVKESVIALYRRKCLLELNAKAASLFETNDDHSVT EGINVMNELIIPCIHLIINNDISKDDLDIEVMRNHWCYSYLGQDIAENLQLCLGEFLP RLLDPSAEIIVLKEPPTIRPNSPYDLCSRFAAVMESIQGVSTVTVK		
	SEQ ID NO: 277	3231 bp	
NOV96c, CG59708-03 DNA Sequence	GCGCTTCGGCCATGACTGCGGAGCTGCAGCAGGACGACGCGGCCGCGGCAGACGG CCACGGCTCGAGCTGCCAAATGCTGTTAAATCAACTGAGAGAAATCACAGGCATTGAG GACCTTCCTTTCTCCATGAAGCTCTGAGGGCCAGTAATGGTGACATTACTCAGGCAG TCAGCCTTCTCACTGATGAGAGAGTTAAGGAGCCAGTCAAGACACTGTTGCTACAGA ACCATCTGAAGTAGAGGGGAGTGCTGCCAACAAGGAAGTATTAGCAAAAGTTATAGAC CTTACTCATGATAACAAGATGATCTTCAGGCTGCCATTGCTTTGAGTCTACTGGAGT CTCCCAAAATTCAGCTGATGGAAGAGATCTTAACAGGATGTCATGAAGCAACCTCTGC AGAAACTAAACGCTCAAAGAGAAAACGCTGTGAAGTCTGGGGAGAAAACCCCAATCCC AATGACTGGAGGAGAGTTGATGGTTGGCCAGTTGGGCTGAAAAATGTTGGCAATACAT GTTGGTTTAGTGCTGTTTATTCACTCTCTTTCAATTGCCTGAATTTTCGAAGACTTGT TCTCAGTTATAGTCTGCCACAAAATGTACTTGAAAATTTGTCGAAGTCATACAGAAAAG AGAAATATCATGTTTATGCAAGAGCTTCAGTATTGTTGTTGCTCTAATGATGGGATCAA ATAGAAAATTTGTAGACCCGCTCTGCAGCCCTGGATCTATTAAAGGGAGCATTCGGATC ATCTGAGGAACAGCAGCAAGATGTGAGTGAATTCACACACAAGCTCCTGGATTGGCTA GAGGACGCATTCCAGCTAGCTGTTAATGTTTAAACAGTCCCGAGAACAAATTTGAAAATC CAATGGTGACAGCTGTTCTATGGTACTTCTCTGACTGAAGGGGTTCTGTAAGGAAAACC		

	CTTTTGTAACCAATGAGACCTTCGCGCCAGTATCCTCTTCAGGTAAACAGGTTATCGCAAC TTAGACGAGTGTTTTGAAGGGGCCATGGTGGAGGGTGATGTTGAGCTTCTTCCCTCCG ATCACTCGGTGAAGTATGGACAAGAGCGTTGGTTTACAAAGCTACCTCCAGTGTGGAC CTTTGAACCTCTCAAGATTTGAGTTAATCAGTCCCTTGGCGAGCCAGGAAATTCAC AATAAGCTGGAATTTCTCAGATTATTTATATATGGACAGGTACATGTACAGGAGCAAGG AGCTTATTGAAAAAAGAGAGAGTGTATTGAAAAAGTTGAAGGAGGAAATAAAAAATCT GCAGCAAAAAATTGGAAGGGTATGTGAAATATGGCTCAGGCCAGCTCGGTTCCCGCTC CCGGACATGCTGAAATATGTTATTGAATTTGCTAGTACAAAACTGCCTCAGAAAGCT GTCCACCTGAAAGTGACACACATATGACATTACCACCTTTCTTCATGTCAGTGTCTCGGT TTCTAACACGACATCCAAGGAAAGTACAAGTACAGAAAGCTCTTCTCAGGATGTTGAA AGTACCTTTTCTTCTCCTGAAGATTCTTTACCCAAGTCTAAACCACTGACATCTTCTC GGTCTTCCATGGAATGCCTTTCACAGCCAGCTCCACGAAAGTACAGATGAGGAGAT AAATTTTGTGAAGCTGTCTTCAGAGATGGAGGAGTGAGATTGAAACAAGATATACAA GATTTAAAGACTTGATTGCAAGTACTACTCAGACTATTGAACAGATGTACTGCGATC CTCTCTCTCGTCAGGTGCCTTATCGCTTGCATGCAGTCTCTGTTCATGAAGGACAAGC AAATGCTGGACACTATTGGGCCTATATCTATAATCAACCCGACAGAGCTGGCTCAAG TACAATGACATCTCTGTTACTGAACTCTTCTGGGAAGAAGTTGAAAGAGATTCTTATG GAGGCTGAGAAAAATGTTAGTGCTTACTGTCTGATGTACATTACGACAACTACCTTA CTTCAATGCAGAGGCAGCCCCAAGTGAATCAGATCAAATGTGAGAAGTGAAGCCCTA TCTGTGGAAGCTCAAGCATTACATTGAGGAGGATAACTGGCGGTTTGAAGCAGGAAGTAG AGGAGTGGGAAGAAGAGCAGTCTTGCAAAATCCCTCAAATGGAGCTCTCCACCAACTC CTCATCAGGACTACTCTACATCACAGAGCCTTCAGTAGCTCTTCTCATGGGGTT CGCTGCTTGTCTATCTGAGCATGCTGTGATTGTAAGGAGCAAACTGCCAGGCTATTG CAAAACAGCCCGTGCCTATGAGAAGAGCGGTGTAGAAGCGGCACAGTGTAGGCGATT CCATGAAGAAATACTCCAGGCTCTATCAGCTTGCCAAAGAGACCCCACTCTCACAGT GATCCTCGACTTCAGCATGTCTTGTCTACTTTTTCCAAAATGAAGCACCACCAAGGG TAGTAGAACGAACCTTCTGGAACAGTTTGCAGATAAAAAATCTTAGCTATGATGAAAG ATCAATCAGCATTATGAAGGTGGCTCAAGCGAACTGAAGGAAATTTGGTCCAGATGAC ATGAATATGGAAGAGTACAAGAAGTGCAATGAAAGATTATGTTTGGTCCGAAAAGTGT CTGTGTTATCTCCTAACAGGCCTAGAATCTATCAAAAAGGAAAGTACCAAGAGGCACT TTCTTACCTGGTATATGCTTACCAGAGCAATGCTGCCCTGTGATGAAGGGCCCCGC CGGGGGGTCAAAGAATCCGTGATTGCTTTATACCGAAGAAAATGCCTTCTGGAGCTGA ATGCCAAAGCAGCTTCTCTTTTGAACAAATGATGATCACTCCGTAACCTGAGGGCAT TAATGTGATGAATGAACGTGATCATCCCTGCATTACCTTATCATTAATGACATT TCCAAGGATGATCTGGATGCCATTGAGGTGATGAGAAACCATTTGGTGTCTCTTACCTTG GGCAAGATATTGCAAAAAATCTGCAGCTGTGCCTAGGGGAGTTTCTACCCAGACTTCT AGATCCTTCTGCAGAAATCATCGTCTTGAAGAGCCTCCAATATTCGACCCAAATCT CCCTATGACCTATGTAGCCGATTGTCAGCTGTGATGGAGTCAATTGAGGAGTTTCAA CTGTGACAGTGAATAAGCTCCACATGTTCAAGGCCCATCTCGGTTCTCGGTGCGCT GCCTCTTGACAGAAAGTTCGTTGTCATAGTGCTCACCTTGG		
	ORF Start: ATG at 12	ORF Stop: TAA at 3147	
	SEQ ID NO: 278	1045 aa	MW at 119107.7kD
NOV96c, CG59708-03 Protein Sequence	MTAELQDDAAGAADGHSSCQMLLNQLREITG IQDPSFLHEALRASNGDITQAVSLT DTERVKEPSQDVTATEPSEVEGSAANKVELAKVIDLTHDNKDDLQAAIALSLLESPI QADGRDLNRMHEATS ETKRSKRKRCEVWGENPNPNDRWRVGDWPVGLKNVNGTCWFS AVIQSLFQLPEFRRRLVLSYSLPQNVLENCRSHTKEKNIMFMQELQVLFALMMGNSRKF VDPSAALDLLKGAFRSSEEQQQDVSEFTHKLLDWLEDAFQLAVNVNSPRNKFENPMVQ LFYGTFLTEGVREGKPF CNNETFFGQYPLQVNGYRNLDCELEGAMVEGDVELLPSDHSV KYGQERWFTKLPVLVTFELSRPEFNQSLGQPEKIHNLKLEFPQI IYMDRYMRSKELIR NKRECIRKLNKEEIKILOQKLEGYVVKYSGSPARFPLPDMLYKVI EFAS TKPASESCPPE SDTHMTLPLSSVHCSVSNQTSKESTSTESSQDVESTFSSPEDSLPSKPKPLTSSRSSM EMPSQAPARTVTDDEEIN FVKTC LQRWRSEIEQDIQDLKTCIASTQT IEQMYCDPLLR QVPYRLHAVLVHVGQANAGHYWAYIYNQPRQSWLKYNDISVTESSWEEVERDSYGGGLR NVSAYCLMYINDKLPPYFNAEAAPTESDQMSVEALSVELKH YIQEDNWRFEQAEVEEWE EEQSKIPQMESSTNSSQDYSTSQEPSVASSHGVRCLSESHAVIVKEQTAQAIANTA RAYEKSGVEAALSEAFHEEYSRLYQLAKETPTSHSDPRLQHVLVYFFQNEAPKRUVVER TLEQFADKNLSYDERSISIMKVAQAKLKEIGPDDMMNMEYKWHEDYSRFLKRVSVYL LTGLELYQKGQYQALSYLVYAYQSNAAALLMKGPRRGVKESVIALYRLKCLLELNKA ASLPETNDDHSVTEGINVMNELIIPC IHLIINNDISKDDLDAIEVMRNHWCSYLGQDI AENLQCLGFEFLPRLLDPSAEIIVLKEPPTIRPNSPYDLCSRFAAVMESIQGVSTVTV K		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 96B.

2020E00062600T

Table 96B. Comparison of NOV96a against NOV96b through NOV96c.		
Protein Sequence	NOV96a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV96b	209..1045 138..974	805/837 (96%) 805/837 (96%)
NOV96c	1..1045 1..1045	979/1045 (93%) 981/1045 (93%)

Further analysis of the NOV96a protein yielded the following properties shown in Table 96C.

Table 96C. Protein Sequence Properties NOV96a	
PSort analysis:	0.8800 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV96a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 96D.

Table 96D. Geneseq Results for NOV96a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV96a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE04874	Human protease protein-1 (PRTS-1) - Homo sapiens, 1055 aa. [WO200146443-A2, 28-JUN-2001]	22..1036 18..1047	524/1035 (50%) 713/1035 (68%)	0.0
AAB31552	A human ubiquitin specific protease 25 (USP25) - Homo sapiens, 1055 aa. [WO200079267-A2, 28-DEC-2000]	22..1036 18..1047	524/1035 (50%) 713/1035 (68%)	0.0
AAB31546	A human ubiquitin specific protease 25 (USP25) - Homo sapiens, 1055 aa. [WO200078934-A2, 28-DEC-2000]	22..1036 18..1047	524/1035 (50%) 713/1035 (68%)	0.0
AAB74491	Human SYK kinase binding protein	22..1036 18..1047	522/1035 (50%) 710/1035 (68%)	0.0

	sapiens, 1055 aa. [WO200121654-A2, 29-MAR-2001]			
AAB31556	A human ubiquitin specific protease (USP) - Homo sapiens, 1087 aa. [WO200079267-A2, 28-DEC-2000]	22..1036 18..1079	525/1067 (49%) 717/1067 (66%)	0.0

In a BLAST search of public sequence databases, the NOV96a protein was found to have homology to the proteins shown in the BLASTP data in Table 96E.

Table 96E. Public BLASTP Results for NOV96a				
Protein Accession Number	Protein/Organism/Length	NOV96a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RU2	UBIQUITIN SPECIFIC PROTEASE - Homo sapiens (Human), 1077 aa.	1..1045 1..1077	1041/1077 (96%) 1042/1077 (96%)	0.0
Q9P213	KIAA1515 PROTEIN - Homo sapiens (Human), 757 aa (fragment).	304..1045 16..757	738/742 (99%) 739/742 (99%)	0.0
P57080	Ubiquitin carboxyl-terminal hydrolase 25 (EC 3.1.2.15) (Ubiquitin thiolesterase 25) (Ubiquitin-specific processing protease 25) (Deubiquitinating enzyme 25) (mUSP25) - Mus musculus (Mouse), 1055 aa.	22..1036 18..1047	527/1033 (51%) 710/1033 (68%)	0.0
Q9UHP3	Ubiquitin carboxyl-terminal hydrolase 25 (EC 3.1.2.15) (Ubiquitin thiolesterase 25) (Ubiquitin-specific processing protease 25) (Deubiquitinating enzyme 25) (USP on chromosome 21) - Homo sapiens (Human), 1087 aa.	22..1036 18..1079	525/1067 (49%) 717/1067 (66%)	0.0
Q9H9W1	CDNA FLJ12512 FIS, CLONE NT2RM2001730, WEAKLY SIMILAR TO PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) - Homo sapiens (Human), 737 aa.	313..1036 2..729	363/733 (49%) 510/733 (69%)	0.0

PFam analysis predicts that the NOV96a protein contains the domains shown in the Table 96F.

Table 96F. Domain Analysis of NOV96a			
Pfam Domain	NOV96a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UIM: domain 1 of 1	96..113	9/18 (50%) 14/18 (78%)	8.4
UCH-1: domain 1 of 1	162..193	14/32 (44%) 28/32 (88%)	2.6e-11
UCH-2: domain 1 of 1	580..649	26/72 (36%) 56/72 (78%)	1.5e-19

Example 97.

- 5 The NOV97 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 97A.

Table 97A. NOV97 Sequence Analysis			
	SEQ ID NO: 279		1601 bp
NOV97a, CG59559-01 DNA Sequence	<u>AGGGCAGAGGCCACAGCGCCATCCCCTTCCCCTATGGTCTCCCTACCCCCAACCTGCAC</u> <u>TGGGCGCTCCGCCCAGAGGTGAGTCCCTCCCAGCCCTTCTCTCTTCTGTCTAGCCA</u> <u>TCCGCAGAGCCATCCTGTGCAAAGGAAGGAGCTAGGCTGTGCGCCCTGGGCGTATGA</u> <u>TCCTTCTGCGGGCCTCCGAAGTGCGGCAGCTGCTTCAACAATAAGTTCTGTGGTCACTCCT</u> <u>GGGGGACTCTGTGCATAGGGCAGTATACAAGGACCTGGTGCTTCTGTCTCAGAAGGAC</u> <u>CGCCTGCTCACTCCCGGCAGCTTAGAGCAAGGGGGAGCTGAACCTTCGAACAAGATG</u> <u>AGCTGGTGGACGGAGGCCAGCGGGGCCACATGCACAACGGCCTTAACTACCGTGAGGT</u> <u>CCGCGAGTTCCGCTCCGACCACCATCTGGTACGTTTTTACTTCCTCACCCGCGGTGATC</u> <u>TCCGATTACCTCCAGACCATCTTGAAGAGCTGCAGTCCGGCGAGCACGCCCCGACC</u> <u>TGGTCATCATGAATTCCTGCCTCTGGGACATCTCCAGGTATGGTCGGAACCTCTGGAG</u> <u>AAGCTACCTGGAGAACCTGGAGAACCTGTTCCAGTGCCTGGGCCAGGTGCTGCCCGAG</u> <u>TCTTGCTCCTGGTGTGGAACACGGCCATGCCTGTGGGCGAGGAAGTCAACGGGGGTT</u> <u>TTCTTTCGCCCCAAGCTCCGGCGGCAGAAGGCCACCTTCCTGAAAAACGAAGTGGTCAA</u> <u>AGCCAACTTCCACAGCGCCACCGAGGCACGTAAACATAACTTCGATGTACTTGGACTTG</u> <u>CATTTCCACTTCCGCCACGCGAGGGAGAACCTGCATGGGACGGGGTGCACTGGAATG</u> <u>GACGTGTGCACCGCTGCCTCTCCAGCTGCTGCTGGCCACGTGGCCGACGCTGGGG</u> <u>TGTGGAGCTGCCCCACCGCCACCCCGTGGGCGAGTGGATCAAGAAGAAAAAACCCTGGC</u> <u>CCGAGAGTCGAAGGGCCGCCCCAGGCCAACAGAAATCACCCGGCCTTACCTCTGTCCC</u> <u>CACCTTACCTTCCCCACATACCGCCCCCTGCTTGGGTTCCACCCCCAGCGCTTGGC</u> <u>GCTGCTCCCGTCCGTGTCCCACAGCCTCCTCCTCCCATCTCCATCACCAGGGAATG</u> <u>CCCCGGTTCCCCAGGGTCCCCCAGATGCCTGTTTTTCCCTCAGACCATACCTTTCCAGT</u> <u>CGGATCAATTCTATTGCCATTAGATGTCCCTCATCAGCCATGCAGGTTTCTTCGT</u> <u>CGAAGACAATTTATGGTTGGTCCCTCAGCTGCCTATGCCCTTCTTCCCCACACCCCGT</u> <u>TATCAGCGGCCTGCCCCAGTGGTACATAGGGGTTTTGGCAGGTATCGTCCCCGTGGCC</u> <u>CCTATACGCCCTGGGGACAGCGGCCTCGACCTTCAAAGAGAAGGGCCCCAGCCAATCC</u> <u>TGAGCCAAGGCCTCAATAGACGGACCTAGGCCTTATTTCTCTTTATGAACATGGATT</u> <u>GGACAGATCTGACACTTCCTTTCCATTGCTTGGCCTGAACAGACTGACCTTGTTAACT</u> <u>TAAGCCTGGAGTCCATGCCTCGTCTCTCTTTTGT</u>		
	ORF Start: ATG at 171		ORF Stop: TAG at 1467
	SEQ ID NO: 280		432 aa MW at 49726.6kD
NOV97a,	MILLRASEVRQLLHNKFVVILGDSVHRAVYKDLVLLQKDRLLTPGQLRARGELNFEQ DELVDGGQRGHMHNGLNYREVREFRSDHHLVRFYFLTRVYSDYLQTIKELQSGEHAP		

CG59559-01 Protein Sequence	DLVIMNSCLWDISRYGPNWSRSYLENLENLFQCLGQVLPESCLLVWNTAMPVGEEVTG GFLPPKLRRQKATFLKNEVVKANFHSATEARKHNFDVLDLHFHFRHARENLHWDGVHW NGRVHRCLSQLLLAHVADAWGVELPHRHPVGEWIKKKKPGPRVEGPPQANRNHPALPL SPPLPSPTYRPLLGFPQRLPLPLSPQPPPIILHHQGMPRFPQGPDPACFSSDHTF QSDQFYCHSDVPSSAHAGFFVEDNFMVGPQLPMPFFPTPRYQRPAPVVHRGFGGRYRPR GPYTPWQQRPRPSKRRAPANPEPRPQ
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Further analysis of the NOV97a protein yielded the following properties shown in Table 97B.

Table 97B. Protein Sequence Properties NOV97a	
PSort analysis:	0.5937 probability located in mitochondrial matrix space; 0.5103 probability located in microbody (peroxisome); 0.4900 probability located in nucleus; 0.3252 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV97a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 97C.

Table 97C. Geneseq Results for NOV97a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV97a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG74241	Human colon cancer antigen protein SEQ ID NO:5005 - Homo sapiens, 281 aa. [WO200122920-A2, 05-APR-2001]	34..294 1..266	162/268 (60%) 191/268 (70%)	1e-82
AAE03639	Human extracellular matrix and cell adhesion molecule-3 (XMAD-3) - Homo sapiens, 386 aa. [WO200142285-A2, 14-JUN-2001]	1..421 1..366	197/435 (45%) 231/435 (52%)	2e-82

In a BLAST search of public sequence databases, the NOV97a protein was found to have homology to the proteins shown in the BLASTP data in Table 97D.

Table 97D. Public BLASTP Results for NOV97a				
Protein Accession Number	Protein/Organism/Length	NOV97a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96HM7	SIMILAR TO HYPOTHETICAL PROTEIN FLJ22376 - Homo sapiens (Human), 432 aa.	1..432 1..432	432/432 (100%) 432/432 (100%)	0.0
Q96B20	HYPOTHETICAL 31.4 KDA PROTEIN - Homo sapiens (Human), 279 aa.	121..310 1..190	190/190 (100%) 190/190 (100%)	e-116
Q9H1Q7	BA12M19.1.3 (NOVEL PROTEIN) (CDNA FLJ31791 FIS, CLONE NT2RI2008749, WEAKLY SIMILAR TO SPLICEOSOME ASSOCIATED PROTEIN 49) - Homo sapiens (Human), 454 aa.	1..421 18..434	234/437 (53%) 273/437 (61%)	e-111
Q9H1Q6	BA12M19.1.1 (NOVEL PROTEIN) - Homo sapiens (Human), 403 aa.	1..421 18..383	197/435 (45%) 231/435 (52%)	7e-82
Q9H6D1	CDNA: FLJ22376 FIS, CLONE HRC07327 - Homo sapiens (Human), 403 aa.	1..421 18..383	196/435 (45%) 231/435 (53%)	1e-81

PFam analysis predicts that the NOV97a protein contains the domains shown in the Table 97E.

Table 97E. Domain Analysis of NOV97a			
Pfam Domain	NOV97a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 98.

- 5 The NOV98 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 98A.

Table 98A. NOV98 Sequence Analysis			
	SEQ ID NO: 281		981 bp
NOV98a, CG59669-01 DNA Sequence	GCGCCGGGTCCCAGAATCTAGTCCTACGCCACGGTTTTGACCACGCGTGACCCGCTGC CCAGCCGGCCCGGCCATCAGGTGGTCCGTGTGCCCTCTGACATGTCTGCTCTGCAGCC GCGTGGCCCTGGTAACTGGGGCTAACAAAGGCATCGGCTTTGCGATCACGCGTGACCT GTGTGCGAAATCTCCGGGGACGTGGTGCTCAGGCGCGGGACGAGGCGCGGGGCGCG GCGGCGGTGCAGCAGCTGCAGGCGGAGGGCCTGAGCCCACGCTTCCACCAGCTGGACA TCGACGACCCGACAGCATCCGTGCGCTGCGCGACTTCTGCGCAAGGAGTACGGGGG ACTTAACGTGCTGGTCAACAACGCGGGCATCGCCTTTAGAAGTACTGATCTCACCCAC TTTCACATTCTAAGAGAAGCTGCAATGAAAACTAACTTTTGGTACCCAGGCCGTCT GCACAGAGCTACTCCCTCTAATAAAAAACCAAGGTAGAGTGGTGAATATATCAAGCCT AATAAGTCTAGAGGCCCTGAAAAACTGCAGCCTGGAGCTACAGCAGAAGTTTCGAAGT GAGACCATCACAGAGGAGGAGCTGGTGGGGCTCATGAACAAGTTTGTGGAGGATACAA AGAAAGGAGTCCATGCAAAGAAGGCTGGCCTAATAGTGCATACGGGGTGTCTAAGAT TGGAGTGACAGTCTGTCCAGAATCCTTGCCAGGAACTCAATGAGCAGAGGAGAGGG GACAAGATCCTTCTGAATGCCTGCTGCCCTGGCTGGGTGAGAACCACATGGCAGGAC CACAAGCCACCAAAAGCCCAGAAGAAGGAGCAGAGACCCCTGTGTACTTGGCCCTTTT GCCTCCAGATGCAGAGGGACCTCATGGGCAGTTTGTTCAGATAAAAAAGTGGAACAA TGGTGAACCTCAGCTCTTTGTACAGCTCCCATCTGTAGCCTGCTCTAAAGGGGA		
	ORF Start: ATG at 101		ORF Stop: TGA at 932
	SEQ ID NO: 282		277 aa MW at 30547.7kD
NOV98a, CG59669-01 Protein Sequence	MSSCSRVALVTGANKGIGFAITRDLCRKFSGDVVLTAARDEARGRAAVQQLQAEGLSPR FHQLDIDDPQSIRALRDLFLRKEYGGLNVLVNNAGIAFRSTDLTTHFHLREAAMKTNFF GTQAVCTELLPLIKTQGRVNNISLISLEALKNCSELELQKFRSETITEEELVGLMKNK FVEDTKKGVHAKEGWPNSAYGVSKIGVTVLSRLARKLNEQRRGDKILLNACCPGWVR TDMAGPQATKSPEEGAETPVYLALLPPDAEGPHGQFVQDKKVEQW		

Further analysis of the NOV98a protein yielded the following properties shown in Table 98B.

Table 98B. Protein Sequence Properties NOV98a	
PSort analysis:	0.4766 probability located in mitochondrial matrix space; 0.4500 probability located in cytoplasm; 0.1822 probability located in mitochondrial inner membrane; 0.1822 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV98a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 98C.

Table 98C. Geneseq Results for NOV98a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV98a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW51011	Human liver carbonyl reductase - Homo sapiens, 277 aa. [US5756299-A, 26-MAY-1998]	1..277 1..277	236/277 (85%) 252/277 (90%)	e-134

AAU33100	Novel human secreted protein #3591 - Homo sapiens, 175 aa. [WO200179449-A2, 25-OCT-2001]	142..277 39..174	119/136 (87%) 128/136 (93%)	2e-66
AAM73641	Human bone marrow expressed probe encoded protein SEQ ID NO: 33947 - Homo sapiens, 123 aa. [WO200157276-A2, 09-AUG-2001]	1..97 1..97	86/97 (88%) 92/97 (94%)	7e-43
AAM60948	Human brain expressed single exon probe encoded protein SEQ ID NO: 33053 - Homo sapiens, 123 aa. [WO200157275-A2, 09-AUG-2001]	1..97 1..97	86/97 (88%) 92/97 (94%)	7e-43
AAM33832	Peptide #7869 encoded by probe for measuring placental gene expression - Homo sapiens, 123 aa. [WO200157272-A2, 09-AUG-2001]	1..97 1..97	86/97 (88%) 92/97 (94%)	7e-43

In a BLAST search of public sequence databases, the NOV98a protein was found to have homology to the proteins shown in the BLASTP data in Table 98D.

Table 98D. Public BLASTP Results for NOV98a				
Protein Accession Number	Protein/Organism/Length	NOV98a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q924V2	CARBONYL REDUCTASE 2 - Cricetulus griseus (Chinese hamster), 277 aa.	1..277 1..277	243/277 (87%) 260/277 (93%)	e-139
Q91X28	SIMILAR TO CARBONYL REDUCTASE 1 - Mus musculus (Mouse), 277 aa.	1..277 1..277	244/277 (88%) 256/277 (92%)	e-139
Q924V3	CARBONYL REDUCTASE 1 - Cricetulus griseus (Chinese hamster), 277 aa.	1..277 1..277	241/277 (87%) 256/277 (92%)	e-137
P48758	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) - Mus musculus (Mouse), 276 aa.	2..277 1..276	240/276 (86%) 253/276 (90%)	e-136
JC5284	carbonyl reductase (NADPH) (EC 1.1.1.184), inducible - rat, 277 aa.	1..277 1..277	236/277 (85%) 249/277 (89%)	e-134

PFam analysis predicts that the NOV98a protein contains the domains shown in the
5 Table 98E.

Table 98E. Domain Analysis of NOV98a			
Pfam Domain	NOV98a Match Region	Identities/ Similarities for the Matched Region	Expect Value
adh_short: domain 1 of 1	4..274	67/286 (23%) 185/286 (65%)	1.6e-38

Example 99.

The NOV99 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 99A.

Table 99A. NOV99 Sequence Analysis			
	SEQ ID NO: 283	1001 bp	
NOV99a, CG58624-01 DNA Sequence	CTTGGTATAAGTAAGTGCTCGTCAATGTTGGCTACTCTCAATGTGCAGAGCCGCAGCCGCGGGGCGCAGAGCGCGATCTCTACCGGGACACGTGGGTGCGATACCTGGGCTATGCCAATGAGGTGGGCGAGGCTTTCGCTCTCTTGTGCCAGCGCGGTGGTGTGGCTGAGCTATGGCGTGGCCAGCTCCTACGTGCTGGCGGATGCCATTGACAAAGGCAAGAAGGCTGGAGAGGTGCCAGCCCTGAAGCAGGCCGAGCGCCAGGGTGACTGTGGCTGTGGTGGACACCTTTGTATGGCAGGCTCTAGCCTCTGTGGCCATTCCGGGCTTCACCATCAACCGCGTGTGTGCTGCCTCTCTCTATGTCTCTGGGCACTGCCACCCGCTGGCCCTTGGCTGTCCGCAAGTGGACCAACCGCGCTTGGGCTGTTGACCATCCCCATCATTTACACCCCATTGACAGGGATCATCCACTCTCCAGTGATGAGAGTGGATCATCCAGTCTCCAGCACGAAGGCCAGGGGTCCCACAGGTGAGTGGAGCCCCAGCAGCCCCCTCAGCTCTGCGTGCCCATGTACTGGTCTTCTCTCCCTGGCTCTATACTCAGTGTTCAAGGGGTTGGACGGGGCTTGGGCCGCGAGCTGCGCTGGCTTTGCTGCTCCACAAGGGCACCGTGGCTGTGAGCTGTGCCTGCTCCTGCAACTGCTGCAGAGCCACGTAGGGTTACAGGTGGTGGCTGGCTGTGGGATCCACTTCTTGTGCATGACACTTCTAGGCATCCGGCTGGGTGCGGCTCTGGCACAGTCAGCAGGGCCTCTGCACCAAGCTGGCCAGTCTGTGCTAGAGGGCATGGTGGCTGGCACCTTCTCTATACCACCTTTCTGGAATCTTTCCACAGGAGCTGGCGACTTCTGAGCAAAGGATCTCTCAAGGTCACTTCTGCTCCTAGAAAGGTGTGCCCTGCTCACTGGCTGCTCTTCATCCATATCTATAGGGGGCTT		
	ORF Start: ATG at 41	ORF Stop: TAG at 992	
	SEQ ID NO: 284	317 aa	MW at 33737.8kD
NOV99a, CG58624-01 Protein Sequence	MSEPQPRGAERDLYRDTWVRYLYGANEVGEAFRSLVPAAVVWLSYGVASSYVLADAIIDKGKKAGEVPSPEAGRSARVTVAVVDTFVWQALASVAIPGFTINRVCAASLYVLGTATRWPLAVRKWTTTALGLLTIPIIHPIIDRDHPLSSDESGSSSLQHEGPGVPQVSGAPAAPSALRAHVLVFSALALYSVFKGLDGAWAAELRLALLLHKGTVAVSLSLQLLQSHVGLQVVAGCGIHFLCMTLLGIRLGAALAQSAAGPLHLQAQSVLEGMVAGTFLYTTTFLEIFPQELATSEQRILKVILLLEGCALLTGLLFIHI		

Further analysis of the NOV99a protein yielded the following properties shown in
5 Table 99B.

Table 99B. Protein Sequence Properties NOV99a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 55 and 56

A search of the NOV99a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 99C.

Table 99C. Geneseq Results for NOV99a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV99a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM93835	Human polypeptide, SEQ ID NO: 3905 - Homo sapiens, 324 aa. [EP1130094-A2, 05-SEP-2001]	140..317 141..324	134/184 (72%) 145/184 (77%)	3e-63
AAV52394	Human transmembrane protein HP10528 - Homo sapiens, 324 aa. [WO9955862-A2, 04-NOV-1999]	140..317 141..324	134/184 (72%) 145/184 (77%)	3e-63
AAV84895	A human proliferation and apoptosis related protein - Homo sapiens, 324 aa. [WO200023589-A2, 27-APR-2000]	140..317 141..324	134/184 (72%) 145/184 (77%)	3e-63
AAB43291	Human ORFX ORF3055 polypeptide sequence SEQ ID NO:6110 - Homo sapiens, 323 aa. [WO200058473-A2, 05-OCT-2000]	140..317 140..323	134/184 (72%) 145/184 (77%)	3e-63
AAM93650	Human polypeptide, SEQ ID NO: 3514 - Homo sapiens, 324 aa. [EP1130094-A2, 05-SEP-2001]	140..317 141..324	133/184 (72%) 144/184 (77%)	2e-62

- 5 In a BLAST search of public sequence databases, the NOV99a protein was found to have homology to the proteins shown in the BLASTP data in Table 99D.

Table 99D. Public BLASTP Results for NOV99a				
Protein Accession Number	Protein/Organism/Length	NOV99a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UDX5	WUGSC:H_DJ0539M06.2 PROTEIN - Homo sapiens (Human), 166 aa.	1..152 1..152	145/152 (95%) 145/152 (95%)	6e-78
Q9CRB8	2610507A21RIK PROTEIN (1700020C11RIK PROTEIN) - Mus musculus (Mouse), 166 aa.	1..168 1..164	133/168 (79%) 143/168 (84%)	8e-69

Q9CZX4	2610507A21RIK PROTEIN - Mus musculus (Mouse), 166 aa.	1..143 1..143	125/143 (87%) 133/143 (92%)	2e-68
Q9NY26	IRT1 PROTEIN (SIMILAR TO ZINC/IRON REGULATED TRANSPORTER-LIKE) (HYPOTHETICAL 34.2 KDA PROTEIN) (UNKNOWN) (PROTEIN FOR MGC:14180) - Homo sapiens (Human), 324 aa.	140..317 141..324	134/184 (72%) 145/184 (77%)	1e-62
Q9Y380	CGI-71 PROTEIN - Homo sapiens (Human), 324 aa.	140..317 141..324	134/184 (72%) 145/184 (77%)	1e-62

PFam analysis predicts that the NOV99a protein contains the domains shown in the Table 99E.

Table 99E. Domain Analysis of NOV99a			
Pfam Domain	NOV99a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Syndecan: domain 1 of 1	235..255	9/21 (43%) 16/21 (76%)	6.9
Zip: domain 1 of 1	174..313	52/178 (29%) 108/178 (61%)	2.3e-15

Example 100.

The NOV100 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 100A.

Table 100A. NOV100 Sequence Analysis		
	SEQ ID NO: 285	987 bp
NOV100a, CG59679-01 DNA Sequence	AGACGCTCACACAGACAACTCAAGTCCAGCAACATCTTAGTAGCCAAAATCGACTG CTTTAGTTCTTCTGGTGGGTGCCCTCTCACTGTCCACTCGGCTATGCCATCCTGCAGTC GCATTGCACTGGTGACTGGAGCTAATAAGGGCATTGGCTTTGCGATCACTCGTGACCT GTGTCAGCAATTCTCAGGGGATGTGGTGCTCACTGCACGGGACGAGGCACGGGGCCTT GCGGCAGTGCAGAAGCTGCAGGCTGAGGGCCTGATTCTCGCTTCCACCAGCTGGACA TCAATGACCTCAGAGCATCCATGCACCTTCGCACTTTCTGCTCAAGGAGTACGGAGG CCTGGATGTGCTGGTCAACAACGCGGCATTGGCGTGCTTTCAAAGTGGATGACCCA ACACCTTCGACATTCAAGCTGAGGTGACACTGAAGACGAACCTTTTGGCCACTAGAA ATGCTGCACTGAGTTACTGCCTATAATGAAACCACATGGTAGAGTGGTGAACATCAG CAGTCTGCAGGGGTTAAAGCCCTTGAGAACTGCAGGGAAGATCTTCAGGAAAAGTTC CGATGTGACACACTTACCGAGGTGGACCTGGTCGACCTCATGAAAAGTTTGTGGAGG ATACAAAAATGAAGTCCATGAGAGGGAAGGTTGGCCGAGCTCGGCTTACGGGGTGTC GAAGCTGGGGGTGACAGTCCTTACGAGGATCCTGGCCCGGAGCTGGATGAAAAGAGG AAAGCGGACAGGATTCTGCTCAATGCCTGCTGCCCGGATGGGTGAAGACCGACATGG CGAGGGACCGAGGCTCCCGGACCGTGGAAAGAGGGGGCCGAAACCCCGTTACTTGGC TCTCTGCCTCCAGATGCCACTGAACCTCACGGCCAGCTAGTCCGTGACAAAGTTGTG CAAACCTGGTGAACGCTGCTCTGGGGCTTAATTGTTTGATAAACGTTAGCGGGAGAG A	

	ORF Start: ATG at 101	ORF Stop: TGA at 938	
	SEQ ID NO: 286	279 aa	MW at 31007.2kD
NOV100a, CG59679-01 Protein Sequence	MPSCSRIALVTGANKGIGFAITRDLCQQFSGDVLTARDEARGLAQVQLQAEGLIPR FHQLDINDPQSIHALRNFLKEYGGLDVLVNNAGIGVLFKVDPTFFDIQAEVTLKTN FFATRNVCTELLPIMKPHGRVNNISLQGLKALENCREDLQEKFRCDTLTEVDLVDLM KKFVEDTKNEVHEREGWPSAYGVSKLGVTVLTRILARQLDEKRAKADRIILLNACCPGW VKTDMARDQGSRTVEEGAETPVYLALLPPDATEPHGQLVRDKVVQVQW		

Further analysis of the NOV100a protein yielded the following properties shown in Table 100B.

Table 100B. Protein Sequence Properties NOV100a	
PSort analysis:	0.3600 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1808 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV100a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 100C.

Table 100C. Geneseq Results for NOV100a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV100a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW51011	Human liver carbonyl reductase - Homo sapiens, 277 aa. [US5756299-A, 26-MAY-1998]	1..279 1..277	198/279 (70%) 233/279 (82%)	e-112
AAU33100	Novel human secreted protein #3591 - Homo sapiens, 175 aa. [WO200179449-A2, 25-OCT- 2001]	145..279 40..174	88/135 (65%) 110/135 (81%)	2e-48
AAG46601	Arabidopsis thaliana protein fragment SEQ ID NO: 58644 - Arabidopsis thaliana, 302 aa. [EP1033405-A2, 06-SEP-2000]	3..259 20..283	106/268 (39%) 157/268 (58%)	6e-43
AAG46600	Arabidopsis thaliana protein fragment SEQ ID NO: 58643 - Arabidopsis thaliana, 316 aa. [EP1033405-A2, 06-SEP-2000]	3..259 34..297	106/268 (39%) 157/268 (58%)	6e-43

AAG46599	Arabidopsis thaliana protein fragment SEQ ID NO: 58642 - Arabidopsis thaliana, 327 aa. [EP1033405-A2, 06-SEP-2000]	3..259 45..308	106/268 (39%) 157/268 (58%)	6e-43
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In a BLAST search of public sequence databases, the NOV100a protein was found to have homology to the proteins shown in the BLASTP data in Table 100D.

Table 100D. Public BLASTP Results for NOV100a				
Protein Accession Number	Protein/Organism/Length	NOV100a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JJN7	CARBONYL REDUCTASE (EC 1.1.1.184) (CARBONYL REDUCTASE 3) - Cricetulus griseus (Chinese hamster), 277 aa.	1..279 1..277	246/279 (88%) 262/279 (93%)	e-140
AAH02812	CARBONYL REDUCTASE 3 - Homo sapiens (Human), 277 aa.	1..279 1..277	227/279 (81%) 246/279 (87%)	e-126
O75828	Carbonyl reductase [NADPH] 3 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 3) - Homo sapiens (Human), 276 aa.	3..279 2..276	226/277 (81%) 245/277 (87%)	e-126
Q924V2	CARBONYL REDUCTASE 2 - Cricetulus griseus (Chinese hamster), 277 aa.	1..279 1..277	206/279 (73%) 244/279 (86%)	e-119
Q91X28	SIMILAR TO CARBONYL REDUCTASE 1 - Mus musculus (Mouse), 277 aa.	1..279 1..277	204/279 (73%) 240/279 (85%)	e-116

5 PFam analysis predicts that the NOV100a protein contains the domains shown in the Table 100E.

Table 100E. Domain Analysis of NOV100a			
Pfam Domain	NOV100a Match Region	Identities/ Similarities for the Matched Region	Expect Value
adh_short: domain 1 of 1	4..277	77/316 (24%) 186/316 (59%)	5.2e-31

Example 101.

The NOV101 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 101A.

Table 101A. NOV101 Sequence Analysis			
	SEQ ID NO: 287	1011 bp	
NOV101a, CG59644-01 DNA Sequence	<div>CTCCTCGGGGGGGCGGCGGCGGCGATGTTCTCGGTCTCTCGTACGGGCGGCTGGTGG CCGCGCGCGGTGCTCGGCGGCCTCTCGCAGACCGACCCAGGGCCGGCGGCGGCGGCG CGGCGCGGTGCTCGGCGGCCTCTCGCAGACCGACCCAGGGCCGGCGGCGGCGGCGGCG GGCGACTACGGAAGTGGTACGGCGGCTGCGGCTTCGGGAAGGACTTCCGTAAGGGCC TCCTCAAGAAGGGCGCGTGTCTACGGGGACGACGCGTGTCTCGTGGCCCGGACCGTTC CGCGGACGTGCTCGGTGTTGCAGATGGTGTAGGAGCTGGAGAGACTATGGAGTTGAT CCATCTCAATTCTCAGGACTTTAATGCGGACGTGTGAACGTTTAGTAAAAGAAGGAC GGTTGCTACCTAGTAATCCCATTTGGAATTTCTACCACAAGCTACTGTGAGTTGCTGCA AAATAAAGTCCCTTTGCTCGGTAGCAGCACCGCCTGCATTGTGGTGTGCGGACAGAAC AGCCACCGCTTACACACAGCAAACCTGGGCGATTCAAGGCTTCTGGTTGTCTAGGGGTG GTGAAGTCGTGCACCGATCAGATGAGCAGCAGCATTACTTCAACACTCCATTCCAGCT CTCAATCGCTCCCCCTGAAGCCGAGGGAGTCGTCTTGAGCGACAGTCCGGATGCTGCT GATAGCAGCTCTTTCGATGTCCAGCTAGGAGACATTATCTGACGGCAACAGATGGAC TCTTTGACAACATGCCTGATTATATGATTCTTCAGGAGCTAAAAAGTTAAAGAATTC AAATTATGAGAGTATACAAAGACTGCCAGAAGCATTGCTGAGCAAGCTCATGAGCTG GCCTATGACCCAAATTATATGTCACCTTTTGACAGTTTGCATGTGACAATGGATTGA ATGTGAGAGGTGGTGGAAAGCCAGATGACATCACCCTCCTTCTTCAATAGTGGCTGA GTATACAGACTAGCTGAGGTGTCAA</div>		
	ORF Start: ATG at 25	ORF Stop: TAG at 997	
	SEQ ID NO: 288	324 aa	MW at 34311.1kD
NOV101a, CG59644-01 Protein Sequence	<div>MFSVLSYGRIVARAVLGGLSQTDPRAGGGGGGAVLGGLSQTDPRAGGGGGGGLVLTVA GCGFGKDFRKGLLKKGACYGDDACFVARHRSADVGVADGVGGWRDYGVDPSQFSGLT MRTCEERLVKEGRFVPSNPIGILTTSYCELLQNKVPLLSSTACIVVLDRTSHRLHTAN LGDSGFLVVRGGEVVHRSDEQQHYFNTPFQLSIAPPEAEGVVLSDSPDAADSTSFVQ LGDIILLATDGLFDNMPDYMILQELKKLKNYSIESIQQTARSIAEQAHELAYDPNYS PFAQFACDNLNVRGGGKPPDITVLLSIVAETD</div>		

Further analysis of the NOV101a protein yielded the following properties shown in
5 Table 101B.

Table 101B. Protein Sequence Properties NOV101a	
PSort analysis:	0.5708 probability located in mitochondrial matrix space; 0.4996 probability located in mitochondrial intermembrane space; 0.2852 probability located in mitochondrial inner membrane; 0.2852 probability located in mitochondrial outer membrane
SignalP analysis:	Likely cleavage site between residues 23 and 24

A search of the NOV101a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 101C.

Table 101C. Geneseq Results for NOV101a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV101a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB85357	Human phosphatase (PP) (clone ID 3402521CD1) - Homo sapiens, 304 aa. [WO200153469-A2, 26-JUL-2001]	1..324 1..304	304/324 (93%) 304/324 (93%)	e-173
AAU32112	Novel human secreted protein #2603 - Homo sapiens, 304 aa. [WO200179449-A2, 25-OCT-2001]	25..324 6..304	272/300 (90%) 274/300 (90%)	e-156
AAG52267	Arabidopsis thaliana protein fragment SEQ ID NO: 66421 - Arabidopsis thaliana, 348 aa. [EP1033405-A2, 06-SEP-2000]	71..320 99..340	101/261 (38%) 133/261 (50%)	4e-33
AAG52266	Arabidopsis thaliana protein fragment SEQ ID NO: 66420 - Arabidopsis thaliana, 374 aa. [EP1033405-A2, 06-SEP-2000]	71..320 125..366	101/261 (38%) 133/261 (50%)	4e-33
AAG52265	Arabidopsis thaliana protein fragment SEQ ID NO: 66419 - Arabidopsis thaliana, 467 aa. [EP1033405-A2, 06-SEP-2000]	71..320 218..459	101/261 (38%) 133/261 (50%)	4e-33

In a BLAST search of public sequence databases, the NOV101a protein was found to have homology to the proteins shown in the BLASTP data in Table 101D.

Table 101D. Public BLASTP Results for NOV101a				
Protein Accession Number	Protein/Organism/Length	NOV101a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9W0E2	CG12091 PROTEIN - Drosophila melanogaster (Fruit fly), 321 aa.	1..320 1..320	163/322 (50%) 218/322 (67%)	1e-83
Q9W3R1	CG15035 PROTEIN - Drosophila melanogaster (Fruit fly), 374 aa.	55..319 109..373	127/266 (47%) 178/266 (66%)	1e-64
O18183	W09D10.4 PROTEIN - Caenorhabditis elegans, 330 aa.	4..320 7..330	136/331 (41%) 198/331 (59%)	2e-60

Q9VAH4	CG7615 PROTEIN - Drosophila melanogaster (Fruit fly), 314 aa.	35..319 26..309	122/285 (42%) 168/285 (58%)	2e-56
Q9SUK9	HYPOTHETICAL 36.2 KDA PROTEIN - Arabidopsis thaliana (Mouse-ear cress), 335 aa.	71..320 86..327	101/261 (38%) 133/261 (50%)	1e-32

PFam analysis predicts that the NOV101a protein contains the domains shown in the Table 101E.

Table 101E. Domain Analysis of NOV101a			
Pfam Domain	NOV101a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PP2C: domain 1 of 1	147..191	13/48 (27%) 36/48 (75%)	0.26

Example 102.

- 5 The NOV102 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 102A.

Table 102A. NOV102 Sequence Analysis			
	SEQ ID NO: 289	523 bp	
NOV102a, CG59662-01 DNA Sequence	AGTCCCAGTACTATCAGCCATGGTCAACCACACCATGTTCTTCGACGTTGCTGTCGACAGTGAGCCCTTGGACCACGTCCTCTTGAGCTGTTTGCAGAAAAGTTTCCAAAGACAGCAGAAAACGTTTCGTGCTCTGAGCACTGAAGAGAAAAGGATTGGTTATAAGGGTCCCTGCTTTTCACAGAATTATACCAGCATTTATGTGTGTCAGGGTGGTGACTTCACGCACCATAATGGCACTGGTGGCAAGTCCATCTACGGGGAGAAAATTGAAGATGAGAAATTTATCCTAAAGCGTACAGGTCTGGCATCTTGTCATGGCAAATTCGGACCCAAACACAAACTGTTTCGTTTTTTTTCATCTGCACTGCCAAGACGGGGTGGTTGGATGGCAAGCATGTAGTCTTTGGCAAGGTGAAAGAAGGCATGAATATTTGGAGGCCATAGAGCAATTTGGGTCCAGGATATGGCAAGACCAGCAAGAAGACCACCATTTGCTGACTGTGGACAGCTCTGGTAAAGTTTGA		
	ORF Start: ATG at 20	ORF Stop: TAA at 515	
	SEQ ID NO: 290	165 aa	MW at 18237.7kD
NOV102a, CG59662-01 Protein Sequence	MVNHTMFFDVAVDSEPLDHVSFELFAEKFPKTAENVRLSTEERGFYKGPCFHR IIPAFMCQGGDFTHNGTGGKSIYGEKFEDEKFLKRTGPGILSMANSGPNTNCSVFFICTAKTGWLDGKHVVFGVKEGMNILEAIEQFGSRNGKTSKTTIADCGQLW		

Further analysis of the NOV102a protein yielded the following properties shown in Table 102B.

Table 102B. Protein Sequence Properties NOV102a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)

TTTCGCACGCTCTGGGCAAGGATGTCCCCGCGATGGCAAAGCCGAGTTCGCTTGCGAG
CAAGTGTGCTTTTCATGCTTGATCGAATCTATCGATTGACACAGTTATTGCCCGGATT
GAAGCGCTTTCTATTGAGCGCTTGCAAAAGCTGCTACTGGAGAAGGATCGGCTCAAGT
TCTGCATTGCCAGTATGTATCGGAAGAATAACGATGACTCTGGCGCGGAGATCAAGGC
GGGGAATGGGACGGTTGACATGTCCGTCTTACCCGATGCGAGATACTCTGCACTGCTC
CAGGAGGACTTCGCCTATTCAAGGTTTGAGTGCTGGGTGGAGAATGAGGATCAGATCC
AGGAGCCACACAGCTGCCATGGTTCAGAAGGCCCTGGAAACCGACCCAGGAGATGCCG
TGGTTGTGCCGCTTTGCGGTTGCTGATTCTGACTATGAAGCCATTTGTAAGGTACCT
CGAAAGGTGGCCAGAAGTATCTCTGCGGCCCTTCTAGCAGGTGGTTCGACCAAGCATTT
GCACTGAAGAACCAGCGTTGTCTGAGGTTGGGCCACCCGACTTAGCAAGCAAAAGGT
ACCCCCAGATGGAGAAAGCATGGAGGAAGAGACGCCCTGGTTCCTCTGTGGAATCTTTG
GATGCAAGCGTCCAGGCTAGCCCTCCACAACAGAAAGATGAGGAGATCAGGATCAGATCC
CAAAGGAACCTGGAAAGTGTGACTGTTGTTTCAGATGATCAGGCTCCGCAGCATGGGTG
TAATCACAAGCTGGAAATTAGCTCTTAGCATGATTAAAGGTCTTGATTATAAGCCCATC
CAGAGCCCCGAGGGAGCAGGCTTCCGATTCCAGTGAAATCCAGGCTCAGGAGTCCCA
AGCCTGGCCCTAGCATGACAGATGGAGTTAGTTCGCGTTTCCCTTAACAGGTCTTTGAA
ACCCCTTTACAAGACACCTGTGAGTTATCCCTTGGAGCTTTTCAGACCTGCAGGAGCTG
TGGGATGATCTCTGTGAAGATTATTTGCGCTCCGGGTCCAGCCCATGACTGAAAGAT
TGCTGAAACAACAAAGCTGAATTTCATGAGACCACTATAACTCAGCAGTCTGTATC
TGATTCCCCTTGGCAGAACTCCAGGAAAAATCCAGCAAACAGAGGCCACCAACAAG
ATTCTCAAGAGAACTTAATGAAATGAGCTATGAACTAAAGTGTGCTCAGGAGTCTGT
CTCAAAGCAAGATGGTACAATTACAGAACCTCAAGGAACTCTGAAAGCAGGGAAACG
TGAGACTGAGGAGTTGTACCAGGTAATTGAAGGTCAAATGACACAATGGCAAAGCTT
CGAGAAATGCTGCCAAAGCCAGCTTGGACAACCTCAGAGTGTGCTCAGGAGTCTTCTC
CAGCTCAGCAACAGGTAGCTCTGCTTGATCTTCAGAGTGCTTTATCTGCAGCCAACT
TGAAATACAGAAGCTCCAGAGGGTGGTACGACAGAAAGAGCGCAACTGGCTGATGCC
AAACAATGTGTGCAATTTGTAGAGGTGCAGCACACGAGAGTGAACAGGAGGAGG
CTTCTTGGAAACATAACCAGGAATTGCGAAAAGCCTTGCAGCAGTACAAGAAGAAAT
GCAGAAATAAGAGCCAAACAGCTTCGTGCCTGGGAGGCTGAAAAATACAATGAGATTGCA
ACCCAGGAACAAAACATCCAGCACCTAAACCATAGTCTGAGTCAACAGGAGGAGTGC
TTCAGGAATTTCCGGGAGCTCCTACAGTATCGAGATAACTCAGACAAAACCTTGAAGC
AAATGAAATGTTGCTTGAGAACTTCGCCAGCGAATACATGATAAAGCTGTTGCTCTG
GAGCGGGCTATAGATGAAAAATTTCTCTGCTCTAGAAGAGAAAGAAAAAGAACTGCGCC
AGCTTCGTCTTGCTGTGAGAGAGCGAGATCATGACTTAGAGAGACTGCGCGATGTCTCT
CTCTCCATGAAGCTACTATGCAAAGTATGGAGAGTCTCTGAGGGCCAAAGGCCCTG
GAAGTGGAAACAGTATCTACTACCTGTCAAACCTCCAGTGGTGAAGAGAAATGG
AAACCAAATTTAGCCGTGGCAGAAGGAACAAGAGAGTATCATTCAGCAGTTACAGAC
GTCTCTTCATGATAGGAACAAAGAAGTGGAGGATCTTAGTGCAACACTGCTCTGCAAA
CTTGGACAGGGCAGAGTGAGATAGCAGAGGAGCTGTGCCAGCTCAGAGGCAAGAGG
AAAGGATGTGTCAGGACCTTCTAAGTATCGAAATAAACAAGTGTGGAACATGAAAT
GGAGATTCAAGGCCTGCTTCAGTCTGTGAGCACAGGGGAGCAGGAAAGCCAAGCTGTCT
GCAGAGAAAGTTGGTCAAGCCTTAATGGAAAGAAATTCAGAAATACAGGCCCTGCGCC
AATATTTAGAGGGAGAGACTCCCTGATGTCCCAAGCACCCTCTCTAACCAACAAGC
TGAAGTTACCCCACTGGCCGCTTGGAAAAACAGACTGATCAAGGTTCAATGCAGATA
CCTTCAGAGATGATAGCACTTCATTGACTGCCAAAGAGGATGTCAGCATACCCAGAT
CCACATTAGGAGACTTGGACACAGTTGCAGGGCTGGAAAAAGAACTGAGTAAATGCCAA
AGAGGAACCTTGAACCTCATGGCTAAAAAAGAAAGAGAAAGTCAAGTGAACCTTTCTGCT
CTACAGTCCATGATGGCTGTGCAGGAAGAAGAGCTGCAGGTGCAGGCTGCTGATATGG
AGTCTCTGACCAGGAACATACAGATTAAAGAAGATCTCATAAAGACCTGCAATGCA
ACTGGTTGATCCTGAAGACATACCAGCTATGGAACGCTGACCCAGGAAGTCTTACTT
CTTCGGGAAAAATGCTTCAGTAGAATCCAGGGTCAAGAAATTCAGGAACCCGAA
GACAACAGTTGCTGCTGATGTAGAAGGACTAGTAGATGAACGGAGTCCGCTCAATGA
GGCCTTACAAGCAGAGAGACAGCTCTATAGCAGTCTGGTGAAGTTCCATGCCCATCCA
GAGAGCTCTGAGAGAGACCGAACTCTGCAGGTGGAACCTGGAAGGGCTCAGGTGTTAC
GCAGTCCGCTAGAAGAAGTTCTTGGAAGAAGCTTGGAGCGCTTAAACAGGCTGGAGAC
CCTGGCCGCCATTGGAGGTGCAGCTGCAGGGGATGACCCGAAGATACAAGCACTGAG
TTCCTGACAGTATTGAGGAGGAGGCTGCACACCATAGTCACCAACCTTGTCAAGG
TGGCTTTGGAGAAAAGTCTGGCAACTGTGGAGACCCAGAACCCATCTTTTCCCTCC
TTCTCCGATGGGAGGGGACAGTAACAGGTGCTTCAGGAAGAAATGCTCCACCTGAGG
GCTGAGTTCCACCAGCACTTAGAAGAGAAGAGGAAGCTGAGGAGGAAGTGAAGGAGC
TAAAGGCTCAAATTGAGGAAGCAGGATTCTCCTCAGTGTCCACATCAGGAACACCAT
GCTGAGCCTTTGCTTGTAGAATGCGGAGCTGAAAGAGCAGATGGGAGAAGCAATGTCT
GATGATGGGAGATCGAGGAAGACAAGGAGAAGGGCGAGGTGATGGTTAGAGTGTGG
TAACCAAAGAGGGTCTGAGTGAGAGTAGCCTTCAGGCTGAGTTACAGAAAGCTCCAGGG
AAAACCTGAAGAATGCCACAATATCATCAACCTCCTCAAAGAACAACCTGTGTGAGT
AGCAAGGAAGGGAATAGTAAACTTACTCCAGAGCTCCTTGTGCTATCTGACCAACCA
TTGAAAGAATAAACACAGAAGTGGTTGGTTCCCCTGGGAAGCACCAACCAAGAGGA
GGGGAATGTGACTGTGAGGCCCTTCCCAGACCCAGAGCCTTGACCTTGGGGCTACC
TTCACAGTGGATGCCACCAATTGGATAACCACTCCAGCCTCGTGACCTTGGGCCTC
AGTCAGCGTTTAGCCTACCAGGGTCCACCCAGCACCTGCGCTCCAGCTGTCACAATG
CAAACAACGCTATCAAGATCTCCAGGAGAAGCTGTGCTATCAGAAGCCATGTCTTT
GCTCAGGCTAACGAGCTGGAGAAATACAGAGTTATGCTTACAGGTGAATCCTTGGTGA
AGCAGGACAGCAAGCAGATCCAGGTGGACCTCCAGGACCTGGGCTATGAGACTTGTGG
CCGAAGCGAGAATGAGGCTGAACGGGAGGAAACCACAGTCTGAGTGTGAGGAGCAC
AACAGCCTCAAGGAATGGTCTGATGGAGGGGCTGTGCTCTGAGCAGGGACGCCGG
GCTCAACACTGGCTAGTTCCTCTGAGAGGAAGCCCTTGGAGAACCAGCTAGGGAAGCA
GGAAGAGTTCGGGTATATGGAAGTCAAGAAACATCTTGGTCTACGAAAGGACATC

	AAAGATCTGAAGGCCAGCTGCAGAATGCCAACAAAGGTCAATCAAAACCTCAAGAGCC GGGTCCGGTCCCTCTCAGTTACAAGTGATTATTCGTCTAGTCTGGAAGACCCCGGAA GCTGAGAGCTGTTGGCACCTTGGAGGGGTCTTCACCTCATAGTGTCCCTGATGAGGAT GAGGGGTGGCTGTCTGATGGCACTGGGGCTTTCTACTCTCCAGGGCTTCAGGCCAAAA AGGACCTGGAGAGTCTCATCCAGAGAGTATCCAGCTGGAGGCCAGCTCCCAAAAAA TGGACTAGAAGAGAAGCTGGCTGAGGAGCTGAGATCAGCCTCGTGGCTGGGAAATAT GATTCCTGATTAGGATCAGGCCCGGGAACGTCTTACCTACGGCAAAAAATACGAG AAGGGAGAGGTATTGTTATCTTATCACCCGGCATGCAAAAGATACAGTAAATCTTT TGAGGATCTCCTAAGGAGCAATGACATTGACTACTACCTGGACAGAGCTTCCGGGAG CAACTCGCCAGGGAAGCCAGCTGACAGAGAGGCTCACCAGCAAACTCAGACCAAGG ATCATAAAAGTGAGAAAGTCAAGCTGGACTTGAGCCACTGGCCCTCAGGCTCAGCAG GGAGCTGCAGGAGAAGGAGAAAGTGATTGAAGTCTGCAGGCCAAGCTGGATGCTCGG TCCCTCACACCCTCCAGCAGCCATGCCTTGTCTGACTCCACCGCTCTCCAGCAGCA CCTCTTCTCTGTCTGATGAACTGGAAGCTGCTCTGACATGGACATAGTCAGCGAGTA CACACACTATGAAGAGAAGAAAGCTTCTCCAGTCACCTCAGATCCATCATCTTCG AGTCATTCTGCTGTGTGTCTTCTAAACCATCATCAACCACTGTCATCTCAGGGGGCTA AGGCCGAATCCAACAGCAACCCCATCAGCTTGCCAACTCCCAGAATACCCCAAGGA GGCCAAACAGGCCCATTCAGGCTTTCATTTTCACTCCATACCCAGCTGGCTGCTCTCC CCTCAGGCACCATTGCCCTCAGTCCATCCAGCTTCTGCTTTCAGCCCACTGGCC CTCTCTCTCTGGCTGCTGTGAGACACCAGTGGTCTCTTGGCTGAGGCTCAGCAGGA GCTACAGATGCTGCAGAAGCAGTTGGGAGAAAGTGCCAGCAGCTGTTCTCTCTCTCC ACAGCTACATTGTCTGAGCAACGACTTGAAGCCGACTCTTCTACTACCTCAACTCTG CCCAGCCTCACTCTCTCCAAGGGGCACCATAGAAGTGGGAAGAACTCAGAGCTGAG GTACCTGGGCAGCAGTGGCAAGTGGGATGTGATGAGGCTCAGAAAGGAGTGTATCT GGGGACCTATCCTCAGGCTCCTCTGTGTACCAGCTTAACTCCAAACCCACAGGGCTG ACCTGCTGGAAGAGCATCTTGGTGAATCCGGAACCTGCGCCAGCGCTGGAGGAGTC CATCTGCATCAATGACCGCTACGGGAGCAACTGGAACACCGGCTACCTGCTACTGCT CGTGAAGGGGATCCACTTCTAATTCTACAGTCAGGCTTGGAGTCCATACCTCAGC TCTGCAATGAGAACAGAGTCTCAGGGAAGACAATCGAAGACTTCAGGCTCAACTGAG TCATGTTTCCAGAGAGCACTCCAGGAAACAGAAAGCCTGAGGAGGCTCTGCTGCTCC TCTCGATCCCACTTCAAGAGCTGGAAGAGGCTGGAGCACCAGAGGTGGAAGGC AGCAGCTTTTGAAGACTTGAGGGAGAAGCAGCAAGAGGTCTTGCATTTTCAGGGAGGA ACGTCTTTCCCTCCAGGAAACGACTCCAGACTGCAGCACAAGCTGTTCTCTCTCAG CAACAGTGTGAAGAGAAACAGCAGCTCTTTGAGTCCCTCCAGTCAGAGCTACAAATCT ACGAGGCACTTTATGGCAATCCAAAGAGGGGCTGAAAGGCTTGGGTTTGGATACTTC TCCAGTAATGAAGACCCCTCCCAAGCTAGAGGGTGATGCTACTGATGGCTCTTTGCC AATAAGCATGGCCGCCATGTCTTGGCCACATGTGACTACAGTCCCTTAAGACAGC AGATTGCGGAGGGCAAGCTGCTGGTCAAAAAGATAGTGTCTCTTGTGAGATCAGCGTG CAGCTTCCCTGGGCTTGAAGCCCAAGGCACAGAGGTGCTAGGCAAGATTCCTCTTGC GAGCTTCGGAGCAGCACCAGTGCCTGCACCATGCCCTAGAGGAGTGGGCTTCCCTCC TCACCATGTTCTGGAGAGCAGCCCTGCCAAGCACCACATCCCTGTGCTGCCTGGCAA AGTGGGAGAATCAACAGAAAGGGAACCTTCTGGAAGTGAAGAACCAAGATTCCAAACAG GAGCGGCTCCTTCAGAGCACACTGAGCATCTGAAGAAGCCCAACAGCAGAGGAGA GCATGGAGCAGTTCATCGTCAGCCAGCTAACCAGAACACATGATGTTTAAAGAAAGGC AAGGATAACTTAGAGGTGAAATCCCTAAGGCTCTGCCATGTACTCCAGCCTTGTGA CCCTTGCCTTCCAGGAACCATGCAAGAAGCGCAGCCACCAGAAGTCTTAAACAGCA GGAAAGGTGGGCTGTCCCTCTTTGTGTCAGTACCTATCTGTGAGGAGCATCTGGG CCTCATCTCCAGTCCAGGGAGGGTCCAGAAGAGGGAGTCCAGAGATGTATCTCTGG TGGAGCTGGGAGAAAGGCAGAAAGCCTTCTGACAGCTATGGAATACGATTAGCCAAAG GTCCACTTGGCCAGCACTAAGAAAAAGATGCGTAGTTTGACAGAAAGTTTGTGAT CCTGCTCTCAACAGCCAGCAGCTTGGGAAGTACAGCAAGCATTTCTTGGCTCA TCAGTGTCTGAGATGGAAGAACTCAGTGGATATAGGACCTGATTCCGATGAAGGG GCACGTGGTCCCAATGCTGGAGCTCCTCTGGCAGGTTCTAAAAGCACACTACTGAGCA CGGTGCTCCTGCCGACACTGCTGGCGGGGGCTCAGTGAGCACTACTCAGCATCCAC ACCTGACCTGTGTTGGGTGAGTCAGGCTGGGCTTGGTCTGCACTGTAGCACCTGTGT TCTTTGAGTTCACATCATGAATGTGGTGACTTCCCAGATACCATCTCAGGCTTAACTT AGCACATCCTATTCTTTTCTTCTATGATATCCAAATGGACTGACCTCACTTCAAAG TTGCTGTCCCATTTTGTCACTTATCTATCTCGGGGAAATGTCAGACTGATGGCCAG ACCAACTCTGTTGAAATCTTGCATAGAGCAAACCTGTGCTCAITTTTAAAGTGGCATG GGAGAGGCCCCAGCCTAGTAAAGCCTAGTCTGTGTCTTACAGTGTCTGGTAGAATGT GTTTGTGTATATAATATATATATAGATTTATATATGTTGCTAACGCCATATATTGA AGGCCAACATAACTGGTGGACAGGGTGGGTGACAGAAATGAAAGCCTTTTGGTGAT TGTTAAAGCAAGATGTGTATAAAGAAATAAATAGTTTTCTTTC		
	ORF Start: ATG at 658	ORF Stop: TGA at 7828	
	SEQ ID NO: 292	2390 aa	MW at 268843.7kD
NOV103a, CG59773-01 Protein Sequence	MKEICRICARELCGNQRRWIFHTASKLNLQVLLSHVLGKDVPRDGKAEFACSKCAFML DRIYRFDTVIARIEALSIERLQKLLLEKDRKFICIASMYRKNNDDSGAEIKAGNGTVD MSVLPDARYSALLQEDFAYSGFECWVENEDQIQEPHSCGSEGPNNRPRRCRGCAALR VADSDYEAICKVPRKVARISICGPPSSRWSTICTEEPALSEVGPPDLASTKVPDPGES MEEETPGSSVESLDASVQASPPQKDEETERSAKELGKDCSSDDQAPQHGCHNKLLEL ALSMIKGLDYKPIQSPRGSRLPIPVKSSLPGAKPGPSMTDGVSSGFLNRSLLKPLYKTP VSYPLELSDQLQELWDDLCEDYLPLRVQPMTEELLKQKLNSHETTITQQSVSDSHLAE LQEKIQQTEATNKILQEKLNEMSYELKCAQESSQKQDGTIQNLKETLKSRREREELY		

	<p>QVIEGQNDTMAKLEMLHQSQQLGQHSSEGTSPAQQQVALLDLQSAIFCSQLEIQKLO RVVRQKERQLADAKQCVQFVEAAAHSEEQKEASWKHNQELRKALQQLQEELQNKSSQ LRAWAEKYNEIRTQEQNIQHLNHSLSHKEQLLQEFRELLQYRDNSDKTLEANEMLLE KLRQRIHDKAVALERAIDEKFSALEEKEKELRQLRLAVRERDHDLERLRDLVSSNEAT MQSMESLLRAKGLEVEQLSTTCQNLQWLKEEMETKFSRWQKEQESIQQQLQTSLHDRN KEVEDLSATLLCKLPGQSEIAEELCQRLQKERMQLDQLSDRNKQVLEHEMEIQGLL QSVSTREQESQAAAEKLVQALMERNSELQALRQYLGGRLDLSMSQAPISNQAEVPTG RLGKQTDQGSQMPIPSRDDSTSLTAKEDVSI PRSTLGLDLDTVAGLEKELSNAAKEELEM AKKERESQMEALSALQSMMAVQEEELQVQAADMESLTRNIQIKEDLIKDLQMLQVDPED I PAMERLTQEVLLREKVASVESQGGQESGNRRQQLLLMLEGLVDESRSLNEALQAER QLYSSSLVKFHAHPESSERDRTLQVELEGAQVLRSLRLEEVLRSLERLNRLETAAIGG AAAGDDTETSTFTDSTIEEEAAHSHQQLVKVALEKSLATVETQNPSPFPPSPMGGD SNRCLQEEMHLHRAEFHQHLEEKRAEBELKELKAQIEEAGFSSVSHIRNTMLSLCLE NAELKEQMGEAMSDGWEIEEDKEKGEVMVETVVTKEGLSESSLQAEFRKLGKLNKNAH NI INLLKEQLVLSSKEGNSKLTPELLVHLTSTIERINTELVGSPGKHQHEEGNVTVR PFPRQSLDLGATFTVDAHQLDNQSQPRDPGPQSAFSLPGSTQHLSRQSLQCKQRYQD LQEKLLSEATVFAQANELEKYRVMLTGESLVKQDSKQIQVDLQDLGYETCGRSENEA EREETSPCEEHNSLKEMVLMBGLCSEQGRRGSTLASSERKPLENQLGQEEFVRVY GKSENI LVLKDIKDLKAQLQNAKVIQNLKSRVRSLSVTSDYSSSLERPRKLRAVGT LEGSSPHSVPEDEDEGLSDGTGAFYSPGLQAKKDLESILQVRSQLEAQLPKNGLEEK AEELRSASWPQKYDSLIDQARELSYLRQKIREGRGICYLITRHAKDTVKSFDLLRS NDIDYLLGQSFREQLAQGSQLTERLTSKLSTKDHKSEKDAQGLEPLALRLSRELEKE KVIEVLQAKLDARSLTPSSSHALSDSHRSPSSTSFLSDELEACSDMDIVSEYTHYEEK KASPSHSDSIHSSHSVAVLSSKPSSTSASQGAESNSNPISLPTPQNTPEANQAHS GFHFHSIPKLASLPQAPLPSAPSSFLPFSPTGPLLLGCCETPVVSLAEAQQLQMLQK QLGESASTVFPASTATLLSNDLEADSSYYLNSAQPHSPPRGTIELGRILEPGYLGSSG KWDVMRPQKQSVSGDLSSGSSVYQLNSKPTGADLLEHLGELIRNLRLQRLSEISICNDR LREQLEHRLTSTARGRGSTSNFYSGLESIPQLCENNRVLREDNRRLQAQLSHVREH SQETESLREALSSRSHLQELEKELEHQKVERQQLLEDLREKQQEVLFHREERLSLQE NDSRLQHKLVLLQQQCEEKQQLFESLQSELQIYEALYGNSSKGLGLDLSVPMKTP PKLEGDATDGSFANKHGRHVIGHIDYALRQQAEGKLLVKKIVSLVRSACSPFPLE AQGTEVLGSKGIELHRSSTALHHALESASLLTMFWRAALPSTHIPVLPGKVGESTE RELLELRTKVSKQERLLQSTTEHLKNANQQKESMEQFIVSQLTRTHDVLKARTNLEV KSLRALPCTPAL</p>
	<div>SEQ ID NO: 293</div> <div>7161 bp</div>
NOV103b, CG59773-02 DNA Sequence	<p>GTTGAGGGGGCAATCGGGCAGCGTCTCTCCCATGGGTGCCCATCATGTCTAATGGAT ATCGCACTCTGTCCAGCACCCTCAATGACCTGAAGAAGGAGAACTTCAGCCTCAAGCT CGCGATCTACTTCTGGAGGAGCGCATGCAACAGAAGTATGAGGCCAGCCGGGAGGAC ATCTACAAGCGGAACATTGAGCTGAAGGTGGAAGTGGAGAGCTTGAACACGAGAATCTC AGGACAAGAAACAGCATCTGGATAAAACATGGGCTGATGTGGAGAATCTCAACAGTCA GAATGAAGCTGAGCTCCGACGCCAGTTTGAGGAGCGACAGCAGGAGACGGAGCATGTT TATGAGCTCTTGGAGAATAAGATCCAGCTTCTGCAGGAGGAATCCAGGCTAGCAAGA ATGAAGCTGCGCGATGGCAGCTCTGTTGGAAGCAGAGAAGGAGTGTAACTGGAGCT CTCAGAGAACTGAAGGGAGTCACCAAAACTGGGAAGATGTACCAGGAGACAGGTC AAGCCCGACCAATACACTGAGGCCCTGGCCAGAGGAGCAGGAGATTGAAGAATCTGA ATCAGAGCCTGGCTGCCAGGAGAGGCTTGTAGAAGCTATCTCGGGAGAAACAACA ACTGCTACATCTGTTGGAGGAGCAACTAGCATGGAAGTGCAGCCCATGACTGGAAG TTGCTGAAACAACAAAAGCTGAATTACATGAGACCACTATAACTGAGCTAGTGAT CTGATTCCCACTTGGCAGAACTCCAGGAAAAATCCAGCAACAGAGGCCACCAACA GATTCTTCAAGAGAACTTAATGAAATGAGCTATGAACTAAAGTGTGCTCAGGAGTCG TCTCAAAAGCAGAATGGTACAATTGAGAACCCTCAAGGAACTCTGAAAAGCAGGAAC GTGAGACTGAGGAGTTGTACCAGTAATTGAAGGTCAAAATGACACAATGGCAAAGCT TCGAGAAATGCTGCACCAAGCCAGCTTGGACAACCTTCAGAGCTCAGAGGGTACTTCT CCAGCTCAGCAACAGGTAGCTCTGCTTGATCTTCAGAGTGCCTTTATCTGCAGCCAAC TTGAAATACAGAAGCTCCAGAGGTGTACGACAGAAAGAGCGCAACTGGCTGATGC CAACAATGTGTGCAATTGTAGAGGTGCAGCACACGAGAGTGAACAGCAGAAAGAG GCTTCTTGAAACATAACAGGAATTGCGAAAAGCCTTGACAGCTACAAGAAGAAT TGCAGAATAAGAGCCAACAGCTTCGTGCTGGGAGGCTGAAAAATACAATGAGATTG AACCAGGAACAAAACATCCAGCACCTAAACCATAGTCTGAGTCACAAGGAGCAGTTG CTTCAGGAATTTGGGAGCTCTACAGTATCGAGATAACTCAGACAAAACCTTTGAAG CAATGAAATGTTGCTTGAGAACTTCGCCAGCGAATACATGATAAAGCTGTTGCTCT GGAGCGGGCTATAGATGAAAAATCTCTGCTCTAGAAGAGAAAAGAAAAGAACTGCGC CAGCTTCGTCTTGTGTGAGAGAGCGAGATCATGACTTAGAGAGCTGCCGAGTGTCC TCTCTCCAATGAAGCTACTATGCAAAGTATGGAGAGTCTCCTGAGGGCCAAAGGCC GGAAGTGGAAACAGTTATCTACTACCTGTCAAACCTCCAGTGGCTGAAAGAAGAAATG GAAACCAATTTAGCCGTTGGCAGAAGGAACAAGAGAGTATCATTACAGAGTTACAGA CGTCTCTTCATGATAGGAACAAAGAAGTGGAGGATCTTAGTGCAACACTGCTCTGCAA ACTTGGACAGGGCAGAGTGAGATAGCAGAGGAGCTGTGCCAGCGCTCTACAGCGAAAG GAAAGGATGCTGCAGGACCTTCTAAGTGATCGAAATAAACAGTGCTGGAAACATGAAA TGGAGATTCAAGGCCTGCTTCAGTCTGTGAGCACCAGGGAGCAGGAAAGCCAAGCTGC TGCAGAGAAGTTGGTGCAAGCCTTAATGGAAAGAAATTCAGAATTACAGGCCCTGCGC CAATATTTAGGAGGAGAGACTCCCTGATGTCCCAAGCACCCTCTTACCAACAAG CTGAAGTTACCCCCACTGGCCGCTTGGAAAAACAGACTGATCAAGGTTCAATGCAGAT ACCTTCCAGAGATGATGACCTTCATTGACTGCCAAAGAGGATGTGAGCATACCCAGA TCCACATTAGGAGATTTGGACACAGTTGCAGGGCTGAAAAAGAACTGAGTAATGCCA</p>

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	SEQ ID NO: 294	2327 aa	MW at 263034.6kD
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AGCAGCCGTGCTGTGCTGACTCCCACCGCTCTCCAGCAGCACCTCTTTCTGTCTG
ATGAGCTGGAAGCTGCTGTGACATGGACATAGTCAGCGAGTACACACTATGAAGA
GAAGAAAGCTTCTCCAGTCACTCAGGTAGCAGTGCATCTCAGGGGGCTAAGGGCGAA
TCCAACAGCAACCCCATCAGCTTGCCAACCTCCCAAGAAATACCCCAAGGAGGCCAAC
AAGCCCATTCAGGCTTTTCAATTTCACTTCAACCAAGCTGGCTAGCCCTTCTCAGGC
ACCATTGCCCTCAGCTCCATCCAGCTTCTGCTTTCAGCCCTTCCAGCCCTGCCCTCCTCT
CTTGGCTGCTGTGAGACACCAGAGGTCTCCTTGGCTGAGTCTCAGCAGGAGCTACAGA
TGCTGCAGAAGCAGTTGGGAGAAAGTAGCACTGTTCTCTCTGCTTCCAGAGCTACATT
GCTGAGCAACGACTTGAAGCCGACTCTTCTACTACCTCAACTCACTGCTGCCAGCTCAC
TCTCTCCAAGGGGCACCATAGAACTGGGAAGAATCCTAGAGCCTGGGTACCTGGGCA
GCAGTGGCAAGTGGGATGTGATGAGGCCCTCAGAAAGGAGTGTATCTGGGGACCTATC
CTCAGGCTCCTCTGTGACTTACAGCTTAACTCCAAACCCACAGGGGCTGACCTGTGGAA
GAGCATCTTGGTGAAATCTGGAACTGCGCCAGCGCTGGAGGAGTCCATCTGCATCA
ATGACTGCTACGGGAGCAACTGGAAACCCGGCTGACCTCTACTGCTCTGGAAGGGG
ATCCACTTCTAATCTTACAGTCAGGGCTGGAGTCCATACCTCAGCTCTGCAATGAG
AACAGAGTCTCAGGGAAGAAATCGAAGACTTCAGGCTCAACTGAGTCATGTTTCCA
GAGGTCACTCCAGGAAACAGAAAGCTGAGGGAGGCTCTGCTGTCTCTCGATCCCA

	CCTTCAAGAGCTGGAAAAGGAGCTGGAGCACCAGAAGGTGGAAAGGCAGCAGCTTTG GAAGACTTGAGGGAGAAGCAGCAAGAGGTCTTGCATTTCAGGGAGGAACGCTTTTCCC TCCAGGAAAACGACTCCAGACTGCAGCACAAAGCTGGTTCTCCTGCAGCAACAGTGTGA AGAGAAACAGCAGCTCTTTGAGTCCCTCCAGTCAGAGCTACAAATCTACGAGGCACTT TATGGCAATTCCAAGAAGGGGCTGAAAGCTTACAGCCTGGATGCCTGTCAACCAATCC CTTTGAGCAGTGACCTGAGCCACCTGGTGGCAGAGGTACAAGCTCTGAGAGGGCAGCT GGAGCAGAGCATTAGGGGAACAATTGTCTGCGACTGCAGCTGCAACAGCAGCTGGAG AGCGGTGCTGGCAAAGCCAGCCTCAGCCCCCTCCTCCATTAAACCAGAACTTCCAGCCA GCACTGACCTGGAAACAGCAGCTGCTCCTCCAAGGTTCAAGCTGTGTCCCCCTCCAGT CCGGGATGTTGGTATGAATCCCCAGCTCTGGTCTTCCCCAGCTCTGCTTCTCTACT CCTGGCTCAGATTAGTTGTGTGTGCTATTTCTTTTCAGGCTTGGGTTTGGATACTT CTCCAGTAATGAAGACCCTCCCAAGCTAGAGGGTGATGCTACTGATGGCTCCTTGC CAATAAGCATGGCCGCGCATGTCTATTGGCCACATTGATGACTACAGTGCCCTAAGACAG CAGATTGCGGAGGGCAAGCTGCTGGTCAAAAAGATAGTGTCTCTTGTGAGATCAGCGT GCAGCTTCCCTGGCCTTGAAGCCCAAGGCACAGAGGCAGAAAGGCATTATGAGCT TCGGAGCAGCACCAGTGCCCTGCACCATGCCCTAGAGGAGTCGGCTTCCCTCCTCACC ATGTTCTGGAGAGCGGCCCTGCCAAGCACCCACATCCCTGTGCTGCTGGCAAACAGG GAGAATCAACAGAAAGGGAACCTTCTGGAACAGAGAACCAGGATCCAAACAGGAGCA GCTCCTTCAGAGCACAACCTGAGCATCTGAAGAACGCCAACAGCAGAAGGAGAGCATG GAACAGTTCATTGTGTCAGCGTAACCAGAACACATGATGTTTAAAGAAGGCAAGGACTA ACTTAGAGGTGAAATCCCTAAGGGCTCTGCGGTGTAAGCTCCAGCCTTGTGACCCCTTGC TTCCAGGAACCATGCAAGAAGCGCAGCCACCAGAAGTCCCTTAAACAGCAGGAAAGGT GAGCCTGTCCCCCTTTTGTGAGCTACCTATCTGCTGAGGAGCATCTGGGCTCATTCT CTCCAAGT		
	ORF Start: ATG at 155	ORF Stop: TGA at 6950	
	SEQ ID NO: 296	2265 aa	MW at 255081.5kD
NOV103c, CG59773-03 Protein Sequence	MRPAGRTSTSGDVENLNSQNEAELRRQFEERQOQTEHVYELLENKIQLLQEE SRLAK NEAARMAALVEAEKECNLESEKLKGVTKNWEDVPGDQVQPDQYTETLAQRDKRIEEL NQSLAAQERLVEQLSREKQQLHLLEPTSMVQPMTEELLKQKLNSHETTITQQSV SDSHLAELOEKIQTEATNKILQEKLNEMSYELKCAQESSQKQDGTIQNLKETLKSRE RETEELYQVIEGQNDTMAKLRMLHQSQLGQLQSSSEGTSPAQQQVALLDLQSFALFCSQ LEIQKLQRVVRQKERQLADAKQCVQFVEAAAHSEQQKEASWKNQELRKALQQLQEE LQNKSQLRAWAEKYNEIRTEQEQNIQHLNHSLSHKEQLLQEFRELLQYRDNSDKTLE ANEMMLEKLRLRIHDKAVALERAIDEKFSALEEKEKELRQLRLAVRERDHLERLQV LSSNEATQSMESLLRAKGLVEQLSTTCQNLQWLKEEMETKFSRWQKEQESI IQQLQ TSLHNRNKEVEDLSATLLCKLPGQSEIAEELCQRLQRKERMLQDLLSDRNKQVLEHE MEIQGLLQSVSTREQESQAAAEKLQALMERNSELQALRQYLGGRDLSMQAPISNQ AEVPTGRLGKQTDQGSQMI PSRDDSTSLTAKEDVSI PRSTLGDLDTVAGLEKELSN KEEELMAKKERESQMEALSALQSMMAVQEEELQVQAADMESLTRNIQIKEDLIKDLQM QLVDPEDIPAMERLTQEVLLLREKVASVESQGEISGNRRQQQLLLMLEGLVDSERSRL NEALQAERQLYSSLVKFHAHPESSEDRDTLQVELEGAQVLRSLVEELGRSLERLNR ETLAAIGGAAGDDTDTSTEFSTDSIEEAAHSHQQLVKVALEKSLATVETQNPFSFS PPSPMGDSNRCLQEEMLHLRAEIQHLEEKRAEELKELKAQIEEAGFSSVSHIRN TMLSLCLENALKEQMGETMSDGEIEEDKEKGEVMVETVTVKEGLSESLQAEFRKL QGKLNHANI INLLKEQLVLSSKEGNSKLTPELLVHLTSTIERINTELVGSPGKHQHQ EEGNVTVRPFPQPSQLDLGATFTVDAHQQLDNQSPRDPGPQAFSLPGSTQHLSRSL SQCKQRYQDLQEKLLSEATVFAQANELEKYRVMLSESLVKQDSKQIQVDFQDLGYET CGRSENEAEREETTSPECEEHNSLKEMVLMGLCSEQGRRGSTLASSSERKPLENQLG KQEEFRVYKSENILVLRKDI EDLKAQLQANANKVIONLKSRRVRSLSVTSYSSSLERP RKLRAVGTLEGSSPHSVPEDEGWLSDGTGAFYSPGLQAKKDLES LIQVRSQLEAQLP ENGLEEKLAELRSASWPGKYDSL IQDQARELSYLRQKIREGRGICYLITQHAKDTVK SFEDLLRSNDIDYLGQSFREQLAQQSQLTERLTSKLSTEDHKSEKDQAGLEPLALRL SRELQEKEKVIEVLQAKLDARSLTPSSSRALS DSHRSPSSTLSDELEACSDMDIVS EYTHYEKKASPSHSGSSASQAKAESNSNPISLPTPQNTPEANQAHSGFHFHSIPK LASLPQAPLPAPSSFLPFPSTPGPPLGCCETPEVSLAESQQLQMLQKQLGESSTVP PASTATLLSNDLEADSSYYLNSAQPHSPPRGTIELGRILEPGYLGSSGKWDVMPQKG SVSGDLSSGSSVYQLNSKPTGADLLEEHLGEIWNLRQRLEESICINDCLREQLHRLT STARGRGSTSNFYSGLESIPQLCENNRVLREENRRLQAQLSHVSRGHSQETESLREA LLSSRSHLQLELEKELEHQKVERQQLLEDLREKQQEVHLHFREERLSLQENDSRLOHKL LLQQQCEEKQQLFESLQSELQIYEALYGNSSKKGLKAYSLDACHQIPLSSDLSHLVAEV QALRGQLEQSIQGNNCLRLQLQQQLESGAGKASLPSSINQNPASTDPGNKQLLLQG SAVSPVPRVDVGMSPALVFPSSASSTPGSDSVVLSFSFSGGLDLPSPVMKTPPKEGD ATDGSFANKHGRHVIGHIDDYSALRQQAEGKLLVKKIVSLVRSACSPFPLEAQGTGEG SKGIELHRSSTSLHHALEESASLLTMFWRAALPSTHIVPLPGKGESTERELLELR KVSKQEQLLQSTTEHLKNAANQKESMEQFIVSVTRTHDVLKARTNLEVKSLRALPCT PAL		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 103B.

Table 103B. Comparison of NOV103a against NOV103b through NOV103c.		
Protein Sequence	NOV103a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV103b	365..2196 202..2016	1510/1834 (82%) 1518/1834 (82%)
NOV103c	365..2196 140..1954	1510/1834 (82%) 1518/1834 (82%)

Further analysis of the NOV103a protein yielded the following properties shown in Table 103C.

Table 103C. Protein Sequence Properties NOV103a	
PSort analysis:	0.5855 probability located in mitochondrial matrix space; 0.4200 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.2957 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 39 and 40

A search of the NOV103a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 103D.

Table 103D. Geneseq Results for NOV103a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV103a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY71159	Human phosphodiesterase interacting protein, myomegalin - Homo sapiens, 2517 aa. [WO200027861-A1, 18-MAY-2000]	1..2196 1..2204	2193/2204 (99%) 2193/2204 (99%)	0.0
AAM40183	Human polypeptide SEQ ID NO 3328 - Homo sapiens, 1883 aa. [WO200153312-A1, 26-JUL-2001]	635..2196 1..1570	1557/1570 (99%) 1559/1570 (99%)	0.0
AAY71158	Rat phosphodiesterase interacting protein, myomegalin - Rattus sp, 2326 aa. [WO200027861-A1, 18-MAY-2000]	365..2197 202..2017	1433/1837 (78%) 1572/1837 (85%)	0.0

AAY67600	Human adipose tissue protein #3 - Homo sapiens, 944 aa. [JP2000037190-A, 08-FEB-2000]	1..934 1..934	925/934 (99%) 927/934 (99%)	0.0
AAU01768	Human secreted protein #47 - Homo sapiens, 934 aa. [WO200123546-A1, 05-APR-2001]	365..1102 197..934	730/738 (98%) 733/738 (98%)	0.0

In a BLAST search of public sequence databases, the NOV103a protein was found to have homology to the proteins shown in the BLASTP data in Table 103E.

Table 103E. Public BLASTP Results for NOV103a				
Protein Accession Number	Protein/Organism/Length	NOV103a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O75042	KIAA0454 PROTEIN - Homo sapiens (Human), 1882 aa (fragment).	636..2196 1..1569	1558/1569 (99%) 1558/1569 (99%)	0.0
Q9WUJ3	MYOMEGALIN - Rattus norvegicus (Rat), 2324 aa.	365..2197 202..2015	1444/1838 (78%) 1581/1838 (85%)	0.0
O75065	KIAA0477 PROTEIN - Homo sapiens (Human), 1132 aa.	1..1132 1..1132	1132/1132 (100%) 1132/1132 (100%)	0.0
Q25893	LIVER STAGE ANTIGEN - Plasmodium falciparum (isolate NF54), 1909 aa.	356..1459 605..1651	243/1129 (21%) 488/1129 (42%)	4e-35
Q13439	Golgi autoantigen, golgin subfamily A 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (72.1 protein) - Homo sapiens (Human), 2230 aa.	229..1749 267..1814	349/1638 (21%) 679/1638 (41%)	4e-34

PFam analysis predicts that the NOV103a protein contains the domains shown in the Table 103F.

Table 103F. Domain Analysis of NOV103a

Pfam Domain	NOV103a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Somatomedin_B: domain 1 of 1	150..189	14/47 (30%) 25/47 (53%)	7.6
recA: domain 1 of 1	621..650	8/30 (27%) 22/30 (73%)	8.1
Ribosomal_L10: domain 1 of 1	604..695	20/109 (18%) 59/109 (54%)	9.9
Dishevelled: domain 1 of 1	844..914	19/74 (26%) 37/74 (50%)	2.7
Transposase_22: domain 1 of 1	1135..1416	71/376 (19%) 127/376 (34%)	4.6
Phe_tRNA-synt_N: domain 1 of 1	2079..2152	13/79 (16%) 49/79 (62%)	4.9

Example 104.

- 5 The NOV104 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 104A.

Table 104A. NOV104 Sequence Analysis

	SEQ ID NO: 297	736 bp
NOV104a, CG57460-01 DNA Sequence	AAAGCACCCGAGATGACCCCGGCTCCTCCACAGGAGCGCGGCCGGCGCGCGTCCC TAGCGGGCTTCGCGGGGTGGCGTCTCTGGGGCTGGGGACCCCGCGCGCGCTGA CCCGCGCCTCTGCCCCAGCGCTGTGCTTCGCCGTGAGCGCTCGCTGCTGTGACG TGCCTGGTGCCGCGCGCTGCTGGGCTGCGCTACTACTACAGCCGCAAGGTGATCC GCGCTACCTGGAGTGC GCGCTGCACACGGACATGGCGGACATCGAGCAGTACTACAT GAAGCCGCCGGTGTCTCCCTGACCGCCTATCCCTGCAGGCTCCTGCTTCTGGGTG GCCGTGCTGGATGGCAACGTGGTGGGCATTGTGGCTGCACGGGCCACGAGGAGGACA ACACGGTGGAGCTGCTGCGGATGTCTGTGGACTCACGTTTCCGAGGCAAGGGCATCGC CAAGGCGCTGGGCGGAAGGTGCTGGAGTTCGCCGTGGTGCACAACTACTCCGCGTG GTGCTGGGCACGACGCCGTCAAGGTGGCGGCCACAAGCTCTACGAGTCGCTGGGCT TCAGACACATGGGCGCCAGTGACCACTACGTGCTGCCGGGCATGACCTCTCGCTGGC TGAGCGCCTCTTCTTCAGTCCGCTACCACCGCTACCGCTGCAGCTGCGCGAGGAG TGACCGCGCGCGCTCGCCCGCGCCCCCGCGCGCCT	
	ORF Start: ATG at 13	ORF Stop: TGA at 697
	SEQ ID NO: 298	228 aa MW at 24767.5kD
NOV104a, CG57460-01 Protein Sequence	MTPAPPPGARPGAASLAGFAGVASLGPDPRRAADPRPLPALCFAVSRSLLLTCLVP AALLGLRYYYSRKIVIRAYLECALHTDMADIEQYMKPPGVSLTALSPAGSCFWAVLD GNVVGIVAARAHEEDNTVELLRMSVDSRFRKGIAKALGRKVLFEFAVHNYSVAVLGT TAVKVAHKLYESLGRHMGASDHVYVLPGMTLSLAERLFFQVRYHRYRLQLREE	

Further analysis of the NOV104a protein yielded the following properties shown in Table 104B.

Table 104B. Protein Sequence Properties NOV104a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 64 and 65

5 A search of the NOV104a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 104C.

Table 104C. Geneseq Results for NOV104a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV104a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB19986	Human camello 3 (Hcml3) protein (partial) - Homo sapiens, 144 aa. [WO200077024-A1, 21-DEC-2000]	42..195 1..144	144/154 (93%) 144/154 (93%)	7e-76
AAB19985	Human camello 2 (Hcml2) protein - Homo sapiens, 227 aa. [WO200077024-A1, 21-DEC-2000]	47..200 56..203	63/158 (39%) 92/158 (57%)	1e-21
AAB19984	Human camello 1 (Hcml1) protein - Homo sapiens, 227 aa. [WO200077024-A1, 21-DEC-2000]	41..196 50..199	60/160 (37%) 88/160 (54%)	7e-20
AAY57959	Human TSC501 protein SEQ ID NO:1 - Homo sapiens, 227 aa. [JP11332579-A, 07-DEC-1999]	41..196 50..199	59/160 (36%) 87/160 (53%)	4e-19
AAB19987	Mouse camello 1 (Mcm11) protein - Mus sp, 222 aa. [WO200077024-A1, 21-DEC-2000]	41..194 50..197	63/158 (39%) 87/158 (54%)	1e-18

In a BLAST search of public sequence databases, the NOV104a protein was found to have homology to the proteins shown in the BLASTP data in Table 104D.

Table 104D. Public BLASTP Results for NOV104a				
Protein Accession Number	Protein/Organism/Length	NOV104a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UHF3	PUTATIVE N-ACETYLTRANSFERASE CAMELLO 2 - Homo sapiens (Human), 227 aa.	47..200 56..203	63/158 (39%) 92/158 (57%)	5e-21
Q9UHE5	PUTATIVE N-ACETYLTRANSFERASE CML1 - Homo sapiens (Human), 227 aa.	41..196 50..199	60/160 (37%) 88/160 (54%)	3e-19
Q9UQ17	GLA PROTEIN - Homo sapiens (Human), 227 aa.	41..196 50..199	60/160 (37%) 88/160 (54%)	3e-19
Q96QI8	KIDNEY-AND LIVER-SPECIFIC GENE - Homo sapiens (Human), 227 aa.	41..196 50..199	59/160 (36%) 87/160 (53%)	1e-18
O75839	TSC501 PROTEIN - Homo sapiens (Human), 227 aa.	41..196 50..199	59/160 (36%) 87/160 (53%)	1e-18

PFam analysis predicts that the NOV104a protein contains the domains shown in the Table 104E.

Table 104E. Domain Analysis of NOV104a			
Pfam Domain	NOV104a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Acetyltransf: domain 1 of 1	111..191	28/82 (34%) 64/82 (78%)	2.2e-17

Example 105.

The NOV105 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 105A.

Table 105A. NOV105 Sequence Analysis		
	SEQ ID NO: 299	1230 bp
NOV105a, CG57464-01 DNA Sequence	<p>CTTCCCGCGGCTGCGCGATGGACAGCCCCGAGGTGACCTTCACTCTCGCCTATCTGG TGTTCGCGGTGTGCTTCGTGTTACGCCCCAACGAGTTCACGCGGCGGGGCTCACGGT GCAGAACCTGCTGTGCGGGCTGGCTGGGCAGCGAGGACGCCCTTCGTGCCCTTCCAC TTGCGCCGCACGCGCCGACGCTGTGTGCCACTCGCTGCTGCCGCTCGGTGAGGCTG CTCGGGCCGCGCGCCGATCCTCTCCTGCGCAGGGCTTGCTGGGAGGTCAGGAGGAG GCCTCCGCCAGCTCCCCGAGGCCCGAAAGCGCCTGGGCGCAGCTGGGGAGAGGCGCC GGTCTCATCCAGAGGGACCGCGCGTGGGCTGAGCGCGCTTAGGGGTGCCCGCGCC TGGCCTGGCGGCTCTTCTGTGCTGGCCGTGACCTCCCTCCATCGCTGCATCCT</p>	

	GATCTACTACTGGTCCCCTGACCGGTGGGCTGCCACCCACTGGCGCGCACCCCTGGCCCTCTACGCCCTCCACAGTCTGGCTGGCAGGCTGTTGCCTCTCTGTCAACACTGAGTTCCGGCGGATTGACAAGTTTGCCACCGGTGCACCAAGTGCCCGTGTGATTGTGACAGACACGTGGGTGATGAAGGTAACCACTACCGAGTGACGTGGCCAGCAGCAGGACGTGCACCTGACTGTGACGGAGTCTCGGCAGCATGAGCTCTGCCAGACTCGAACTTGCCCGTGCAGCTCCTCACCATCCGTGTGGCCAGCACCAACCCTGCTGTGCAGGCCTTTGACATCAGGCTGAATCCACTGAGTACGGGAGCTCTGCGAGAAGCTCCGGGCACCCATCCGCAGGGCAGCCCATGTGGTCATCCACCAGAGCCTGGGCGACCTGTTCTGGAGACATTTCCTCCCTGGTAGAGGTCAACCGGCCCTACTCAGTGCCAGCAGCCAGGTGGGGGGCCTGGAGGCTGCATAGGCTGCATGCAGACACGTGCCAGCGTGAAGCTGGTGAAGACCTGCAGGAGGCAGCCACAGGCGAGTGCCAGCAGTGTTACTGCCGCCCATGTGGTGCCTCACTGCATGGGCAAGTGGTTCGCCAGCCGCCAGGACCCCTGCGCCCTGACACCTGGCTGGCCAGCCGCTGCCCTGCCACCTGCCGCGCACGCTTCTGCATCCTGGATGTGTGCACCGTGCCTGA		
	ORF Start: ATG at 19		ORF Stop: TGA at 1228
	SEQ ID NO: 300	403 aa	MW at 44585.0kD
NOV105a, CG57464-01 Protein Sequence	MDSPEVTFTLAYLVFAVCFVFTPNEFHAAGLTVQNLLSGWLGSEDAAPFVPHLRRTAATLLCHSLLPLGEAARAGRPHPLRRACWEVRRRPPAPRGPESAWAQLGRGAGPHPEGPRRGLSALRGAAGLAWRLFLLLAVTLPSIACILIYYWSRDRWACHPLARTLALYALPQSGWQAVASSVNTFERRIDKFATGAPGARVIVTDTWVMKVTTYRVHVAQQQDVHLTVTESRQHELSPDSNLPVQLLTIRVASTNPVQAFDIRLNSTEYGELCEKLRAPIRRAHVVIHQSLGDLFLETFASLVEVNPAYSVPSQVGGLEACIGCMQTRASVKLVKTCQEAATGECQQCYCRPMWCLTCMGKWFASRQDPLRPDTWLASRVPCPTRARFCILDVCTVR		

Further analysis of the NOV105a protein yielded the following properties shown in Table 105B.

Table 105B. Protein Sequence Properties NOV105a	
PSort analysis:	0.6760 probability located in plasma membrane; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Likely cleavage site between residues 29 and 30

A search of the NOV105a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 105C.

Table 105C. Geneseq Results for NOV105a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV105a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81377	Human AFP protein sequence SEQ ID NO:272 - Homo sapiens, 362 aa. [WO200129221-A2, 26-APR-2001]	1..403 1..362	344/409 (84%) 345/409 (84%)	0.0

In a BLAST search of public sequence databases, the NOV105a protein was found to have homology to the proteins shown in the BLASTP data in Table 105D.

Table 105D. Public BLASTP Results for NOV105a				
Protein Accession Number	Protein/Organism/Length	NOV105a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC38627	SEQUENCE 271 FROM PATENT WO0129221 - Homo sapiens (Human), 362 aa.	1..403 1..362	345/409 (84%) 346/409 (84%)	0.0
Q9DCF3	0610039G24RIK PROTEIN - Mus musculus (Mouse), 362 aa.	1..403 1..362	311/403 (77%) 328/403 (81%)	e-176
Q96GP5	SIMILAR TO RIKEN CDNA 0610039G24 GENE - Homo sapiens (Human), 232 aa.	1..265 1..226	211/271 (77%) 212/271 (77%)	e-109
Q9VN16	CG14646 PROTEIN - Drosophila melanogaster (Fruit fly), 409 aa.	1..399 1..383	123/409 (30%) 202/409 (49%)	1e-55
Q95TM4	LD39811P - Drosophila melanogaster (Fruit fly), 393 aa.	20..399 4..367	117/390 (30%) 192/390 (49%)	1e-51

PFam analysis predicts that the NOV105a protein contains the domains shown in the Table 105E.

5

Table 105E. Domain Analysis of NOV105a			
Pfam Domain	NOV105a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 106.

The NOV106 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 106A.

Table 106A. NOV106 Sequence Analysis		
	SEQ ID NO: 301	1136 bp
NOV106a, CG57466-01 DNA Sequence	TTTCTGCAATGGGAGCCTCCGCCACCCACCTGGAGCCACAGAAGGCCAGAGCCAA ATGGACAGCTGGTGAACCCCAACAACCTTCTGGAAGAACCCGAAAGATGTGTGCGCCCA CGCCCATGGCCTCTCAGGGCCAGGCCTGGGACGTGACCACCACTAAGTCTCAGCCA ATATCAACTTGACCCACAGCCCTGGTTCAGGTCTGGAGCCGAGTTCGGCAGTT TCTCTTCTACCGCACTGCCGCTACTTCCCATGCTGCTGAACCAACCCGAGAAGTGC AGGGGCGATGTCTACCTGCTGGTGGTGTCAAGTCGGTCATCAGCAGCACGACCGCC	

	GCGAGGCCATCCGCCAGACCTGGGCGCGAGCGGCAGTCCGCGGGTGGGGCCGAGCGC CGTGCGCACCCCTCTTCTGTCTGGGCACGGCCTCCAAGCAGGAGGAGCGCACGCACTAC CAGCAGCTGCTGGCCTACGAAGACGCCCTCTACGGCGACATCCTGCAGTGGGGCTTC TCGACACCTTCTTCAACCTGACCCTCAAGGAGATCCACTTCTCAAGTGGCTGGACAT CTACTGCCCCACGTCCCTTCATTTTCAAAGGCGACGATGACGTCTTCGTCAACCCC ACCAACCTGCTAGAATTTCTGGCTGACCGGCAGCCACAGGAAAACCTGTTCTGTGGGCG ATGTCCTGCAGCAGCTCGGCCCATTCGCAGGAAAGACAACAAATACTACATCCCGGG GGCCCTGTACGGCAAGGCCAGCTATCCGCCGTATGCAGGCGGCGGTGGCTTCCTCATG GCCGGCAGCCTGGCCCGCGCCTGCACCATGCCTGCGACACCTGGAGCTCTACCCGA TCGACGACGCTCTTCTGGGCATGTGCTTGAGGTGCTGGGCGTGCAGCCACGGCCCA CGAGGGCTTCAAGACTTTCGGCATCTCCCGGAACCGCAACAGCCGATGAACAAGGAG CCGTGCTTTTCCGCGCATGCTCGTGGTGCAAGCTGCTGCCCCCTGAGCTGCTCG CCATGTGGGGGCTGGTGACAGCAATCTCACCTGCTCCCGCAAGCTCCAGGTGCTCTG <u>ACCCGAGCCGGGCTACTAGGACAGGCCAGGGCAC</u>		
	ORF Start: ATG at 9	ORF Stop: TGA at 1101	
	SEQ ID NO: 302	364 aa	MW at 41853.8kD
NOV106a, CG57466-01 Protein Sequence	MGASATHPGATEGPEAKWTAGEPQQLLEPERCVRPRPWPLRAQAWDVTTNCSANIN LTHQPFQVLEPQFRQFLFYRHCYFPMLLNHPEKCRGDVYLLVVVKSIVTQHDRREA IRQTWARAAVRGWGPSAVRTLFLGLTASKQEERTHYQQLLAYEDALYGDILQWGFLLDT FFNLTLKEIHFLKWLDIYCPHVFFIFKGDDDVFNPTNLLEFLADROPQENLFGVDVL QHARPIRRKDNKYYIPGALYGKASYPPYAGGGGFLMAGSLARRLHHACDTLELYPIDD VFLGMCLEVLGVQPTAHEGFKTFGISRNRNSRMNKEPCFFRAMLVVHKLLPELLAMW GLVHSNLTCSRKLQVL		

Further analysis of the NOV106a protein yielded the following properties shown in Table 106B.

Table 106B. Protein Sequence Properties NOV106a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.3122 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV106a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 106C.

Table 106C. Geneseq Results for NOV106a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV106a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB24035	Human PRO4397 protein sequence SEQ ID NO:42 - Homo sapiens, 402 aa. [WO200053750-A1, 14- SEP-2000]	72..352 84..380	149/300 (49%) 191/300 (63%)	4e-76
AAU29167	Human PRO polypeptide sequence #144 - Homo sapiens, 372 aa. [WO200168848-A2, 20-SEP-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76

AAB88404	Human membrane or secretory protein clone PSEC0159 - Homo sapiens, 372 aa. [EP1067182-A2, 10-JAN-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76
AAB49750	Human beta 1,3-N-acetylglucosamine transferase protein G4 - Homo sapiens, 372 aa. [WO200100848-A1, 04-JAN-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76
AAB49749	Human beta 1,3-N-acetylglucosamine transferase protein G4 - Homo sapiens, 372 aa. [WO200100848-A1, 04-JAN-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76

In a BLAST search of public sequence databases, the NOV106a protein was found to have homology to the proteins shown in the BLASTP data in Table 106D.

Table 106D. Public BLASTP Results for NOV106a

Protein Accession Number	Protein/Organism/Length	NOV106a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL32295	BETA-3-GALACTOSYLTRANSFERASE - Brachydanio rerio (Zebrafish) (Zebra danio), 418 aa.	46..364 101..417	199/319 (62%) 249/319 (77%)	e-121
AAL32297	BETA-3-GALACTOSYLTRANSFERASE - Brachydanio rerio (Zebrafish) (Zebra danio), 412 aa.	29..360 82..409	180/337 (53%) 244/337 (71%)	e-104
Q96EK0	UNKNOWN (PROTEIN FOR MGC:20513) - Homo sapiens (Human), 377 aa.	60..352 46..355	152/313 (48%) 198/313 (62%)	9e-76
CAC39768	SEQUENCE 175 FROM PATENT EP1067182 - Homo sapiens (Human), 372 aa.	26..363 27..371	149/348 (42%) 207/348 (58%)	3e-75
Q9C0J2	BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE BGNT-3 - Homo sapiens (Human), 372 aa.	26..363 27..371	149/348 (42%) 207/348 (58%)	3e-75

PFam analysis predicts that the NOV106a protein contains the domains shown in the Table 106E.

Table 106E. Domain Analysis of NOV106a			
Pfam Domain	NOV106a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PI3_PI4_kinase: domain 1 of 1	195..205	8/12 (67%) 10/12 (83%)	8.5
Galactosyl_T: domain 1 of 1	112..308	69/212 (33%) 148/212 (70%)	7.7e-45

Example 107.

5 The NOV107 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 107A.

Table 107A. NOV107 Sequence Analysis		
	SEQ ID NO: 303	4091 bp
NOV107a, CG57468-01 DNA Sequence	AAGCAAGAGGCTGAGATGGATCTTGAGGCGGCAAAGAACGGAACAGCCTGGCGCCCCA CGAGCGCGGAGGGCGACTTTGAAC TGGGCATCAGCAGCAAACAAAAAGGAAAAAAC GAAGACAGTGAATGATTGGAGTATTAACATTGTTTCGATACTCCGATTGGCAGGAT AAATTGTTTATGTCGCTGGGTACCATCATGGCCATAGCTCACGGATCAGGTCTCCCCC TCATGATGATAGTATTTGGAGAGATGACTGACAAATTTGTTGATACTGCAGGAACTT CTCCTTTCCAGTGAACCTTTCTTGTGCTGCTAAATCCAGGCAAAATTTCTGGAAGAA GAAATGACTAGATATGCATATTACTACTCAGGATTGGGTGCTGGAGTTCTTGTGCTG CCTATATACAAGTTTCATTTTGGACTTTGGCAGCTGGTGCAGATCAGGAAATTAG GCAGAAGTTTTTTCATGCTATTCTACGACAGGAAATAGGATGGTTTGACATCAATGAC ACCACTGAACTCAATACGCGGCTAACAGATGACATCTCCAAATCAGTGAAGGAATTG GTGACAAGGTTGGAATGTTCTTCAAGCAGTAGCCACGTTTTTTCAGGATTATAGT GGGATTCATCAGAGGATGGAAGCTCACCTTGTGATAATGGCCATCAGCCCTATTCTA GGACTCTCTGCGAGCCGTTTGGGCAAAGATACTCTCGGCATTTAGTGACAAAGAACTAG CTGCTTATGCAAAGCAGGCGCCGTGGCAGAAGAGGCTCTGGGGCCATCAGGACTGT GATAGCTTTCGGGGGCGCAACAAAGAGCTGGAAAGGTATCAGAAACATTTAGAAAA GCCAAAGAGATTGGAATTAAGAAAGCTATTTAGCAAAACATTTCCATGGGTATTGCCCT TCCTGTTAATATATGCATCATATGCACTGGCCTTCTGGTATGGATCCACTCTAGTCAT ATCAAAGAATATACTATTGGAATGCAATGACAGTTTTTTTTTCAATCCTAATTGGA GCTATGGCCATCGGAGAAACGCTCGTTTTTGGCTCCTGAATATTCAAAGCCAAATCGG GGGCTGCGCATCTGTTTGCCTTGTGGAAGAAACCAATATAGACAGCCGCACTCA AGAAGGAAAAAGCCAGTAAGCGACACATGTGAAGGGAATTTAGAGTTTCGAGAAGTC TCTTTCTTCTATCCATGTGCGCCAGATGTTTTCATCCTCCGTGGCTTATCCCTCAGTA TTGAGCGAGGAAAGACAGTAGCATTGTGTTGGGAGCAGCGGCTGTGGGAAAGCACTTC TGTTCAACTTCTGCGAGAGCTTTATGACCCCGTGCAAGGACAAAGTGGATGGTGTGGAT GCAAAAGAAATTGAATGTACAGTGGCTCCGTTCCCAATAGCAATCGTTCTCAAGAGC CTGTGCTCTTCAACTGCAGCATTGCTGAGAACATCGCCTATGGTGACAACAGCCGTGT GGTGCCATTAGATGAGATCAAAGAACCGCAATGCAGCAAAATATCCATTCTTTTATT GAAGGTCTCCCTGAGAAATACAACACACAAGTTGGACTGAAGGAGCAGCAGCTTCTG GCGGCCAGAAACAAAGACTAGCTATTGCAAGGGCTCTTCCAAAAACCCAAATTTT ATTGTTGGATGAGGCCACTTCAGCCCTCGATAATGACAGTGAGTGGCAGGTGGTTTTCAG CATGCCCTTGATAAAGCCAGGACGGGAAGGACATGCCTAGTGGTCACTCAGAGCTCT CTGCAATTGAGAACGCAGATTGATAGTGGTTCTGCACAATGGAAGATAAAGGAACA AGGAACTCATCAAGAGCTCCTGAGAAATCGAGACATATATTTAAGTTAGTGAATGCA CAGTCAGCGAGCAAAGGTCGGAATACAAATCGTGGTAGCACACCGACTTCTACTATTTC GAAGTGCAGATTGATTGTGACCCTAAAGGATGGAATGCTGGCGGAGAAAGGAGCACA TGCTGAACTAATGGCAAAACGAGGTCTATATTACTTGTGATGTCACAGGTAATG CTTATGGGGACTCTTTCAGACTGTGGTAATAGTCTTCTGAAAGTCTCTCTATTAAGAA TTTTAAAGTTAAACAAGCCTGAATGGCCTTTTGTGGTCTGGGGACATTGGCTTCTGT TCTAAATGGAAGTGTTCATCCAGTATTTTCCATCATCTTTCAGAAATTTATACCGTA ATGTTTGAATAATGATCTTTTGTCTTCTCCTCAAAATTTTTTATATTCATTCCTTT	

	<p>TGTTTTCTCTCAAAACAAGTTTTCAGCGTAGATTTTGTGTTTGTCTTTTCAGGGATT ATTTTACGGCAGAGCAGGGGAAATTTTAACGATGAGATTAAGACACTTGGCCTTCAA GCCATTGTTATATCAGGATATGCTCGTGGTTTGATGAAAAGGAAAAACAGCAGCAGGAGCT TGACAAACAATATTAGCCATAGATATAGCACAATTCAGGAGCAACAGGTTTCAGGAT TGGCGTCTTAAACACAAAATGCAACTAACATGGGACTTTTCAGTTATCATTTCCTTTATA TATGGATGGGAGATGACATTCCTGATTCTGAGTATTGCTCCAGTACTTGGCGTGACAG GAATGATTGAAACCGCAGCAATGACTGGATTGTGCCAACAAAGATAAGCAAGAACTTAA GCATGCTGGAAAGGTAAGATAGCAACTGAAGCTTTGGAGAATATACGTACTATAGTG TCATTAAACAAGGGAAAAAGCCTTCGAGCAAAATGTATGAAGAGATGCTTCAGACTCAAC ACAGGAGAAATACCTCGAAGAAGACAGATATTGGAAGCTGTTATGCATTACGCCA TGCCTTTATATATTTTGGCTATGCGGCAGGGTTTCGATTGGAGCCTATTTAATTCAA GCTGGACGAATGTCAAATGCTTTATCTTTTGATGAGGTTTTTACTGCAATTGCATATG GAGCTATGGCCATCGGAGAAACGCTCGTTTTGGAGCTCTGGAATATTCGAAAGCCAAATC GGGGGCTGCGCATCTGTTTGCCTTGTGGAAAAGAAACCAATATAGACAGCCGCAGT CAAGAAGGGAAAAAGCCACTTTCACAGGACACATGTGAAGGGAATTTAGAGTTTCGAG AAGTCTCTTCTTCTATCCATGTCGCCCAGATGTTTTCATCTCCGTGGCTTATCCCT CAGTATTGAGCGAGAAAGACAGTAGCATTGTGGGGAGCAGCGCTGTGGGAAAAGC ACTCTGTTCAACTTCTGCAGAGACTTATACCCCGTGAAGGACCAACAGCTGTTTG ATGGTGTGGATGCAAAAGAATTGAATGTACAGTGGCTCCGTTCCCAAATGCAATCGT TCCTCAAGAGCCTGTGCTCTTCAACTGCAGCATTGCTGAGAACATCGCCTATGGTGAC AACAGCCGTGTGGTGCCATTAGATGAGATCAAAGAAGCCGCAATGACAGCAAAATATCC ATTTCTTTTATGAGGCTCTCCCTAAATACAACACACAAGTTGGACTGAAGAGGACACA GCTTTCTGGCGCCAGAAACAAAGACTAGCTATTGCAAGGGCTCTTCTCCAAAAACCC AAAAATTTTATGTTGGATGAGGCCACTTCAGCCCTCGATAATGACAGTGAGAAGGTAC AGGTGGTTCAGCATGCGCTTGATAAAGCCAGGACGGGAAGGACATGCCTAGTGGTCAC TCACAGGCTCTCTGCAATTGAAACGCAGATTGATAGTGCTTCTGCACAATGGAAG ATAAGGAACAAGGAACATCAAGAGCTCCTGAGAAATCGAGCATATATTTTAAAGT TAGTGAATGCACAGTCAGCGAGCAAGGTCGGACTACAATCGAGGTAGACACCGACT TTCTACTATTGCAAGTGCAGATTGATGTGACCCTAAAGGATGGAATGCTGGCGGAG AAAGGAGACATGCTGAACTAATGGCAAAACGAGGTCTATATTATTCACTTGTGATGT CACAGGTAAATGCTTATGTGACATAATGCTAT</p>		
	ORF Start: ATG at 16	ORF Stop: TGA at 4078	
	SEQ ID NO: 304	1354 aa	MW at 149167.3kD
NOV107a, CG57468-01 Protein Sequence	<p>MDLEAAKNGTAWRPTSAEGDFELGISSKQKRKKTKTVMKIGVLTFRYSWQDKLFMS LGTIMAI AHGSGLP LMMIVFGEMTDK FVD TAGNFSFPVNFSLNSLNP GK ILEEMTRY AYYYSGLGAGVLVAA YIQVSFWTLAAGRQIRKIRQKFHAILRQEIFWFDINDTEL N TRLTDDISKISEGIGDKVGMMFFQAVATFFAGFIVGFI RGWKLT L VIMATSPILGSLAA VWAKILSAFSDKELAA YAKAGAVAEELGAIRTVIAFGGQNKELERYQKHLENAKEIG IKKAIISANILGAMAIGFLLIYASYALAFWYGSTLVISKEYTIGNAMTVFFSILIGAMAIG ETLVLAPEYSKAKSGAAHLFALLEKKPNIDSRSQEGKKPVSDTCEGNLEFREVFFFP CRPDVFI LRGLSLSIERGKTVA FVGSSGCGKSTSVQLLQRLYDPVQGGQVDGVDAKELN VQWLR SQIAIVPQEPVLFNC SIAENIAYGDN SRVPLDEI KEAANAANIHSFIEGLPE KYNTQVGLKGAQLSGGQKQRLAIARALLQKPKILLDEATSALDNDSEQVQVQH ALDK ARTGRTCLVVTHRLSAIQNADLIVLVLHNGKIKEQGTHQELLNRNDIYFKLVNAQSASK GRTTIVVAHRLSTIRSADLIVTLKDGMLAEKGAAELMAKRGLYYSLVMSQVMLMGTL SDCGNSLPEVSL LKILKLNKPEWPFVVLGTLASVLN GTVHPVFSIIFAKIITVMFGNN DLLFFLKIFLYSFLFLFLKQGFSVDFCLFAPQGLFYGRAGEILTMLRLHLAFKAMLYQ DIAWFDEKENSTGGLT LILAIDIAIQIGWATSGIRIGVLTQNA TMLGSLNISFIYGWEM TFLILSIAPVLAVTGM IETAAMTGFANKDKQELKHAGKVKIATEALENIRTVISLTRE KAPEQMYEEMLQTQHRRTSKKAQIIGSCYAFSHAFIYFAYAAGFRFGAYLIQAGRMS NALSFDRVFTA IAYGAMAIGETLVLAPEYSKAKSGAAHLFALLEKKPNIDSRSQEGKK PLSQDTCEGNLEFREVFFFP CRPDVFI LRGLSLSIERGKTVA FVGSSGCGKSTSVQL LQRLYDPVQGGQQLFDGVDAKELNVQWLR SQIAIVPQEPVLFNC SIAENIAYGDN SRV PLDEI KEAANAANIHSFIEGLPKYNTQVGLKGAQLSGGQKQRLAIARALLQKPKILL DEATSALDNDSEKVQVQVQH ALDKARTGRTCLVVTHRLSAIQNADLIVLVLHNGKIKEQ THQELLNRNDIYFKLVNAQSASKGRTTIVVAHRLSTIRSADLIVTLKDGMLAEKGAA ELMAKRGLYYSLVMSQVMLM</p>		

Table 107B. Protein Sequence Properties NOV107a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV107a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 107C.

Table 107C. Geneseq Results for NOV107a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV107a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB81064	Cynomologous monkey P-glycoprotein variant 1 - Macaca fascicularis, 1280 aa. [WO200123565-A1, 05-APR-2001]	1..1299 1..1278	750/1312 (57%) 964/1312 (73%)	0.0
AAB81065	Cynomologous monkey P-glycoprotein variant 2 - Macaca fascicularis, 1283 aa. [WO200123565-A1, 05-APR-2001]	1..1299 1..1281	749/1312 (57%) 967/1312 (73%)	0.0
AAB81959	Human MDR1 - Homo sapiens, 1280 aa. [WO200121762-A2, 29-MAR-2001]	1..1299 1..1278	749/1324 (56%) 967/1324 (72%)	0.0
AAY58186	Human wild-type multidrug resistance-1 (MDR-1) protein - Homo sapiens, 1280 aa. [WO9961589-A2, 02-DEC-1999]	1..1299 1..1278	749/1324 (56%) 967/1324 (72%)	0.0
AAW44073	Human multidrug resistance P-glycoprotein MDR1 - Homo sapiens, 1280 aa. [WO9740160-A1, 30-OCT-1997]	1..1299 1..1278	749/1324 (56%) 967/1324 (72%)	0.0

- 5 In a BLAST search of public sequence databases, the NOV107a protein was found to have homology to the proteins shown in the BLASTP data in Table 107D.

Table 107D. Public BLASTP Results for NOV107a				
Protein Accession Number	Protein/Organism/Length	NOV107a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P23174	Multidrug resistance protein 3 (P-glycoprotein 3) - <i>Cricetulus griseus</i> (Chinese hamster), 1281 aa.	1..1299 1..1279	818/1303 (62%) 999/1303 (75%)	0.0
P21440	Multidrug resistance protein 2 (P-glycoprotein 2) - <i>Mus musculus</i> (Mouse), 1276 aa.	1..1299 1..1274	823/1306 (63%) 998/1306 (76%)	0.0
Q08201	Multidrug resistance protein 2 (P-glycoprotein 2) - <i>Rattus norvegicus</i> (Rat), 1278 aa.	1..1299 1..1276	823/1309 (62%) 999/1309 (75%)	0.0
CAC37764	SEQUENCE 1 FROM PATENT WO0123565 - <i>Macaca fascicularis</i> (Crab eating macaque) (<i>Cynomolgus</i> monkey), 1280 aa.	1..1299 1..1278	750/1312 (57%) 964/1312 (73%)	0.0
CAC37765	SEQUENCE 3 FROM PATENT WO0123565 - <i>Macaca fascicularis</i> (Crab eating macaque) (<i>Cynomolgus</i> monkey), 1283 aa.	1..1299 1..1281	749/1312 (57%) 967/1312 (73%)	0.0

PFam analysis predicts that the NOV107a protein contains the domains shown in the Table 107E.

Table 107E. Domain Analysis of NOV107a			
Pfam Domain	NOV107a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ABC_membrane: domain 1 of 2	57..350	115/301 (38%) 252/301 (84%)	3.3e-83
MVIN: domain 1 of 1	57..447	70/531 (13%) 263/531 (50%)	5.8
SAA_proteins: domain 1 of 1	518..524	6/7 (86%) 7/7 (100%)	3
ABC_tran: domain 1 of 2	424..609	76/199 (38%) 150/199 (75%)	3.1e-56

DsbD: domain 1 of 1	722..926	39/249 (16%) 126/249 (51%)	9.6
ABC_membrane: domain 2 of 2	722..1008	80/297 (27%) 222/297 (75%)	2.2e-43
ABC_tran: domain 2 of 2	1083..1270	77/202 (38%) 154/202 (76%)	7.1e-54
GidB: domain 1 of 1	1170..1312	29/202 (14%) 97/202 (48%)	6.6

Example 108.

The NOV108 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 108A.

Table 108A. NOV108 Sequence Analysis			
	SEQ ID NO: 305	520 bp	
NOV108a, CG59609-01 DNA Sequence	<u>CCCCGTTCTATCAGCCATGGTCAACCCACCAGGTTCTTAGACATCATCGTGGATGGT</u> GAGCTCTTGGGACGTGTCTCCTTTGAGCTGTTTGCAGACAAGATTCCAAAGACAGCAG AAAATTTTGTGCTCTAATCATTGGAGAGAAAGGATTGGTTATAAAGGTTCTCTACTT TCACAGAATTGTTCTCTGGGTTTATGTGTCAAGGTGGTGACTTCACACAGCATAATGGC ACTGGTGGCAAGTCCATCTACGGGAAGAAATTGATGATGAGAAGTTCGTCCTAAATT ATACAGGCTCTGGCATCTTGTCCGTGGAGAATGCTGGACCAACACAAATGGTTCCCA GTTTTTCATCTGCACTGCCATGTCTGAGTGGTTGGATGGCATGCAGGTGGTCTTTGGC AAGGGAAGGAAGGTGAGTATTGTGGAAGCCATGGAGTGCTTTGGGTCCACAAATGGCA AGACCAGCAAGAAGATCACCATTGCTGACTGTGGACAAC <u>CTAATAGGTTTGACTT</u>		
	ORF Start: ATG at 17	ORF Stop: TAA at 506	
	SEQ ID NO: 306	163 aa	MW at 17734.1kD
NOV108a, CG59609-01 Protein Sequence	MVNPTRFLDIIVDGLGRVSFELFADKIPKTAENFCALIGEKGFYKGSYFHRIVP GFMCQGGDFTHNGTGGKSIYGKKFDDENFVLNYTGPGLSVENAGPNTNGSQPFICT AMSEWLDGMQVVFVGKGRKVSIVEAMECFGSTNGKTSKKITITADCGQL		

Further analysis of the NOV108a protein yielded the following properties shown in
5 Table 108B.

Table 108B. Protein Sequence Properties NOV108a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.6000 probability located in plasma membrane; 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV108a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 108C.

Table 108C. Geneseq Results for NOV108a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV108a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU01195	Human cyclophilin A protein - Homo sapiens, 165 aa. [WO200132876-A2, 10-MAY-2001]	1..163 1..164	134/164 (81%) 147/164 (88%)	2e-75
AAW56028	Calcineurin protein - Mammalia, 165 aa. [WO9808956-A2, 05-MAR-1998]	1..163 1..164	134/164 (81%) 147/164 (88%)	2e-75
AAR13726	Bovine cyclophilin - Bos taurus, 163 aa. [US5047512-A, 10-SEP-1991]	2..163 1..163	133/163 (81%) 146/163 (88%)	5e-75
AAG65275	Haematopoietic stem cell proliferation agent related human protein #2 - Homo sapiens, 164 aa. [JP2001163798-A, 19-JUN-2001]	2..163 1..163	133/163 (81%) 146/163 (88%)	9e-75
AAP90431	Cyclophilin - Homo sapiens (human), 164 aa. [EP326067-A, 02-AUG-1989]	2..163 1..163	133/163 (81%) 146/163 (88%)	9e-75

In a BLAST search of public sequence databases, the NOV108a protein was found to have homology to the proteins shown in the BLASTP data in Table 108D.

Table 108D. Public BLASTP Results for NOV108a				
Protein Accession Number	Protein/Organism/Length	NOV108a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC39529	SEQUENCE 26 FROM PATENT WO0132876 - Homo sapiens (Human), 165 aa.	1..163 1..164	134/164 (81%) 147/164 (88%)	8e-75
Q9BRU4	PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A) - Homo sapiens (Human), 165 aa.	1..163 1..164	134/164 (81%) 146/164 (88%)	2e-74
P04374	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) - Bos taurus (Bovine), and, 163 aa.	2..163 1..163	133/163 (81%) 146/163 (88%)	2e-74

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P05092	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human),, 164 aa.	2..163 1..163	133/163 (81%) 146/163 (88%)	3e-74
Q9TTC6	CYCLOPHILIN 18 - Oryctolagus cuniculus (Rabbit), 164 aa.	1..163 1..164	133/164 (81%) 147/164 (89%)	5e-74

PFam analysis predicts that the NOV108a protein contains the domains shown in the Table 108E.

Table 108E. Domain Analysis of NOV108a			
Pfam Domain	NOV108a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pro_isomerase: domain 1 of 1	5..163	101/181 (56%) 137/181 (76%)	5.2e-79

Example 109.

5 The NOV109 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 109A.

Table 109A. NOV109 Sequence Analysis			
	SEQ ID NO: 307	887 bp	
NOV109a, CG59613-01 DNA Sequence	GATATCATTTTTTATGGCAGCCATTGTTAAGCCTCCAGAACCTATACCTTTAAATGG TTAACAGATAAGCCAGTTTGGATAGAACAAATGGCCACTGAGTAAAGAGAACTGGAGG CTTTAGAGGATTGGTTACTGAACAATTTCTCAATAATCATTTTCCAAAAGTGAACCT ACACAGCATGAAAGTATCACACATTTCTTAGTGCAGCTAACCTGTGTGACCAGGGC TTCAACACATACCACTGTGACCACAACCTAGCCATGAGCATGAGCTCACCAGCATGT CCAAAATGCTAAAATACAACAATGGCAGTGAAGACATCACTACATGGAGGGCTGAAGG TACTATGGATCTCTTGGTGCTAGAATTTGAAGCACTAAATCAAGAGAACTTTGTGGAC TGTGAATTTGAAGTTAATGACTCTAGATGTTGAGCAACTTGAAATTCAGAACAGAGT ACAGCTGTGTAATAAAGATGCATTCTAGTGAATTTGTTTCATATATGCCAAGATCTCAG TCATATTTGGAGAGTCTGCTATAATTTCTTGTGCAAAAGATGGAGTGAATTTTCTGCA AATGGGAGAACTTGACATGGAAACATTGCCACAATTGCCCAACAAGTAATTACAATA AAGAAGAGGAGGCTGTTGCCATAATGATGAATGGGCCAGTTCAGCTAACTTTTGCAC TAACTTACTTAAATTTCTTTATAACAGGCACTCCACTCTCTCAGATGCACCCCTTGCTG GAGAGTATAAGATTGCCGGATATGGAACATTTAAAGTATTATTTGGCTCCCAAAATTG AGGATGAAAAAGGATTTTAGAAATTTCTAGAATCCAAGAAAATAAACTAAGCTCTTT GAAAATTGCTTCTGAGA		
	ORF Start: ATG at 14	ORF Stop: TAG at 830	
	SEQ ID NO: 308	272 aa	MW at 30831.1kD
NOV109a, CG59613-01 Protein Sequence	MAAIVKPPPEIPLKWLTDKPVWIEQWPLSKEKLEALEDLVTEQFSIIIFQKVNLSMK VSHISLVQLTLCDDQGFNTYHCDHNLAMSMSLTSMKMLKYNNGSEDIITWRAEGTMDL LVLEFEALNQENFVDCLEKMLTLDVEQLEIPEQEYSCVIKMHSSEFVHICQDLISHIGE SAIISCAKDGVNFSANGELGHGNIATIAQTSNYNKEEEAVAIMMNGPQQLTFALSILN FFITGTPLSQMHPLESIRLPDMEHLKYLLAPKIEDEKGF		

Further analysis of the NOV109a protein yielded the following properties shown in Table 109B.

Table 109B. Protein Sequence Properties NOV109a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Likely cleavage site between residues 19 and 20

5 A search of the NOV109a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 109C.

Table 109C. Geneseq Results for NOV109a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV109a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY51639	Human PCNA protein fragment - Homo sapiens, 261 aa. [WO200008164-A2, 17-FEB-2000]	25..271 8..260	158/255 (61%) 184/255 (71%)	8e-78
AAY52010	Human PCNA protein - Homo sapiens, 261 aa. [DE19840771-A1, 10-FEB-2000]	25..271 8..260	158/255 (61%) 184/255 (71%)	8e-78
AAB43712	Human cancer associated protein sequence SEQ ID NO:1157 - Homo sapiens, 269 aa. [WO200055350-A1, 21-SEP-2000]	25..271 16..268	158/255 (61%) 184/255 (71%)	8e-78
AAG75139	Human colon cancer antigen protein SEQ ID NO:5903 - Homo sapiens, 268 aa. [WO200122920-A2, 05-APR-2001]	25..269 16..266	157/253 (62%) 182/253 (71%)	5e-77
AAW90758	Human PCNA protein fragment #2 - Homo sapiens, 236 aa. [DE19840771-A1, 10-FEB-2000]	39..268 1..236	149/238 (62%) 171/238 (71%)	7e-73

In a BLAST search of public sequence databases, the NOV109a protein was found to have homology to the proteins shown in the BLASTP data in Table 109D.

Table 109D. Public BLASTP Results for NOV109a

Protein Accession Number	Protein/Organism/Length	NOV109a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P12004	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Homo sapiens (Human), 261 aa.	25..271 8..260	158/255 (61%) 184/255 (71%)	3e-77
P04961	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Rattus norvegicus (Rat), 261 aa.	25..271 8..260	158/255 (61%) 185/255 (71%)	5e-77
P57761	Proliferating cell nuclear antigen (PCNA) - Cricetulus griseus (Chinese hamster), 261 aa.	25..271 8..260	158/255 (61%) 184/255 (71%)	7e-77
Q91ZH2	11 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2700095L20, FULL INSERT SEQUENCE - Mus musculus (Mouse), 261 aa.	25..272 8..261	156/256 (60%) 183/256 (70%)	1e-75
P17918	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Mus musculus (Mouse), 261 aa.	25..270 8..259	155/254 (61%) 182/254 (71%)	5e-75

Pfam analysis predicts that the NOV109a protein contains the domains shown in the Table 109E.

Table 109E. Domain Analysis of NOV109a

Pfam Domain	NOV109a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PCNA: domain 1 of 1	23..143	46/128 (36%) 83/128 (65%)	2.3e-20
PCNA_C: domain 1 of 1	145..265	59/131 (45%) 98/131 (75%)	1.6e-45

Example 110.

- 5 The NOV110 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 110A.

Table 110A. NOV110 Sequence Analysis			
	SEQ ID NO: 309	1233 bp	
NOV110a, CG59619-01 DNA Sequence	<p>TGGCAATGGAAGAAGAGATCCCCGCGCTCTTCATTGACAAATGGCTCCGGCATGTGGAA AGCAGCTTTGCTGGGAGACAATGCCCTCCGAGCCATATTCCCCTCCATCATCGGGCA CCCCGGCACCAGGCGTGAATGGTGGGATGGGCGAGAAGGACTCTACGCTGGGCGACC AGGCCCAGAGCAAGTGCGGCATCCTGACCCCTGAAGTACCCCATCAAGCATGGCATCGT CACAAACTGGGACGACATGGAGAAGATCTGGCACCATGTTTTCTACAACGAGCTGTGC GTGGCCCTGGAGGAGCAGGTGGTGTCTGTGACCGAGGCCCGCTTAAACCCAGGGGCA ATAGGGAGAAGATGACTCAGATCATGTTTAAGACCTTCAACACCCAGGCCATGTACGT GGCCATTGAGGCCGTGTGACCCCTCCACAGCTCTGGTTGCACCACTGGCCATTGTGATG GACTCTGGAGATGGGGTCACCCACACAGTCCCCATCTACGAGCGCCACACCCCTCCCTC ACACCATCTGCACTCTGGACCTGGCTGGCCAGGACCTTACTGACTACCTCATGAAGAT CCCTACCTACCGCAGCTATAGCTTCAACACCATGGCCAAGTGGAAAATCGTGCGCAAC ATCAAGGAGAAGCTATGCTATGTGCTCTGGACTTCGAGGAGGAGATGGCCACTGCTGT CATCTCTCTCTCCCTGGAGAAGAGCTACGAGCTGCCTGACAGCCAGGCCATCATTAT TAGCAATGAGCGGTTCCGGTGTCCGGAGGCACTGTTCAGCCCTTCTTCTGGGCATG GAATCCTGTGGCATCCATGAAAGTACCTTCAACTCCATCATGAAGTGTGATATGGACA TCCCCAAAGACCTGTACGCCAACACAGTGTCTGGCGTCACCAACCATGTACCCCTGG CATCCCCAATAGGATGCAGAAGGAGATCACTGCCCTGGCATCCAGCACCATGAAGATC AAGATATCGTGCCCCATCGTGCCCCCAGAGTGCAAGTACTTTGTGTGGATCGGTGGCT CCATCCTGGCCCTCACTGTCCACCTTCCAGCAGATGTGGATTAGCAAGCAGGAGTACAA CGAGTCGGGCCCTCTCATCATCCACCGCAAATGGACTGCGAGCAGATGCATAGCATTT GCTGCATGGGTTAATTGAGAAGTATAAATTGCCCCCTGGCAAATGCATATACCTCATG CTAGCCTCAGGATAC</p>		
	ORF Start: ATG at 6	ORF Stop: TAA at 1185	
	SEQ ID NO: 310	393 aa	MW at 44147.5kD
NOV110a, CG59619-01 Protein Sequence	<p>MEEIIPALFIDNNGSMWKAALLGDNALRAIFPSIIIGHPRHQGVMMGMQKDSYVGDQ QSKCGILTLKYPKIHGIVTNWDDMEKIWHHVYFYNELCVALEEQVLLTEAPLNPRANR EKMTQIMPTKFTNQAMYYAIQAVLTLHSSGCTTGIVMDSGDGVTHTVPIYERHTLPH ILHLDLAQDLDLTLDYMIKPTIYRSYSFNTPMAKWKIVRNIEKLKCVLDFEEMETAAL SSSLEKSYELPDSQAIISNERFRCPEALFQPSFLGMESCGIHESTFNSIMKCDMDI KDLYANTVLSQGVTTMYPGIPNRMQKEITLASSTMKIKISCPVPECKYFVWIGGSI LASLSTFQMGWISKQEYNESGSIIRKWTASRCIAFAAWNVSEV</p>		

Further analysis of the NOV110a protein yielded the following properties shown in Table 110B.

Table 110B. Protein Sequence Properties NOV110a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.1547 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV110a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 110C.

Table 110C. Geneseq Results for NOV110a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV110a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU32060	Novel human secreted protein #2551 - Homo sapiens, 399 aa. [WO200179449-A2, 25-OCT-2001]	1..376 25..397	315/376 (83%) 336/376 (88%)	e-180
AAB43991	Human cancer associated protein sequence SEQ ID NO:1436 - Homo sapiens, 413 aa. [WO200055350-A1, 21-SEP-2000]	1..376 39..411	311/376 (82%) 336/376 (88%)	e-179
AAP61532	Sequence of beta-actin - Homo sapiens, 375 aa. [EP174608-A, 19-MAR-1986]	1..376 1..373	311/376 (82%) 335/376 (88%)	e-179
AAB12985	Human beta-actin protein sequence - Homo sapiens, 374 aa. [US6087398-A, 11-JUL-2000]	2..376 1..372	310/375 (82%) 334/375 (88%)	e-178
AAR50328	Drug resistant structural protein - Homo sapiens, 375 aa. [JP06038773-A, 15-FEB-1994]	1..376 1..373	309/376 (82%) 335/376 (88%)	e-178

In a BLAST search of public sequence databases, the NOV110a protein was found to have homology to the proteins shown in the BLASTP data in Table 110D.

Table 110D. Public BLASTP Results for NOV110a				
Protein Accession Number	Protein/Organism/Length	NOV110a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P02571	Actin, cytoplasmic 2 (Gamma-actin) - Homo sapiens (Human),, 375 aa.	1..376 1..373	315/376 (83%) 336/376 (88%)	e-179
ATBOG	actin gamma (tentative sequence) - bovine, 374 aa.	2..376 1..372	314/375 (83%) 335/375 (88%)	e-179
P53505	Actin, cytoplasmic type 5 - Xenopus laevis (African clawed frog), 376 aa.	2..376 3..374	313/375 (83%) 335/375 (88%)	e-178
P29751	Actin, cytoplasmic 1 (Beta-actin) - Oryctolagus cuniculus (Rabbit), 375 aa.	1..376 1..373	311/376 (82%) 337/376 (88%)	e-178

Further analysis of the NOV111a protein yielded the following properties shown in Table 111B.

Table 111B. Protein Sequence Properties NOV111a	
PSort analysis:	0.8500 probability located in endoplasmic reticulum (membrane); 0.4400 probability located in plasma membrane; 0.1000 probability located in mitochondrial inner membrane; 0.1000 probability located in Golgi body
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV111a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 111C.

Table 111C. Geneseq Results for NOV111a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV111a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB58174	Lung cancer associated polypeptide sequence SEQ ID 512 - Homo sapiens, 250 aa. [WO200055180-A2, 21-SEP-2000]	166..391 20..243	168/227 (74%) 189/227 (83%)	2e-88
AAO01161	Human polypeptide SEQ ID NO 15053 - Homo sapiens, 122 aa. [WO200164835-A2, 07-SEP-2001]	147..264 1..118	81/119 (68%) 92/119 (77%)	2e-36
AAB53700	Human colon cancer antigen protein sequence SEQ ID NO:1240 - Homo sapiens, 106 aa. [WO200055351-A1, 21-SEP-2000]	42..99 1..58	53/58 (91%) 54/58 (92%)	1e-24

In a BLAST search of public sequence databases, the NOV111a protein was found to have homology to the proteins shown in the BLASTP data in Table 111D.

Table 111D. Public BLASTP Results for NOV111a				
Protein Accession Number	Protein/Organism/Length	NOV111a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BVT4	SELENOPHOSPHATE SYNTHETASE , HUMAN SELENIUM DONOR PROTEIN - Homo sapiens (Human), 392 aa.	1..391 1..392	364/392 (92%) 367/392 (92%)	0.0
P49903	Selenide,water dikinase 1 (EC 2.7.9.3) (Selenophosphate synthetase 1) (Selenium donor protein 1) - Homo sapiens (Human), 383 aa.	1..375 1..376	348/376 (92%) 351/376 (92%)	0.0
AAC50958	SELENOPHOSPHATE SYNTHETASE 2 - Homo sapiens (Human), 448 aa.	2..391 33..441	272/411 (66%) 313/411 (75%)	e-147
Q99611	Selenide,water dikinase 2 (EC 2.7.9.3) (Selenophosphate synthetase 2) (Selenium donor protein 2) - Homo sapiens (Human), 448 aa.	2..391 33..441	272/411 (66%) 313/411 (75%)	e-147
AAC53024	SELENOPHOSPHATE SYNTHETASE 2 - Mus musculus (Mouse), 452 aa.	2..387 36..441	267/407 (65%) 307/407 (74%)	e-146

Pfam analysis predicts that the NOV111a protein contains the domains shown in the Table 111E.

Table 111E. Domain Analysis of NOV111a			
Pfam Domain	NOV111a Match Region	Identities/ Similarities for the Matched Region	Expect Value
AIRS: domain 1 of 1	32..188	29/180 (16%) 113/180 (63%)	3e-18
AIRS_C: domain 1 of 1	191..367	34/197 (17%) 125/197 (63%)	1.1e-20

Example 112.

- 5 The NOV112 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 112A.

Table 112A. NOV112 Sequence Analysis			
	SEQ ID NO: 313	1544 bp	
NOV112a, CG59625-01 DNA Sequence	CGATGGGACACAGACAGGTCACCCAGCTCTGATCTTTGCCATCACAGTTGCTACAAT CGGCTCTTTCCAGTTTGGCTACAACACTGGGGTCATCAATGCTCCTGAGACGGTGCAG ATCATAAAGGAATTTATCAATAAAACTTTGACGGACAAGGCAAATGCCCTCCCTCTG AGGTGCTGCTCACGAATCTCTGGTCTTGTCTGTGGCCATATTTCCGTCGGGGGTAT GATCGGCTCCTTTCCGTCGGACTCTTTGTTAACCGCTTTGGCAGGAGGCGCAATTCA ATGCTGATTGTCAACCTGTTGGCTGCCACTGGTGGCTGCCTTATGGGACTGTGTAAAA TAGCTGAGTCAGTTGAAATGCTGATCCTGGGCGCTTGGTTATTGGCCTCTTCTGCGG ACTCTGCACAGGTTTGTGCCCATGTACATTGGAGAGATCTCGCCTACTGCCCTGAGG GGTGCCTTTGGCACTCTCAACCAGCTGGGCATAGTTATTGGAATTCTGGTGGCCAGG TAATCTTTGGTCTGGAACCTCATCCTTGGGTCTGAAGAGCTATGGCCGGTGTCTATTAG CTTTACCATCCTTCCAGCTATCCTGCAAAGTGCAGCCCTTCCATGTTGCCCTGAAAGT CCGAGATTTTGTCTATTAAACAGAAAAAAGAGGAGAATGTACGCGGGTCTCCAGG GGTTGTGGGGCACCAGGATGTATCCCAAGACATCCAGGAGATGAAAGATGAGAGTGC AAGGATGTGCACAAGAAAAGCAAGTCACCGTGTCTGGAGCTCTTTAGAGTGTCCAGCTAC CGACAGCCCATCATCTTCCATTGTGCTCCAGCTCTCTCAGCAGCTCTCTGGGATCA ATGCTGTGGTGTCTATTACTCAACAGGAATCTTCAAGGATGCAGGTGTTCAACAGCC CATCTATGCCACCATCAGCGCGGGTGTGGTTAATACTATCTTCACTTTACTTTCTGTAT GTAGCTCAGATGCTGTTTTCATGGAAGGAAACTGAAGTTTCAATGTGCATAACTGTTT CTTTGTTATTAAAGCTGGGTTACACTGTCTTTAAATTTAATCTTCTGTGTTCTCTCTC CTTACAGAATCACTATAATGGGATGAGCTTTGTCTGTATTGGGGTATCTTGGTCTTT GTGGCTGTGTTTGAATTGGACCAGGCCCATTCCTGGTTTATTGTGGCCGAACCTCT TCAGCCAGGGCCCCCGCCAGCTGCGATGGCAGTGGCCGGCTGCTCCAAGTGGACCTC CAACTTCTTAGTCGAGATTGCTCTTCCCTCTGCTGCTTACTATTAGGAGCCTACGTT TTTATTATCTTACCGGCTTCTCATTACCTTCTTGGCCTTTACCTCTCTCAAAGTCC CTGAGACCCGTGGCAGGACTTTTGAAGATATCACACGGGCTTTGAAGGGCAGGCACA CGGTGCAGATAGATCTGGGAAGGACGGCGTCATGGGGATGAACAGCATCGAGCTGCT AAGGAGACCACCACCAATGTCTAAGTCATGCCTCT		
	ORF Start: ATG at 3	ORF Stop: TAA at 1530	
	SEQ ID NO: 314	509 aa	MW at 55571.7kD
NOV112a, CG59625-01 Protein Sequence	MGHRQVTPALIFAITVATIGSFQFGYNTGVINAPETVQIIKEFINKLTLDKANAPPSE VLLTNLWSLSVAIFSVGGMIGSFVGLFVNRFGRRRNSMLIVNLLAATGGCLMGLCKI AESVEMLILGRVLIGLFCGLCTGFVPMYIGEISPTALRGAFGLTNQLGIVIGILVAQV IFGLELILGSEELWPVLLGFTILPAILQSAALPCCPESPRFLINRKKEENATRVLQR LWGTQDVSQDIQEMKDESARMSQEKGQVTVLELFRVSSYRQPIIIISIVLQLSQQLSGIN AVFYYSTGIFK DAGVQQPIYATISAGVVNTIFTLLSVVAQMLFSWKGLKFHVITVS LLLKLGYTVFKFNLLCSFLLQNHYNGMSFVCIGAILVVFVACFEIGPGPIPFVIVAELE SQGPRPAAAMAVAGCSNWTSNFLVGLLFPSSAAYYLGAYVFIIFTGLITFLAFTFFKVE ETRGRTFEDITRAFEGQAHGADRSGKDGVMGMNSIEPAKETTTNV		

Further analysis of the NOV112a protein yielded the following properties shown in Table 112B.

Table 112B. Protein Sequence Properties NOV112a	
Psort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 22 and 23

A search of the NOV112a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 112C.

In a BLAST search of public sequence databases, the NOV112a protein was found to have homology to the proteins shown in the BLASTP data in Table 112D.

Protein Accession Number	Protein/Organism/Length	NOV112a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P11169	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Homo sapiens (Human), 496 aa.	1..509 1..496	446/510 (87%) 468/510 (91%)	0.0
P47842	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Canis familiaris (Dog), 495 aa.	1..507 1..494	400/507 (78%) 446/507 (87%)	0.0
P47843	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Ovis aries (Sheep), 494 aa.	1..505 1..492	389/505 (77%) 431/505 (85%)	0.0

P58352	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Bos taurus (Bovine), 494 aa.	1..505 1..492	390/505 (77%) 431/505 (85%)	0.0
Q07647	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Rattus norvegicus (Rat), 493 aa.	1..508 1..492	380/508 (74%) 422/508 (82%)	0.0

PFam analysis predicts that the NOV112a protein contains the domains shown in the Table 112E.

Table 112E. Domain Analysis of NOV112a			
Pfam Domain	NOV112a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Herpes_glycop: domain 1 of 1	1..249	40/417 (10%) 171/417 (41%)	7.2
GntP_permease: domain 1 of 1	65..329	70/478 (15%) 185/478 (39%)	2.5
sugar_tr: domain 1 of 1	12..478	188/503 (37%) 410/503 (82%)	2.2e-158

Example 113.

- 5 The NOV113 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 113A.

Table 113A. NOV113 Sequence Analysis		
	SEQ ID NO: 315	1731 bp
NOV113a, CG59887-01 DNA Sequence	ACTACTTCGCCGACACTCGCCAGCCTCGGGCTACGAGCAAAAAATGCACCGCACCATGA GCTCGTTACCTCGTTTGGCCCTGGCCTTTTCCATGGTCTCGATCAACACCGCGTGGT CACGCTGTTCGCCGACCCGTTCAACCGCGTCGGGGGCATCGGCATCCTCCTGTGGCTG TTGGTGATCCCGCTGGTGTGCTGCATCGTCATGGTCTACTGCCACCTGGCCGGGCGCA TTCCGCTCACC GGCTACGCCTACCAATGGTCAGCGGATGGCGGGCAATCACTTCGG CTGTTTTACCGGCTGGGTGGCGTTCACTCGTTTGTCCGGGTACAGCCGCCACCTCG GCGGCCATCGGTACGGTGTTCGCACCGGAGATCTGGGCCAACCCGACACAGGGTCAGA TCCAGGGCCTGAGCATCGGCGCCACGCTGGTGGTGGGCTTGCTGAATATCTCGGGAT TCGCCTGGCCACCCGATCAACGACATCGGCGCGATCATCGAATCATCGGCACGGTA CTGCTGGCGATTGCGTTGTTCTTCGGGGTGTTCCTTCTTTGAGCACACCCAGGGCG TGGCGATCCTGACCTCCGCGCAACCAAGTGAAGCGGCGGCGCTCAGCTTCAACACCAT CGCCCTCGCCACCTTGCTGCCGGTCTCGGTGCTGCTGGGTGGGAAGGCGCCGCGGAC CTGTCCGAGGAACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGG TGCTGGTGTCCAGCGTATTGGGCTTCGTGGTGTTCGCCTTGCTGAGCATCGCGATCCC GGGCTCGGTACGCAACTGCTCAGCCACAGCGAAACCCGGTGATCAATATCGTGCGC CTGCAACTGGGCAATGCGCGCGGCTGGGCGATGATCGTGATCGCTTTCGCCTCGATCC TCGCCTGCCTGATCGCAACATGGCGGTGGCCACGCGCATGACCTTCGCCCTGTCCCG GGACAACATGTGCGGGGCTCCAAGGTGCTGGCGAAGATCAACCCGCACTTCGGCAGC CCGGTCCGCCATCGTGCTGATCACCGCATCGCGTGTCTGTAACCTGGCGAGTG	

	CGGGGTTTGTACGGCGATCTACTCGATGGTCGGCCTGACCTACTACTGCACTTACCT GCTGACGCTGATTGCCGCGTACCTGGCCTATAAAAAACGGCCGATGCCGGGGGCGCCT CGGGGCGTGTTCAGCCTGGGCGCTGGTTGCTGCCGATGATTATCCTCGGCGGCCTGT GGGCCATCGCGGTGATCCTGACCCTGAGCGTGCCGGAAGAAGCCACACTGGCGCTAT CACCACCGGGGTTACACTCGGCGTGGGCGTGTGTGGTGGTTGTTTCTACTGCGCAGC CGCCTTAACAATGGCACCGCGGGCCGAGCGGCAAATTGCTCGACCACTAGCCGCTGA TTGCAGCCAAAAGACAAAACCCCGAACACGGGGTTTTGTCTTGTACCTCAAAGGAG CTTCCCGATGTTTGAACAGGCCAGCTGGCTCAATCAACCCAGCATTTGGCGCCGAGAA GGCGAGCGACTCAAGGTCGCGACCGATGCCAGTACCGATTCTTGGCGTGAAACCCACT ATGGTTTTGTACGCGACAACGGGCATTTCCTGTTTGTGAAACCGCGCGACTTTAC CGCCCAAGTCAAAATCCACAGTGAGTTTACCCACCTGTATGACCTTCGC		
	ORF Start: ATG at 43	ORF Stop: TAG at 1441	
	SEQ ID NO: 316	466 aa	MW at 49070.4kD
NOV113a, CG59887-01 Protein Sequence	MHRTMSSFTSFALAFSMVSINTGVVTLFADPFNRVGGIGILLWLLVPLVCCIVMVYC HLAGRIPLTGYAYQWSSRLAGNHFGWFTGWVAFSTFVAGTAATSAAIGTVFAPEIWAN PTQQIQGLSIGATLVVGLLNICGIRLATRINDIGAIIEIIGTVLLAIALFFGVFFFF EHTQGVAILTSAQPVSGGTLSTFTIALATLLPVSVLLGWEGAADLSEETKDPRAAPR AMIRAVLVSSVLGFVVFALLSIAIPGSVSELLSHSENPNVINIVRLQLGNAAGVGMIVI AFASILACLIANMAVATRMFTFALSRDNMLPGSKVLAKINPHFGTPVAAIVLITAI AVL LNLASGGFVTAIYSMVGLTYCTYLLTLIAAYLAYKNGRMPGAPAGVFSLGRWLLPMI ILGLWAIIVILTLSPVESHTGAITTGVTGLGVGLWWLFLSLRTRLNNGTAGPSGKLL DH		
	SEQ ID NO: 317	1433 bp	
NOV113b, CG59887-02 DNA Sequence	AAAAATGCACCGCACCATTGAGCTCGTTACCTCGTTTGCCTGGCCTTTTCCATGGTC TCGATCAACACCGCGTGGTCACGCTGTTCCGCCGACCCGTTCAACCGCGTCGGGGGCA TCGGCATCCTCCTGTGGCTGTTGGTGATCCCGCTGGTGCTGCTCATCGTCATGGTCTA CTGCCACCTGGCCGGGCGCATTCCGCTCACCGGCTACGCCATACCAATGGTCCAGCCGA TTGGCGGGCAATCACTTCGGCTGGTTTACCGGCTGGGTGGCGTTACCTCGTTTGTGCG CCGGTACAGCGCGCCACCTCGGCGGCCATCGGTACGGTGTTCCGACCGGAGATCTGGGC CAACCCGACACAGGGTCAGATCCAGGGCCTGAGCATCGGCGCCACGCTGGTGGTGGGC TTGCTGAATATCTCGGGGATTGCGCTGGCCACCCGGATCAACGACATCGGCGCGATCA TCGAAATCATCGGCACGGTACTGCTGGCGATTGCGTTGTTCTTCGGGGTGTTTTCTT CTTTGAGCACACCCAGGGCGTGGCGATCCTGACCTCCGCGCAACCAAGTGAAGCGCGC ACGCTCAGCTTACCACCATCGCCCTCGCCACCTTGTGTCGGGTCTCGGTGCTGCTGG GTTGGGAAGGCGCGCCGACCTGTCCGAGGAAACCAAGACCCACGCGCGCCGCGCC CCGGGCGATGATTGCTGCGGTGCTGGTGTCCAGCGTATTGGGCTTCGTGGTGTTCGCG TTGCTGAGCATCGCGATCCCGGGCTCGGTACGCGAACTGCTCAGCCGACGCGAAACCC CGGTGATCAATATCGTGCGCCTGCAACTGGGCAATGCCGCGCGCTGGGCGATGGCTGCT GATCGCTTTCGCTCGATCCTCGCCTGCCTGATCGCCAACATGGCGGTGGCCACGCGC ATGACCTTCGCCCTGTCCCGGGACAACATGCTGCCGGGCTCCAAGGTGCTGGCGAAGA TCAACCCGCACTTCGGCACGCGCGTTCGCCGCCATCGTGTGATCACCGCCATCGCCGT GCTGCTGAACCTGGCGAGTGGCGGGTTTTGTACCGCGCATCTACTCGATGGTGGCGCTG ACCTACTACTGCACTTACCTGCTGACGCTGATTGCCGCGTACTTGGCCTATAAAAAACG GCCGGATGCCGGGGGCGCCTGCGGGCGTGTTAGCCTGGGCGCTGGTGTGCTGCGCAT GATTATCTCGGCGGCCTGTGGGCCATCGCGGTGATCCTGACCTGAGCGTGCCGGAA GAAAGCCACACTGGCGCTATCACCACGGGGTTACTCGGCGTGGGCGTGTTGTGGT GGTTGTTTTCTACTGCGCACGCGCCTTAACAATGGCACCGCGCGGCGGAGCGGCAAATT GCTCGACCACTAGCCGCTGATTGCAGCCAAAAGACAAAACC		
	ORF Start: ATG at 5	ORF Stop: TAG at 1403	
	SEQ ID NO: 318	466 aa	MW at 49075.4kD
NOV113b, CG59887-02 Protein Sequence	MHRTMSSFTSFALAFSMVSINTGVVTLFADPFNRVGGIGILLWLLVPLVCCIVMVYC HLAGRIPLTGYAYQWSSRLAGNHFGWFTGWVAFSTFVAGTAATSAAIGTVFAPEIWAN PTQQIQGLSIGATLVVGLLNICGIRLATRINDIGAIIEIIGTVLLAIALFFGVFFFF EHTQGVAILTSAQPVSGGTLSTFTIALATLLPVSVLLGWEGAADLSEETKDPRAAPR AMIRAVLVSSVLGFVVFALLSIAIPGSVSELLSRSENPNVINIVRLQLGNAAGVGMVVI AFASILACLIANMAVATRMFTFALSRDNMLPGSKVLAKINPHFGTPVAAIVLITAI AVL LNLASGGFVTAIYSMVGLTYCTYLLTLIAAYLAYKNGRMPGAPAGVFSLGRWLLPMI ILGLWAIIVILTLSPVESHTGAITTGVTGLGVGLWWLFLSLRTRLNNGTAGPSGKLL DH		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 113B.

Table 113B. Comparison of NOV113a against NOV113b.		
Protein Sequence	NOV113a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV113b	1..466	343/466 (73%)
	1..466	344/466 (73%)

Further analysis of the NOV113a protein yielded the following properties shown in Table 113C.

Table 113C. Protein Sequence Properties NOV113a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 59 and 60

- A search of the NOV113a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
- 5 several homologous proteins shown in Table 113D.

Table 113D. Geneseq Results for NOV113a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV113a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG49885	Arabidopsis thaliana protein fragment SEQ ID NO: 63155 - Arabidopsis thaliana, 504 aa. [EP1033405-A2, 06-SEP-2000]	1..449 17..492	122/486 (25%) 217/486 (44%)	3e-31
AAG49884	Arabidopsis thaliana protein fragment SEQ ID NO: 63154 - Arabidopsis thaliana, 516 aa. [EP1033405-A2, 06-SEP-2000]	1..449 29..504	122/486 (25%) 217/486 (44%)	3e-31
AAG20282	Arabidopsis thaliana protein fragment SEQ ID NO: 22407 - Arabidopsis thaliana, 504 aa. [EP1033405-A2, 06-SEP-2000]	1..449 17..492	122/486 (25%) 217/486 (44%)	3e-31
AAG20281	Arabidopsis thaliana protein fragment SEQ ID NO: 22406 - Arabidopsis thaliana, 516 aa. [EP1033405-A2, 06-SEP-2000]	1..449 29..504	122/486 (25%) 217/486 (44%)	3e-31

AAG20280	Arabidopsis thaliana protein fragment SEQ ID NO: 22405 - Arabidopsis thaliana, 528 aa. [EP1033405-A2, 06-SEP-2000]	1..449 41..516	122/486 (25%) 217/486 (44%)	3e-31
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In a BLAST search of public sequence databases, the NOV113a protein was found to have homology to the proteins shown in the BLASTP data in Table 113E.

Table 113E. Public BLASTP Results for NOV113a				
Protein Accession Number	Protein/Organism/Length	NOV113a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9KZF1	PROBABLE AMINO ACID/METABOLITE PERMEASE - Streptomyces coelicolor, 504 aa.	3..450 27..481	139/469 (29%) 214/469 (44%)	2e-41
Q98H14	AMINO ACID/METABOLITE PERMEASE - Rhizobium loti (Mesorhizobium loti), 518 aa.	1..446 27..485	118/466 (25%) 209/466 (44%)	1e-36
Q92N18	PUTATIVE AMINO-ACID PERMEASE PROTEIN - Rhizobium meliloti (Sinorhizobium meliloti), 515 aa.	1..449 25..487	122/475 (25%) 204/475 (42%)	1e-32
O22509	PUTATIVE AMINO ACID OR GABA PERMEASE - Arabidopsis thaliana (Mouse-ear cress), 516 aa.	1..449 29..504	122/486 (25%) 217/486 (44%)	1e-30
Q9ZU50	PUTATIVE AMINO ACID PERMEASE - Arabidopsis thaliana (Mouse-ear cress), 517 aa.	1..449 29..505	120/487 (24%) 216/487 (43%)	2e-28

PFam analysis predicts that the NOV113a protein contains the domains shown in the Table 113F.

5

Table 113F. Domain Analysis of NOV113a			
Pfam Domain	NOV113a Match Region	Identities/ Similarities for the Matched Region	Expect Value
oxidored_q3: domain 1 of 1	162..307	28/182 (15%) 91/182 (50%)	3.7

ISK_Channel: domain 1 of 1	196..326	32/136 (24%) 55/136 (40%)	8.8
ABC2_membrane: domain 1 of 1	122..377	46/273 (17%) 154/273 (56%)	8.3
SSF: domain 1 of 1	7..394	77/470 (16%) 222/470 (47%)	7.8
Aa_trans: domain 1 of 1	29..417	67/483 (14%) 236/483 (49%)	9.7
aa_permeases: domain 1 of 1	1..451	86/516 (17%) 287/516 (56%)	1.1e-05

Example 114.

The NOV114 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 114A.

Table 114A. NOV114 Sequence Analysis			
	SEQ ID NO: 319	876 bp	
NOV114a, CG59861-01 DNA Sequence	AACTTGCTTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCC TCAACAGCGACCTGGCCAATTTAGGGGCCGAGTGCTCCGGATGCTAGACTCTGGGGC CGATTATCTGCACCTGGACGTAATGGACGGGCATTTGTTCCCAACATCACCTTTGGT CACCCTGTGGTGGAAAGCCTTCGAAAGCAGCTAGGCCAGGACCCCTTTCTTTGACATGC ACATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAA TCAGTACACCTTTTCATCTCGAGGCTACTGAGAACCAGGGGCTTTGATTAAAGACATT CGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAAACCAGGAACCTCAGTTGAGTATT TGGCACCATTGGGCTAATCAGATAGATATGGCCTTGGTTATGACAGTGGAACCGGGGTT TGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAG TTCCCATCTTTGGATATAGAGGTCGATGGTGGAGTAGGTCTGACACTGTCCATAAAT GTGCAGAGGCAGGAGCTAACATGATTGTGTCTGGCAGTGCTATTATGAGGAGTGAAGA CCCCAGATCTGTGATCAATCTATTAAGAAATGTTTGTCTCAGAAGCTGCTCAGAAACGT TCTCTTGATCGGTGA <u>AAACCATAAGGAGCCAGTGTCTCTGTT</u> CATGAAATCTCCCTTT TACTGGAAAACAGGAATATTGACTACCAAATCACAATGCAATTGAAGCCGTACTGCTT TTTTGAGCAGTTATTCTATTCAGTGATTAAAACTGATTGTGCAGAATAAAAAA AAAAA		
	ORF Start: ATG at 25	ORF Stop: TGA at 709	
	SEQ ID NO: 320	228 aa	MW at 24901.4kD
NOV114a, CG59861-01 Protein Sequence	MASGCKIGPSILNSDLANLGAECRMLDSGADYLHLDDVMDGHFVPNITFGHPVVESLR KQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGMKVG LAIKPGTSVEYLPFWANQIDMALVMTVEPGFGGQKFMEDMMPKVHWLRTQFPLSDIEV DGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPFRSVINLLRNVCSAAQKRSLDR		
	SEQ ID NO: 321	730 bp	
NOV114b, CG59861-02 DNA Sequence	AACTTGCTTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCC TCAACAGCGACCTGGCCAATTTAGGGGCCGAGTGCTCCGGATGCTAGACTCTGGGGC CGATTATCTGCACCTGGACGTAATGGACGGGCATTTGTTCCCAACATCACCTTTGGT CACCCTGTGGTAGAAAGCCTTCGAAAGCAGCTAGGCCAGGACCCCTTTCTTTGACATGC ACATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAA TCAGTACACCTTTTCATCTCGAGGCTACTGAGAACCAGGGGCTTTGATTAAAGACATT CGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAAACCAGGAACCTCAGTTGAGTATT TGGCACCATTGGGCTAATCAGATAGATATGGCCTTGGTTATGACAGTGGAACCGGGGTT TGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAG TTCCCATCTTTGGATATAGAGGTCGATGGTGGAGTAGGTCTGACACTGTCCATAAAT GTGCAGAGGCAGGAGCTAACATGATTGTGTCTGGCAGTGCTATTATGAGGAGTGAAGA CCCCAGATCTGTGATCAATCTATTAAGAAATGTTTGTCTCAGAAGCTGCTCAGAAACGT TCTCTTGATCGGTGA <u>AAACCATAAGGAGCCAGT</u> G		
	ORF Start: ATG at 25	ORF Stop: TGA at 709	
	SEQ ID NO: 322	228 aa	MW at 24927.5kD

NOV114b, CG59861-02 Protein Sequence	MASGCKIGPSILNSDLANLGAECRLMLDSGADYLHLDVMDGHFVFNITFGHPVVESLR KQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGMKVG LAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMMPKVHWRQTQFPSLDIEV DGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCSAAQKRSLDR
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 114B.

Table 114B. Comparison of NOV114a against NOV114b.		
Protein Sequence	NOV114a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV114b	1..228	227/228 (99%)
	1..228	227/228 (99%)

Further analysis of the NOV114a protein yielded the following properties shown in Table 114C.

Table 114C. Protein Sequence Properties NOV114a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1753 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV114a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 114D.

Table 114D. Geneseq Results for NOV114a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Protein/Organism/Length [Patent #, Date]	NOV114a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41358	Human polypeptide SEQ ID NO 6289 - Homo sapiens, 247 aa. [WO200153312-A1, 26-JUL-2001]	1..228 20..247	227/228 (99%) 227/228 (99%)	e-132
AAM41357	Human polypeptide SEQ ID NO 6288 - Homo sapiens, 247 aa. [WO200153312-A1, 26-JUL-2001]	1..228 20..247	227/228 (99%) 227/228 (99%)	e-132

AAM39571	Human polypeptide SEQ ID NO 2716 - Homo sapiens, 228 aa. [WO200153312-A1, 26-JUL-2001]	1..228 1..228	227/228 (99%) 227/228 (99%)	e-132
AAB71912	Human ISOM-4 - Homo sapiens, 228 aa. [WO200112790-A2, 22-FEB-2001]	1..228 1..228	227/228 (99%) 227/228 (99%)	e-132
AAM39572	Human polypeptide SEQ ID NO 2717 - Homo sapiens, 246 aa. [WO200153312-A1, 26-JUL-2001]	1..228' 1..246	227/246 (92%) 227/246 (92%)	e-129

In a BLAST search of public sequence databases, the NOV114a protein was found to have homology to the proteins shown in the BLASTP data in Table 114E.

Table 114E. Public BLASTP Results for NOV114a				
Protein Accession Number	Protein/Organism/Length	NOV114a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96AT9	HYPOTHETICAL 24.9 KDA PROTEIN - Homo sapiens (Human), 228 aa.	1..228 1..228	227/228 (99%) 227/228 (99%)	e-131
Q9BSB5	HYPOTHETICAL 25.3 KDA PROTEIN - Homo sapiens (Human), 232 aa (fragment).	1..228 5..232	227/228 (99%) 227/228 (99%)	e-131
AAH19126	HYPOTHETICAL 24.9 KDA PROTEIN - Mus musculus (Mouse), 228 aa.	1..228 1..228	221/228 (96%) 226/228 (98%)	e-129
O43767	RIBULOSE-5-PHOSPHATE-EPIMERASE - Homo sapiens (Human), 174 aa (fragment).	55..228 1..174	174/174 (100%) 174/174 (100%)	2e-98
Q96N34	CDNA FLJ31466 FIS, CLONE NT2NE2001372, HIGHLY SIMILAR TO HOMO SAPIENS PUTATIVE RIBULOSE-5-PHOSPHATE-EPIMERASE - Homo sapiens (Human), 178 aa.	69..228 1..178	160/178 (89%) 160/178 (89%)	2e-86

PFam analysis predicts that the NOV114a protein contains the domains shown in
5 the Table 114F.

Table 114F. Domain Analysis of NOV114a

Pfam Domain	NOV114a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Ribul_P_3_epim: domain 1 of 1	6..204	95/209 (45%) 174/209 (83%)	1.9e-105
IGPS: domain 1 of 1	179..213	15/35 (43%) 27/35 (77%)	0.02
trp_syntA: domain 1 of 1	34..222	45/273 (16%) 124/273 (45%)	2.9

Example 115.

The NOV115 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 115A.

Table 115A. NOV115 Sequence Analysis

	SEQ ID NO: 323	1761 bp
NOV115a, CG59857-01 DNA Sequence	AGTGTGGTACCTATCTGTCCCCCTCTGGAGGGGTTGACAAGGGAAAGGGCACCGGGG GGCACAGAGATGCAGGACAGATTGCACATCCTGGAGGACCTGAATATGCTCTACATT GGCAGATGGCACTCAGCCTGGAGGACACGGAGTTGCAGAGGAAGCTAGACCATGAGAT CCGGATGAGGGAAAGGGGCTGTAAGCTGCTGGCAGCCTGCTCCAGCGAGAGCAGGCT CTGGAGGCCACCAAGAGCCTGCTAGTGTGCAACAGCCGATCCTCAGCTACATGGGCG AGCTGCAGCGCGCAAGGAGGCGCAGGTGCTGGGGAAAGACAAGCCGGCGGCTTCTGA CAGTGGCCCGCCCGCTGAGCGCTCCCCCTGCCGCGGCGGGTCTGCATCTCTGACCTC CGGATTCCACTCATGTGAAGGACACAGAATATTCAAGAACAAGACTTGCACCGCT GGGCTGTGTTCTGCTGCTGCAGCTGGGGGAACACATCCAGGACACAGAGATGATCCT AGTGGACAGGACCTCAGACATCTCCTTTCAGAGCAATGTGCTCTTCTGCTGAGGGG GGGCCAGACTTGAAGTCCGGTTAGAGCTGTATGGGGCTGTGTGGAAGAAGAGGGGG CCCTGACTGGCGGCCCCAAGAGGCTTGCCACCAAATCAGCAGTCCCTGGGCGGCTC CTCAGGGAGGCGGTGCCGGGATCGCTGGACAGTGTGGGGTTTCAGGAGCAGTCCC ATCTTGCTCCCCACCCAGTTGTTGGTGGTCTCGTTACCACTCTTGGCTCACACCA CACTCACCTGGCAGTGCAGATGGAATCCGACACATGATGATGATGATGATGATGATG TCATGAGGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT GCTCAGCTCTCTGATGACTCAGCCACTGCAAGTGGTACCCTCAGGCTGCAGCAAG CTGGGGAGATGCAGAACTGGGCACAAGTGCATGGAGTTCTGAAGGCACAACTCTT CTGTTACCGGCAACCTGAGGATGCAGACACTGGGGAAAGAGCCGTGCTTACTATTGCT GTCAACAAGGAGACTCGAGTCCGGGAGGGGAGCTGGACAGGCTCTAGGACGGCCCT TCACCTAAGCATCAGTAACAGTATGGGGATGATGAGGTGACACACACCTTCAGAC AGAAAGTCGGGAAGCACTGCAGAGCTGGATGGAGGCTCTGTGGCAGCTTTCTTTGAC ATGAGCCAATGGAAGCAGTGTGTGATGAAATCATGAAATGAAACTCCTGCTCCCC GGAAACCACCCCAAGCACTGGCAAAGCAGGGGCTCCTGTACCATGAGATGGCTATTGA GCCGCTGGATGACATCGCAGCGGTGACAGACATCCTGACCCAGCGGGAGGGCGCAAGG CTGGAGACACCCACCCCTGGCTGGCAATGTTTACAGACCAGCCTGCCTGCCTAACC CCTGCTCGCTGCTCAGTGGCCCCAGCCCCAGACTGGACCCACCCCTGCCCTGGGG GAGACCCCGAACCTTTCCCTGGATGCTGTCCCCCAGACCACTCCCTAGGGCTCGC TCGGTTGCCCCCTCCACCTCAGCGATCCCCACGGACCAGAGGCCTCTGCAGCAAG GCCAACCTCGCACTTGGCTCCAGTCACCACTGTGAGAGAGAAAGGTGCTGGCATAGGA TCTGCCCAGAAGAGAAATGA	
	ORF Start: ATG at 68	ORF Stop: TGA at 1715
	SEQ ID NO: 324	549 aa MW at 61171.0kD
NOV115a, CG59857-01 Protein Sequence	MQDRLHILEDLNLMIYIRQMALSLEDTELQRKLDHEIRMREGACKLLAACSQREQALEA TKSLLCVNSRIILSYMGELQRRKEAQLGKTSRRPSDSGPPAERSPCRGVCI S D L R I P LMWKDTEYFKNKDLHRWAVFLLLQLGEHIQDTEMLVDRTLTDISFQSNVLF AEAGPD FELRLELYGACVEEGALTGGPKRLATKLSSSLGRSSRRVRASLDSAGSGSSPILL PTPVVGGPRYHLLAHTTLTAAVQDGFRTDHLTLASHEENPAWLPYGVCCRLAAQP LCMTQPTASGTLRVQAGEMQNWAVHGVKGTNLF CYRQPEDADTGEEPLLTIAVNK ETRVRAGELDQALGRPFTLSISNQYGDDEVHTLTQTESREALQSWMEALWQLFFDMSQ	

	WKQCCDEIMKIETPAPRKPPQALAKQGSLYHEMAIEPLDDIAAVTDILTQREGARLET PPPWLAMFTDQPALPNPCSPASVAPADWTHPLPWGRPRTFSLDAVPPDHSPRARSVA PLPPQRSRTRGLCSKGQPRTWLQSPV
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Further analysis of the NOV115a protein yielded the following properties shown in Table 115B.

Table 115B. Protein Sequence Properties NOV115a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1707 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV115a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 115C.

Table 115C. Geneseq Results for NOV115a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV115a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB35241	Human rhotekin - Homo sapiens, 563 aa. [US6183990-B1, 06-FEB-2001]	24..549 37..563	526/527 (99%) 526/527 (99%)	0.0
AAY44559	Human Rhotekin protein - Homo sapiens, 563 aa. [WO9958667-A1, 18-NOV-1999]	24..549 37..563	526/527 (99%) 526/527 (99%)	0.0
AAB35242	Human rhotekin EST-derived protein - Homo sapiens, 527 aa. [US6183990-B1, 06-FEB-2001]	24..549 1..527	522/527 (99%) 523/527 (99%)	0.0
AAY44560	Human Rhotekin variant protein - Homo sapiens, 527 aa. [WO9958667-A1, 18-NOV-1999]	24..549 1..527	522/527 (99%) 523/527 (99%)	0.0
AAB26790	Human Ras correlative GTP binding kinase protein sequence - Homo sapiens, 544 aa. [CN1257924-A, 28-JUN-2000]	24..549 18..544	518/527 (98%) 519/527 (98%)	0.0

In a BLAST search of public sequence databases, the NOV115a protein was found to have homology to the proteins shown in the BLASTP data in Table 115D.

Table 115D. Public BLASTP Results for NOV115a				
Protein Accession Number	Protein/Organism/Length	NOV115a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH17727	SIMILAR TO RHOTEKIN - Homo sapiens (Human), 550 aa.	1..549 1..550	549/550 (99%) 549/550 (99%)	0.0
Q9BST9	SIMILAR TO RHOTEKIN - Homo sapiens (Human), 587 aa (fragment).	24..549 61..587	526/527 (99%) 526/527 (99%)	0.0
Q96PT6	RTKN - Homo sapiens (Human), 544 aa.	24..549 18..544	518/527 (98%) 519/527 (98%)	0.0
Q9HB05	RHOTEKIN - Homo sapiens (Human), 567 aa (fragment).	24..549 41..567	505/527 (95%) 513/527 (96%)	0.0
Q61192	RHOTEKIN - Mus musculus (Mouse), 551 aa.	1..549 1..551	477/551 (86%) 500/551 (90%)	0.0

PFam analysis predicts that the NOV115a protein contains the domains shown in the Table 115E.

Table 115E. Domain Analysis of NOV115a			
Pfam Domain	NOV115a Match Region	Identities/ Similarities for the Matched Region	Expect Value
HR1: domain 1 of 1	23..95	17/87 (20%) 54/87 (62%)	0.27
PH: domain 1 of 1	296..397	19/102 (19%) 72/102 (71%)	1e-06

Example 116.

- 5 The NOV116 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 116A.

Table 116A. NOV116 Sequence Analysis		
	SEQ ID NO: 325	450 bp
NOV116a, CG59855-01 DNA Sequence	CTGGGAGACTGAAAAATGCAGACCACCGGGTATTACTCATTCTCCAGCTCTGATC TGCTGTTGTACCAGGGGTCTAATCAGGCCTGTGTCTGCCTTCTCCTTGAATAGCCCAG AGAATTTCATCTAAACAGCCTTCCTACAGCAGCTCCCCACTCCAGGTGGCCAGACGGGA GTTCCAGACCAGTGTGTCTCCCGGGACACTGACACAGCCGCCAAGTTTATTGGTGTCT GGTCAGCCACAGTTGGTGTGGCTGATTACAGGGGCTGGCATTGGAGCGGTGTTGGCA GCTTGATTATTGTCTATGCCAGGAAGCTGTCTCTCAAGCAGCAACTCTCTCTATGC CATCTGGGCTTTGCCCTGTCTGAGGCCATGGGGCTCTTCTGTTTGATGATCTCCTTC TTCATCCTGTTCCCATGTGAGGCTCCGTGAGGGTCACCTGCCT	

P32876	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Bos taurus (Bovine), 136 aa.	1..136 1..136	113/136 (83%) 117/136 (85%)	1e-54
P17605	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Ovis aries (Sheep), 136 aa.	1..136 1..136	113/136 (83%) 117/136 (85%)	2e-54
Q9CR84	ATP SYNTHASE C CHAIN ISOFORM 1 (EC 3.6.1.34) (LIPID-BINDING PROTEIN) (SUBUNIT C) - Mus musculus (Mouse), 136 aa.	1..136 1..136	112/136 (82%) 117/136 (85%)	1e-53
P48202	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Mus musculus (Mouse), 136 aa.	1..136 1..136	112/136 (82%) 117/136 (85%)	1e-53

PFam analysis predicts that the NOV116a protein contains the domains shown in the Table 116F.

Table 116F. Domain Analysis of NOV116a			
Pfam Domain	NOV116a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ATP-synt_C: domain 1 of 1	67..135	31/70 (44%) 57/70 (81%)	2.3e-18

Example 117.

The NOV117 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 117A.

Table 117A. NOV117 Sequence Analysis		
	SEQ ID NO: 329	1769 bp
NOV117a, CG59807-01 DNA Sequence	GAGGTGATGCTGGAGACCTGCGGACTTCTCATGTCTCTGGGCTGTCCTTTGTTCAAAC CAGAGCTGATCTACCACTGGATCAGACAGGAGCTATGGATGGCTACAAAAGACCT CTCCCAAAGCTCCTATCCAGGTGACACACAAAACCAAGACCACAGAGCCTACCTTT TCTCACCTGGCCTTGCTGAGGAAGTCTTACTCCAGGAACAACGACACAGAAGGAGCCT CAAAGAACTCCCAATTAGGGCAATCCAAGGATCAGGATGGGCCATCTGAAATGCAAGA AGTCCACTTGAAATAGGGATAGGCCCCAGCGGGGAAGCTGCTGGAGAAAATGAGT	

	TCTGAACGTGATGGTTTGGGGTCAGATGATGGTGTATGTACAAAGATTACACAGAAAC AAGTTTCAACAGAAGGTGATCTCTATGAATGTGATTACATGGACCAGTTACAGATGC CTTGATTGCGGAAGAGAAAAATTCCTATAAATGTGAGGAATGCGGGAAGGTGTTAAA AAGAATGCCCTCCTTGTTTTCAGCATGAACGGATTACACTCAAGTGAAGCCCTATGAAT GCACAGAGTGTGGGAAAACCTTTAGCAAGAGCACTCATCTTCTTTCAGCACTCATCAT CCACACTGGGGAGAAGCCCTATAAGTGCATGGAGTGTGGGAAGGCTTTTAACCGCAGG TCACACCTCACACGGCACCAGCGGATTACAGTGGAGAGAAGCCCTATAAGTGCAGTG AATGTGGAAAGGCCCTTCAACCGCGGTTCACCTTCTTGTCTTGCATACAGGAGCCACAC TGGAGAAAAACCTTTGTGTGCAAAGAGTGTGGCAAAGCCTTTTCGAGATAGGCCAGGT TTCATTCGACACTACATCATCCACACGGGAGAGAAGCCCTATGAGTGCATTGAGTGTG GGAAGGCCCTTCAACCGCGGTTCATACCTCAGTGGCACCACAGATTACACTGGAGT GAAACCCCTTGAATGCAACGAGTGTGGAAAAGCCTTTTGCAGAGTGCAGACCTCATT CAACACTACATTATCCACACTGGGAGAAGCCCTATAAGTGCATGGAGTGTGGGAAGG CGTTCAACCGTAGGTACACCTCAAGCAGCATCAACGGATTACACTGGGGAGAGACC TTATGAATGCAGTGAATGTGGAAAGGCCCTTCAACCGCAGCTCACACTTTCCTTCTGAT AAAAGGACCCACACAGGAGAAAAACCTATGAATGCAAAGAATGTGGAAAAGCCTTTA GTGATAGGGCAGACCTCATTGCGCACTTTCAGCATCCACACTGGAGAGAAGCCCTATGA GTGCGTGGAGTGTGGAAAGGCCCTTCAACCGCAGCTCACACTCAGAGGACCAACAG ATTACACTGGAGAGAAGCCCTATGAATGCATCCAGTGTGGGAAGCCTTTTGCCTGGA GCGCAACCTTATTCGACACTCCATCATTACACTGGAGAGAAGCCGTATGAATGCAG TGAGTGTGGAAAGCCTTTAATCGCGGCTCATCCCTCACACATCATCAAGGATTATCAT ACTGGGAGAAGCCCTACCATTGTAACAGATGTGGGAAGACCTTTTATGACTGCACAGA CTTCAGTCAACATCCAGGAACCTTTATAGGGAAGAGTTTTGAATATCACCAGTGA AGAAAATCTGTGGTGAAGGGAACATCTTACCATCTGGCCATTACACTGAAGAGAAA CTTCATAAGCATCTCTCTTTGAGAAAAC		
	ORF Start: ATG at 7	ORF Stop: TGA at 1696	
	SEQ ID NO: 330	563 aa	MW at 64300.6kD
NOV117a, CG59807-01 Protein Sequence	MLETCGLLSLGLCPFKPELIYQLDHRQELWMATKDLSSQSSYPGDNTKPKTTEPTFSH LALPEEVLLQEQLTQGASKNSQLGSKDQDGPSEMGEVHLKIGIPQRGLLEKMSSE RDGLGSDDGVTCTKIQTQKQVSTEGDLYECDSHGPVTDALIREKNSYKCEECGVFKKN ALLVQHERIHTQVKPYECTECGKTFKSTHLLQHLIHTGEKPYKMECGKAFNRSSH LTRHQRIHSGEKPYKCECGKAFTHRSTFVLHHRSHTEGKPFVCKEKGKAFDRPGFI RHYIHTGEKPYECIECGKAFNRSSYLTWHQQIHTGVKPFECNECGKAFCESADLIQH YIHTGEKPYKMECGKAFNRSSHLKQHQRIHTGEKPYECSECGKAFTHCSTFVLHHR THTGEKPYECKEKGKAFSDRADLIRHFSIHTGEKPYECVECGKAFNRSSHLTRHQIHT TGEKPYECIQCGKAFCSRANLIRHSIHTGEKPYECSECGKAFNRSSSLTHHQRIHTG RNPTIVTDVGRPFMTAQTSVNIQELLGKEFLNITTEENLW		

Further analysis of the NOV117a protein yielded the following properties shown in Table 117B.

Table 117B. Protein Sequence Properties NOV117a	
Psort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	Likely cleavage site between residues 19 and 20

A search of the NOV117a protein against the Geneseq database, a proprietary
5 database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 117C.

Table 117C. Geneseq Results for NOV117a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV117a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79549	Human protein SEQ ID NO 3195 - Homo sapiens, 603 aa. [WO200157190-A2, 09-AUG-2001]	1..563 38..603	563/566 (99%) 563/566 (99%)	0.0
AAM78565	Human protein SEQ ID NO 1227 - Homo sapiens, 603 aa. [WO200157190-A2, 09-AUG-2001]	1..563 38..603	563/566 (99%) 563/566 (99%)	0.0
ABB21767	Protein #3766 encoded by probe for measuring heart cell gene expression - Homo sapiens, 551 aa. [WO200157274-A2, 09-AUG-2001]	44..562 10..527	375/519 (72%) 437/519 (83%)	0.0
AAM69575	Human bone marrow expressed probe encoded protein SEQ ID NO: 29881 - Homo sapiens, 551 aa. [WO200157276-A2, 09-AUG-2001]	44..562 10..527	375/519 (72%) 437/519 (83%)	0.0
AAM57172	Human brain expressed single exon probe encoded protein SEQ ID NO: 29277 - Homo sapiens, 551 aa. [WO200157275-A2, 09-AUG-2001]	44..562 10..527	375/519 (72%) 437/519 (83%)	0.0

In a BLAST search of public sequence databases, the NOV117a protein was found to have homology to the proteins shown in the BLASTP data in Table 117D.

Table 117D. Public BLASTP Results for NOV117a				
Protein Accession Number	Protein/Organism/Length	NOV117a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O43296	Zinc finger protein 264 - Homo sapiens (Human), 627 aa.	1..562 43..603	401/562 (71%) 468/562 (82%)	0.0
Q96NL3	CDNA FLJ30663 FIS, CLONE	1..535 38..572	299/535 (55%) 369/535 (68%)	0.0

	SIMILAR TO ZINC FINGER PROTEIN 84 - Homo sapiens (Human), 588 aa.			
Q99676	Zinc finger protein 184 - Homo sapiens (Human), 751 aa.	2..535 58..595	261/542 (48%) 355/542 (65%)	e-151
Q96SE7	ZINC FINGER 1111 - Homo sapiens (Human), 839 aa.	151..541 306..694	233/391 (59%) 281/391 (71%)	e-148
Q03923	Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1) - Homo sapiens (Human), 595 aa.	1..535 33..547	266/544 (48%) 328/544 (59%)	e-148

PFam analysis predicts that the NOV117a protein contains the domains shown in the Table 117E.

Table 117E. Domain Analysis of NOV117a			
Pfam Domain	NOV117a Match Region	Identities/ Similarities for the Matched Region	Expect Value
KRAB: domain 1 of 1	1..34	14/66 (21%) 24/66 (36%)	0.15
zf-C2H2: domain 1 of 13	162..184	11/24 (46%) 19/24 (79%)	3.6e-06
zf-C2H2: domain 2 of 13	190..212	11/24 (46%) 19/24 (79%)	7.1e-06
zf-C2H2: domain 3 of 13	218..240	14/24 (58%) 22/24 (92%)	2.3e-07
zf-BED: domain 1 of 3	203..241	13/52 (25%) 25/52 (48%)	2
zf-C2H2: domain 4 of 13	246..268	11/24 (46%) 20/24 (83%)	4.6e-05
LIM: domain 1 of 1	220..284	16/72 (22%) 50/72 (69%)	0.69
zf-C2H2: domain 5 of 13	274..296	8/24 (33%) 18/24 (75%)	7.6e-05
zf-C2H2: domain 6 of 13	302..324	11/24 (46%) 20/24 (83%)	8.4e-05
Zn_carbOpept: domain 1 of 1	312..330	5/19 (26%) 17/19 (89%)	1.2

The NOV118 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 118A.

Table 118A. NOV118 Sequence Analysis		
	SEQ ID NO: 331	1899 bp
NOV118a, CG59805-01 DNA Sequence	<p> CAAACTCTACTACCTCTATATGACATTTCAGGTGTCTGTGACCTTTTGATGATGTGGCT GTGACTTTCACCAGGAGGAGTGGGGCCAGCTGGACCTAGCTCAGCGGACCCTTGTAC AGGAGGTGATGCTGGAAAACTGTGGGCTCCTGGTATCTCTGGGTGGGTGTCCTGTTCC CAGACCTGAGCTGATCTACCACTAGAGCATGGGCAGGAGCCATGGCACAGGAAGGA GACCTCTCCAAAGGCACCTGTCCAGGTGACAAAGGAAACCCAAAGAGCACAGAACCTA CCACCTGTGAGCTAGCCTTGTCTGAAGGAATCTCTTTTTGGGGACAACTAACACAAGG AGCTTCAGGGGACTCCCAGTTGGGGCAACCCAAGGATCAGGATGGGTTTCAGAAATG CAGGGAGAACGCTTGAGACCAGGGTTAGATTCCAAAAGGAGAAGCTTCTTGAAAAA TGAGCCCCAAACATGATGGTTTAGGGACAGCTGATAGTGTGTGTCAAGGATTATACA GGATCGAGTCTCCTTAGAGATGATGTCATGACTGTGACTCACATGGATCAGGTAA AATCCAGTTATTCAGGAAGAGGAAAATATCTTTAAATGCAATGAATGTGAAAAAGTGT TTAACAAGAAACGCTGCTTGCTCGGCATGAGAGGATTCACTCTGGAGTGAAGCCCTA TGAATGCACAGAGTGTGGAAAACCTTTAGCAAGAGTACATACCTCCCTCGCACCACC ATGGTCCACACTGGGGAGAAGGCCTATAAGTGCATGGAGTGTGGGAAGGCTTTTAATC GGAAGTCACACCTTACCCAGCACAGCGGATTACAGTGGAGAGAAGCCCTTATAAGTG CAGTGAATGTGAAAGGCCTTCACCCACCGCTCCACTTTGTCTTGCATAACCAAGGAGC CACACTGGAGAAAACCCTTTGTGTGCAAAAGAGTGTGGCAAAGCCTTTCGAGATAGGC CAGGTTCATTTCGACATACATCATCCACAGTGGTGAGAATCCCTACGAGTGCTTCGAG ATGTGGCAAGGTCTTCAAACAGATCATACTCATGTGGCACAGCAGACTCATACC GGGGAGAAGGCCTATGAGTGCAGTGAATGTGGGAAGGCCTTCTGTGAGAGCGCAGCGC TGATTCACCACTATGTCATCCACACTGGAGAGAAGGCCTTTGAGTGCCTCGAGTGTGG GAAGGCTTTCAACCACCGATCCTACCTCAAAGGCACCAGCGGATTCACACTGGGGAG AAGCCATATGTGTGTAGTGAATGCGGAAAGGCCTTCACCCACTGCTCTACTTTATCT TGCATAAAAGGGCCCACTGGAGAAAAACCTTTCGAGTGCAAAGAGTGTGGGAAAGC CTTTAGCAATAGGGCAGACCTCATTGCCACTTCAGCATCCACATGGAGAGAAGCCC TATGAGTGCATGGAGTGTGGAAGGCCTTCAACCGCAGGTGAGGCCTCAGAAGCACC AGCGGATTCATAGTGGAGAGAAGGCCTATGAATGCATCGAGTGTGGGAAAACATTTTG CTGGAGCACAAACCTCATTGCACACTCTATCATCCACATGGAGAGAAGCCGATGAG TGCAGTGAATGTGGAAGGCCTTCAGTGCAGCTCGTCCCTCACTCAGCATCAATGGA </p>	

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	TGCATACTGGGAGAAATCCTATCAGTGTAACAGATGTGGGAAGACCTTTTACAAGTGG GCAGACCTCAGTCAACATCCAAGAACTTTTATTTGGGAAAAAAGCTTTTGAATGTCACC ACTGAGGAAAATCTTTTGAAGAGGAAGCATCTTACATGGCATCTGATCGTACATACC AAAGAGAAACCCCAAGTGTCTTCTACTGTGAGAAAACCTTCT		
	ORF Start: ATG at 20		ORF Stop: TGA at 1886
	SEQ ID NO: 332	622 aa	MW at 70677.2kD
NOV118a, CG59805-01 Protein Sequence	MTFQVSVTFDDVAVTFTQEEWGQLDLAQRITLYQEVMLENCGLLVSLGGCPVPRPELIY HLEHGQEPWTRKEDLSQGTCPGDKGPKSTEPTTCELALSEGISFWGQLTQAGSDSQ LGQPKDQDGFSEMQGERLRPGLDSQKEKLPKMSPKHDLGTADSVCSRI IQDRVSLG DDVHDCDSHGSGKNPVIQEEENIFKCNECEKVFNKKRLLARHERIHSVGKPYECTECG KTFSKSTYLLQHHMVHTGEKPYKMECGKAFNRKSHLTQHRIHSGEKPYKCECGKA FTHRSTFVLHNRSHTEKPFVCKEKGAFDRPGFIRHYI IHSGENPYECFECGKVFK HRSYLMWHQQTHTGEKPYECSECGKAFCEAALIHHYVIHTGEKPFECLECGKAFNHR SYLKRHRIHTGEKPYVCSECGKAFTHCSTFILHKRAHTGEKPFCECKEKGAFNRRAD LIRHFSIHTGEKPYECMECGKAFNRRSGLTRHQRHISGEKPYECIECGKTFWCSTNLI RHSIHTGEKPYECSECGKAFSRSSSLTQHQRMTGRNPISVTDVGRPPFTSGQTSVNI QELLGKNFLNVTTEENLLQEEASYMASDRTYQRETPQVSSL		

Further analysis of the NOV118a protein yielded the following properties shown in Table 118B.

Table 118B. Protein Sequence Properties NOV118a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3796 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV118a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded
5 several homologous proteins shown in Table 118C.

Table 118C. Geneseq Results for NOV118a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV118a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB22693	Protein #4692 encoded by probe for measuring heart cell gene expression - Homo sapiens, 468 aa. [WO200157274-A2, 09-AUG-2001]	81..548 1..468	468/468 (100%) 468/468 (100%)	0.0
AAM70526	Human bone marrow expressed probe encoded protein SEQ ID NO: 30832 - Homo sapiens, 468 aa. [WO200157276-A2, 09-AUG-2001]	81..548 1..468	468/468 (100%) 468/468 (100%)	0.0

Table 118E. Domain Analysis of NOV118a			
Pfam Domain	NOV118a Match Region	Identities/ Similarities for the Matched Region	Expect Value
KRAB: domain 1 of 1	7..70	41/66 (62%) 54/66 (82%)	2.2e-33
zf-C2H2: domain 1 of 13	198..220	11/24 (46%) 17/24 (71%)	3.9e-05
BolA: domain 1 of 1	161..238	14/88 (16%) 49/88 (56%)	3.4
zf-C2H2: domain 2 of 13	226..248	10/24 (42%) 18/24 (75%)	6.2e-05
zf-C2H2: domain 3 of 13	254..276	14/24 (58%) 22/24 (92%)	5e-07
TFIIS: domain 1 of 1	257..292	12/39 (31%) 21/39 (54%)	5.7
zf-C2H2: domain 4 of 13	282..304	11/24 (46%) 20/24 (83%)	3.7e-05
LIM: domain 1 of 1	256..320	14/71 (20%) 48/71 (68%)	0.38
zf-C2H2: domain 5 of 13	310..332	8/24 (33%) 18/24 (75%)	7.6e-05
zf-C2H2: domain 6 of 13	338..360	11/24 (46%) 19/24 (79%)	1.1e-05
zf-C2H2: domain 7 of 13	366..388	9/24 (38%) 18/24 (75%)	0.00027
zf-C2H2: domain 8 of 13	394..416	12/24 (50%) 21/24 (88%)	7.9e-07
zf-C2H2: domain 9 of 13	422..444	10/24 (42%) 19/24 (79%)	0.00014
zf-C2H2: domain 10 of 13	450..472	10/24 (42%) 20/24 (83%)	8.3e-06
zf-C2H2: domain 11 of 13	478..500	13/24 (54%) 21/24 (88%)	3e-07
zf-BED: domain 1 of 1	463..501	14/52 (27%) 29/52 (56%)	0.1
zf-C2H2: domain 12 of 13	506..528	11/24 (46%) 17/24 (71%)	0.0016

zf-C2H2: domain 13 of 13	534..556	13/24 (54%) 23/24 (96%)	7.2e-08
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Example 119.

The NOV119 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 119A.

Table 119A. NOV119 Sequence Analysis			
	SEQ ID NO: 333	1546 bp	
NOV119a, CG59928-01 DNA Sequence	<u>GCTCAGTAGGCGTCGGGCTGTGATGCCCAACTGCTCCAGCGTCTGCAGGCGCGCGCG</u> <u>GGCGCGGTAGGCGTACTCGCTGGCCGGATAGCGCGTGATGATGAACCTGGTAGGTCTGC</u> <u>GCCGCATCGACGAACAGGCTCTCGGCTCCAGGCATTGACCGCGCAGCAGGGAATCT</u> <u>CCGGCTGCGAGTAATTGCGTGAGCGGCTCTTGCGCTCGGCCCTGCGACAGCTCCAGCGC</u> <u>GACACGGGCGCAATCGCCTTCGTTGTAGGCGCGATAGGCGTTGTTTCAGATGATGGTCC</u> <u>AGCGAGACACGGGTGCAACCCGCGAGCAACAGGGCCACGGCCAGAATGATCAGGTTAC</u> <u>GCATGGGCAATTCTCTCAAATGAGCAGTGATCGACAGCCCAGGCCAAAACTGAACAGC</u> <u>GGCAAGCCGACGACGGTTTTTCTGGCGGCGCCTTGGCATGACGCCACTGCTCTCATT</u> <u>TTATCAACGCCAGCGCCACGACCGCTCTCTCTCGAACCAGCGCTAAATCCCCCTTCT</u> <u>GCGCTGACCCATATCAATGCCGTTT</u> <u>CAGCGCAACAGGGTGTGTAATGTAGGTACAGACT</u> <u>CCAGGCGAGGACGCTGCCATGAACTGCAACGACTGTTGGTCGTATCGACGCCGAAC</u> <u>ACCAGCAACAAACCCCGCTTGCACCGCGAGCCGATGTGGCAGCGCAAGACCGCGCAAC</u> <u>ATTGCACCTGTTGCAGATCGAATACCACCCAAGCCTGGAAGCGGCCGTGCTGGACAGC</u> <u>CATCTGCTCAACCGCGCCCGTGAAACCATCCTGCGACAGAGCCACGAGGCCCTGCGTG</u> <u>CCAGCTCGCTCACCTGAGCGATGAAGGATTCAAGATCGCAGTGAGCGTGGCGTGGG</u> <u>CAACGTCGTCATGAAGAAATCCTCGCCCGCGTCGCGGTGTTGCAACCGGACATCCTG</u> <u>TTCAAGTCGACTCATCCAGCAGTGCGCTGCGCCGCTGTTGTTTCAGTGATACCACTT</u> <u>GGCAGCTGATTGCGCGCAGCCCGGTGCGCTGTGGCTGGTACACGACGCCGAGCCCCA</u> <u>TGGTCAGAGCCTGTGCGCTGCGCTCGACCCGCTGCACAGCGCGGACAAACCTGCCGCC</u> <u>CTCGATCATCAGTTGATTGATGCCAGCCAGACCCTGCAGGCCGAGCTCGGCTTACAGG</u> <u>CCCAATACCTGCATGCACAGGCGCCTCTGCCGCGGTGCTGCTGTTGTCGACGCCAGGT</u> <u>AGCGCAGGAATATGAAGACTACGTGACCCAGTGACAGCCGCGAGCACCGCAAGCCTTC</u> <u>GACAAGCTGATCGCCAGCACGCCATCGATAGAGCACAGGCCACCTGTTGGACGGTT</u> <u>TTGCCGAGGAAGTCATCCCGGTTTCGTGCTGAGCACAAATATAGGCCTGCTGGTGAT</u> <u>GGGCGCCATCGCCCGCGGCCATCTGGACAGCCTGCTGATCGGCCACACCGCAGAACGG</u> <u>GTGCTGGAACGTGTCGAGTGCGATCTGCTGGTGATCAAATCGCACGGCAAGGGTAGT</u> <u>GCACAGGAACAATGACTACAGCCCGACGCCTACTGAGC</u>		
	ORF Start: ATG at 599	ORF Stop: TAG at 1505	
	SEQ ID NO: 334	302 aa	MW at 33922.3kD
NOV119a, CG59928-01 Protein Sequence	MKLQRLLVVIDAEHQQPALQRAADVARKTGAELHLLQIEYHPSLESGLLDSHLLNRA RETILRQSHEALRASVAHLSDEGFKIAVDVVRWGKRRHEILARVAVLQPDILFKSTHP SSALRRLLFSDTSWQLIRRPVPLWLVDHAEPHGQSLCAALDPLHSADKPAALDHQLI DASQTLQAEGLQAQYLHAQAPLPRSLFLDAEVAQEYEDYVYQCSREHREAFDKLIAQ HAIDRAQAHLLDGFAEEVPIPRFVREHNIGLLVMGAIARGHLDSLLIGHTAERVLERVE CDLLVIKSHGKG		

Further analysis of the NOV119a protein yielded the following properties shown in
5 Table 119B.

Table 119B. Protein Sequence Properties NOV119a	
PSort analysis:	0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.2014 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV119a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 119C.

Table 119C. Geneseq Results for NOV119a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV119a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found				

In a BLAST search of public sequence databases, the NOV119a protein was found to have homology to the proteins shown in the BLASTP data in Table 119D.

Table 119D. Public BLASTP Results for NOV119a				
Protein Accession Number	Protein/Organism/Length	NOV119a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9HW73	HYPOTHETICAL PROTEIN PA4328 - Pseudomonas aeruginosa, 304 aa.	1..297 1..299	156/299 (52%) 200/299 (66%)	1e-79
Q9KS28	HYPOTHETICAL PROTEIN VC1433 - Vibrio cholerae, 315 aa.	5..300 6..304	78/302 (25%) 147/302 (47%)	4e-29
CAC91106	PUTATIVE STRESS PROTEIN - Yersinia pestis, 318 aa.	2..300 3..303	93/310 (30%) 137/310 (44%)	2e-28
AAL20579	PUTATIVE UNIVERSAL STRESS PROTEIN - Salmonella typhimurium LT2, 315 aa.	4..297 5..300	91/305 (29%) 139/305 (44%)	2e-28
CAD01669	CONSERVED HYPOTHETICAL PROTEIN - Salmonella enterica subsp. enterica serovar Typhi, 315 aa.	4..297 5..300	91/305 (29%) 139/305 (44%)	3e-28

PFam analysis predicts that the NOV119a protein contains the domains shown in the Table 119E.

CG59947-01 Protein Sequence	EELGFWGIDETDVEACCWMTYRQHRDAEEALDSFEAPDPAGAANAANAAGAHDGGLDD EAGAGGGGLDGAGGELKRLCFQDAGGGAGGPPGGAGGAGGTWRRWQPRVWALFEDPY SSRAARYVAFASLFFILISITTFCLETHEGFIHISNKTVTQASPIPGAPPENITNVEV ETEPFLTYVEGVVWVTFEFLMRITFCPDKVEFLKSSLNIDCVAILPFYLEVGLSG LSSKAAKDVLGFLRVVRFVRLRIFKLTRHFVGLRVLGHTRASTNEFLLLIIFLALG VLIFATMIYYAERIGADPDDILGSNHTYFKNIPIGFWWAVVTMTLGYGDMYPKTWSG MLVGALCALAGVLTIAMVPVIVNFMGYSLAMAKQKLPKKKNKHI PRPPQPGSPNY CKPDPPPPPPPHHGGSGISPPPIITPPSMGVTVAGAYPAGPHTHPLGLRGGAGGLG IMGLPPLPAPGEPCLAQEEVIEINRADPRNGDPAAAALAHEDCPAIDQFAMSPEDK SPITPGSRGRYSRDRACFLLDYAPSPDGSIRKATGAPPLPPQDWRKPGPPSFLPDNLN ANAAWISP
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Further analysis of the NOV120a protein yielded the following properties shown in Table 120B.

Table 120B. Protein Sequence Properties NOV120a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.5071 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV120a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 120C.

Table 120C. Geneseq Results for NOV120a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV120a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY34120	Human potassium channel K+Hnov4 - Homo sapiens, 601 aa. [WO9943696-A1, 02-SEP-1999]	32..526 4..476	371/510 (72%) 399/510 (77%)	0.0
AAY32016	Caenorhabditis elegans cation channel protein - Caenorhabditis elegans, 556 aa. [WO9947923-A2, 23-SEP-1999]	33..512 27..465	217/486 (44%) 300/486 (61%)	e-113
AAB86319	Human Kv4.2 protein - Homo sapiens, 629 aa. [DE19963612-A1, 12-JUL-2001]	16..521 22..441	173/511 (33%) 256/511 (49%)	5e-69
AAY13523	Amino acid sequence of KV4.2FL ion channel protein - Mammalia, 630 aa. [WO9923880-A1, 20- MAY-1999]	16..521 23..442	173/511 (33%) 257/511 (49%)	8e-68

AAW42996	Putative mature potassium channel 2 protein - Homo sapiens, 494 aa. [US5710019-A, 20-JAN-1998]	17..510 4..425	171/503 (33%) 240/503 (46%)	2e-66
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In a BLAST search of public sequence databases, the NOV120a protein was found to have homology to the proteins shown in the BLASTP data in Table 120D.

Table 120D. Public BLASTP Results for NOV120a				
Protein Accession Number	Protein/Organism/Length	NOV120a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q14003	Voltage-gated potassium channel protein Kv3.3 (KSHIID) - Homo sapiens (Human), 757 aa.	1..705 1..757	704/757 (92%) 704/757 (92%)	0.0
Q01956	Voltage-gated potassium channel protein Kv3.3 (KSHIID) - Rattus norvegicus (Rat), 889 aa.	1..693 1..756	663/757 (87%) 668/757 (87%)	0.0
Q63959	Voltage-gated potassium channel protein Kv3.3 (KSHIID) - Mus musculus (Mouse), 769 aa.	1..671 1..724	650/725 (89%) 653/725 (89%)	0.0
A42073	potassium channel protein Kv3.3 - mouse, 679 aa.	32..607 8..581	557/576 (96%) 559/576 (96%)	0.0
Q9PVD1	KV3.1 POTASSIUM CHANNEL - Xenopus laevis (African clawed frog), 592 aa.	34..671 6..547	441/640 (68%) 479/640 (73%)	0.0

5 PFam analysis predicts that the NOV120a protein contains the domains shown in the Table 120E.

Table 120E. Domain Analysis of NOV120a			
Pfam Domain	NOV120a Match Region	Identities/ Similarities for the Matched Region	Expect Value
K_tetra: domain 1 of 1	36..137	50/112 (45%) 86/112 (77%)	1.6e-47
thaumatin: domain 1 of 1	314..319	4/6 (67%) 6/6 (100%)	0.7

ion_trans: domain 1 of 1	295..486	51/231 (22%) 155/231 (67%)	2.1e-29
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Example 121.

The NOV121 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 121A.

Table 121A. NOV121 Sequence Analysis			
	SEQ ID NO: 337	1943 bp	
NOV121a, CG59938-01 DNA Sequence	<u>AGATCCACGTGATCTCCAAGACCCCTGTTGTGTTGTTGGGAGGTGGATCCTGAAT</u> <u>CCACCCAGAGAAGCCTGATACCAATAAAATCCCTGCTTGCTTTCCAGGAGACCCTTGG</u> <u>TCTTCATGTCTTTGGTGTGTGCACTCTTGAACACATGCCAGGCACACAGGGTGCATGA</u> <u>CGACAAGCCTAATATTGTCCTAATCATGGTTGATGACCTGGGTATTGGAGATCTGGGC</u> <u>TGCTACGGCAATGACACCATGAGGACGCCTCACATCGACCGCCTTGCCAGGGAAGGCC</u> <u>TGCGACTGACTCAGCACATCTCTGCCGCTCCCTCTGCAGCCCAAGCCGGTCCGCGTT</u> <u>CTTGACGGGAAGATACCCCATCCGATCAGGTATGGTTTCTAGTGGTAATAGACGTGTC</u> <u>ATCCAAAATCTTGCACTCCCGCAGGCTCCCTCTTAATGAGACAACACTTGCAGCCT</u> <u>TGCTAAAGAAGCAAGGATACAGCACGGGGCTTATAGGTAAGTTAGGCAATGGCACCT</u> <u>GGGTTTGAGCTGCGCCTCTCGGAATGATCACTGTTACCACCCGCTCAACCATGGTTTT</u> <u>CACTACTTTTACGGGGTGCTTTTGGACTTTTAAGCGACTGCCAGGCATCCAAGACAC</u> <u>CAGAAGTGCACCGCTGGCTCAGGATCAAACTGTGGATCTCCACGGTAGCCCTTGCCCT</u> <u>GGTTCCTTTTCTGCTTCTCATTCCCAAGTTCGCCCGCTGGTTCTCAGTGCCATGGAAG</u> <u>GTCATCTTTGCTTTTGCTCTCCTCGCTTTCTGTTTTTCACTTCTGTTACTCTAGTT</u> <u>ATGGATTTACTCGACGTTGGAATTGCATCCTTATGAGGAACCATGAAATATCCAGCA</u> <u>GCCAATGAAAGAGGAGAAAGTAGCTTCCCTCATGCTGAAGGAGGCACCTTGCTTTCATT</u> <u>GAAAGGTACAAAAGGGAACCTTTTCTCTCTTTTTTCTCCTGTCACATGACATCTC</u> <u>CACTCATCTCCAAAAGAAAGTTTGTGGGCGCAGTAAATATGGCAGGTATGGGGACAA</u> <u>TGTAGAAGAAATGGATTGGATGGTGGGTGGTAAATCCTGGATGCCCTGGACCAGGAG</u> <u>CGCTTGGCCAAACACACCTTGGTGTACTTCACTCTGACAACGGGGCCACCTGGAGC</u> <u>CCCTGGACGGGGCTGTTCACTGGGTGGCTGGAACGGGATCTACAAAGGTGGCAAAGG</u> <u>AATGGGAGGATGGGAAGGAGGTATCCGTGTGCCAGGGATATTCCGGTGGCCGTCAGTC</u> <u>TTGGAGGCTGGGAGAGTGATCAATGAGCCCAACAGCTTAATGGACATCTATCCGACGC</u> <u>TGTCTTATATAGGCGGAGGGATCTTGTCCCAGGACAGAGTGATTGACGGCCAGAACCT</u> <u>AATGCCCTTGCTGGAAGGAAGGGCGTCCCACTCCGACCACGAGTTCCTCTTCCACTAC</u> <u>TGTGGGTCTATCTGCACACGCTCAGGTGGCATCAGAAGGACACTGTGTGGAAGCTC</u> <u>ATTATGTGACTCCTAAATTCTACCCTGAAGGAACAGGTGCCTGCTATGGGAGTGGAAAT</u> <u>ATGTTTCATGTTTCGGGGGATGTAACCTACCACGACCACCACTCCTTTTGACATCTCA</u> <u>AGAGACCCTTCAGAAGCCCTTCCACTGAACCTGACAATGAGCATTATTTGACTCCG</u> <u>TGATCAAAAAGATGGAGGCAGCCATAAGAGAGCATCGTAGGACACTAACACCTGTCCC</u> <u>ACAGCAGTTCTCTGTGTTCAACACAATTTGGAACCATGGCTGCAGCCTTGCTGTGGG</u> <u>ACCTTCCCTTCTGTGGGTGTGACAAGGAAGATGACATCCTTCCCATTGGCTCCCTGAG</u> <u>ACCATGCGGACCAGTGTACCCACCACAACTTACTGTTACAAATGGTCATAGGAGCA</u> <u>GAGCTCACCTGACTGATTTCATTGCAATTTG</u>		
	ORF Start: ATG at 122	ORF Stop: TGA at 1853	
	SEQ ID NO: 338	577 aa	MW at 65099.5kD
NOV121a, CG59938-01 Protein Sequence	MSLVCALLNTCQAHRVHDDKPNIVLIMVDDLGIQDLGCGYNDTMRTPHIDRLAREGVR LTQHISASLCSPSRSAFLTGRYPISGMVSSGNRRVIQNLAVPAGLPLNETTLAALL KKQGYSTGLIGLKGWHLGLSCASRNDHCYHPLNHGFHYFYGVFPGLLSDCQASKTPE LHRWLRIKLWISTVALALVPFLLLI PKFARWFSVPWKVIFVFALLAFLLFTSWYSSYG FTRRWNCILMRNHEIIQQPMKEEKVASLMLKEALAFIERYKREPFLFFSFLHVHTPL ISKKKFVGRSKYGRYGDNVEMDMVVGKILDALDQERLANHTLVYFTSDNGGHLEPL DGAVALGGWNGIYKGGKMGGWEGGIRVPGIFRWPSVLEAGRVINEPTSLMDIYPTLS YIGGGILSQDRVIDGQNLMPLEGRASHSDHEFLFHYCGVYLHTVVRWQKDTVWKAHY VTPKFYPBGTGACYGSGICSCSGDVITYHDPPLLFDISRDPSEALPLNPDNEPLFDSVI KKMEAATREHRRLTLPVPQQFSVFNTIWKFWLPQCCGTFPFCGDKEDDILPMAP		

Further analysis of the NOV121a protein yielded the following properties shown in

5 Table 121B.

Table 121B. Protein Sequence Properties NOV121a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV121a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 121C.

Table 121C. Geneseq Results for NOV121a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV121a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM78688	Human protein SEQ ID NO 1350 - Homo sapiens, 590 aa. [WO200157190-A2, 09-AUG- 2001]	1..572 10..580	388/576 (67%) 449/576 (77%)	0.0
AAM39343	Human polypeptide SEQ ID NO 2488 - Homo sapiens, 589 aa. [WO200153312-A1, 26-JUL- 2001]	20..571 37..587	331/555 (59%) 404/555 (72%)	0.0
AAM41129	Human polypeptide SEQ ID NO 6060 - Homo sapiens, 646 aa. [WO200153312-A1, 26-JUL- 2001]	20..571 94..644	331/555 (59%) 404/555 (72%)	0.0
AAY39920	Human steroid sulphatase protein sequence - Homo sapiens, 583 aa. [WO9950453-A1, 07-OCT-1999]	20..569 26..575	295/559 (52%) 374/559 (66%)	e-166
AAB51185	Human sulfatase protein C SEQ ID NO:14 - Homo sapiens, 583 aa. [US6153188-A, 28-NOV-2000]	20..569 26..575	294/559 (52%) 372/559 (65%)	e-165

- 5 In a BLAST search of public sequence databases, the NOV121a protein was found to have homology to the proteins shown in the BLASTP data in Table 121D.

Table 121D. Public BLASTP Results for NOV121a				
Protein Accession Number	Protein/Organism/Length	NOV121a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P54793	Arylsulfatase F precursor (EC 3.1.6.-) (ASF) - Homo sapiens (Human), 591 aa.	1..572 10..581	379/577 (65%) 441/577 (75%)	0.0
AAH20229	HYPOTHETICAL 64.9 KDA PROTEIN - Homo sapiens (Human), 593 aa.	4..574 24..593	358/574 (62%) 440/574 (76%)	0.0
P51689	Arylsulfatase D precursor (EC 3.1.6.-) (ASD) - Homo sapiens (Human), 593 aa.	4..574 24..593	349/574 (60%) 429/574 (73%)	0.0
P51690	Arylsulfatase E precursor (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	20..571 37..587	334/555 (60%) 405/555 (72%)	0.0
P08842	Steryl-sulfatase precursor (EC 3.1.6.2) (Steroid sulfatase) (Steryl-sulfate sulfohydrolase) (Arylsulfatase C) (ASC) - Homo sapiens (Human), 583 aa.	20..569 26..575	295/559 (52%) 374/559 (66%)	e-166

PFam analysis predicts that the NOV121a protein contains the domains shown in the Table 121E.

Table 121E. Domain Analysis of NOV121a			
Pfam Domain	NOV121a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Sulfatase: domain 1 of 1	21..504	231/530 (44%) 410/530 (77%)	1e-187

Example 122.

- 5 The NOV122 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 122A.

Table 122A. NOV122 Sequence Analysis			
	SEQ ID NO: 339	3005 bp	
NOV122a, CG59746-01 DNA Sequence	<p>ATTTCTTTGGTGTGTCTTCACAGCTGAAGCTGCAAAACAGATTGGAAGCTTCAAGATT ATCAATAATCGGAGATACGTATATTTTATTGTAAAGAAAACATGGCTGCCCTATTCC TACGTGGTTTTGTCCAATAGGGAAGTCAAGACTGGGATATCTAAGTCAAAAGAAGC ATTCAATTGAAGCAGTGGAAAGAAAGAAAGATAGACTGGTGTCTGTATTTCAAAAGT GGAAAATATAGCACTTTTCGGCTAAGTGATAATATTCAAAATGTAGTCTTAATCCT ATAGAGGAAACCAAAATCACCTGCATTTAACTTTACAAAATAAATGGCTGTTTAT TGAAGGATTATCCTCCACAGATGCTGAACAATTGAAGATATTCTTGGACAGAGTTCAT CAAAACGAGGTTTCAGCCACCTGTGAGACCTGGTAAGGGTGGGAGTGTCTTTCTAGCA CAACACAGAAGGAAATCAACAAAACCTTATTCCACAAGTTGATGAGAAATCAAGTAG CAAATCTTTTGAGATAGCAAAAGGAAGTGGGACAGGTGTCCTTCAGAGGATGCCCTTG CTTACATCAAAATTGACACTTACTTGGCGAGAGTTATCAGAAAATCAGCACAGAAGA GGAAAAGAATGCTCTCATCTAGCTCAGAGATGAATGAGGAATCTTGAAGAAAATAA TTCTGTAGAATACAAGAAATCCAAGGCAGATTGTTTCGAGGTGTGTAAGCTATAATCGA GAGAAACAATTGAAGTTAAAAGAGTTAGAAGAGAATAAGAAATTTGGAATGTGAATCTT CATGCATCATGAAGCCCACTGGAAATCCTTACCTAGATGACATTGGTCTTCTCCAAGC TCTCACTGAGAAAATGGTTTTGGTATTTCTGTTACAACAAGGGTATAGTGACGGTTAC ACAAAGTGGGATAAAATAAAACCTATTTTGTGAATTATTTCCAGAGAAAATATGCCACG GCCTCCCCAATTTGGGAAACACCTGTTATATGAATGCAGTGTACAGTCTCTACTTTTC AATCCCATCGTTTGCTGATGATTTACTTAATCAGAGTTTCCCATGGGGTAAAATTCCC CTTAATGCTCTTACCATGTGCTTGGCAGCGCTACTTTTTTTAAAGATACCTATAATA TAGAAATCAAGGAGATGTTACTCTTGAATCTTAAAAGGCCATTTCAGCAGCTGCAGA GATATTCATGGCAATGCACAGAACGATGCTCATGAGTTTTTAGCTCACTGTTTAGAT CAACTGAAAGATAACATGGAAAACCTCAACACAATTTGGAAGCCTAAAAGTGAATTTG GGGAAGATAAATTTTCTAAACAGGTTTTTGTCTGATGATCCTGACACAGTGGGTTTTCT TTGCCCTGTCTATTACTAATTTTGAGTTAGAGTTGTTGCACCTCCATTGCTTGTAAAGCT TGTGGTCAGGTTATTTCTCAAGACAGAACTGAATAATTACCTCTCCATCAACCTTCCCC AAAGAATAAAAGCACATCCTTCATCTATTCACTCTACTTTTGATCTTTTTTTGGAGC AGAAGAGCTTGAGTATAAATGTGCAAAATGTGAGCACAAGACTTCCGTTGGAGTGCAC TCATTCAGTAGGCTACCTAGAATCCTTATTGTTTCACTCAAACGCTATAGCTTGAATG AGTTTTGTGCATTAAGAAGAATGACCAGGAAGTCATCAATTTCCAAATATTTAAAGGT GTCTTCTCATTGCAATGAAGGCACCAGACCCTCTTCCCTTGAGTGAGGATGGAGAA ATTACAGATTTCCAATTATTAAGGTTATTGAAAGATGACTTCTGGAACATCAGTG TATCATGGCTGCAACAAAGGAATCCAAGATATCCTGGCTCCACACATTGGATCAGA TAAGGAGTCTGAACAAAAAAGGCCAGACAGTCTTTAAAGGGGCAAGCAGAAGACAG CAGCAAAAGTACCTTGAAAAAATTTCAAACCAATGAGCTAGAATCTGTATACCTCAG GAGATCGAGCATTCTTGAAGAAAGAACCGTTAGCTCACTTAATGACGTATCTGGAAGA TACCTCACTTTGTGAGTTCCACAAAGCTGGAGGTAAACCTGCCAGCAGCCAGGCACAC CCTCTCTCAAAAGTTGACTTTCAAACAGTGCCCGAAAATCCAAACGAAAGAAATATG TGAAAACCAAGTAAGTTTGTAGCTTTTGATAGGATTATCAATCTCAATAAGATTTGTA TGAAGATAAAATATCAGAATTCAGAAAGATTCCAAAAGTGTCTGAACAGACTCAG CAGTGTGACGGTATGAGAATCTGTGAACAAGCCCCCTCAGCAGGCACTGCCTCAAAGCT TTCCAAAGCCAGGCACCCAGGGGCACACAAAGAACCTCCTAAGACCTACAAAATTA TCTACAGAAGTCTAACAGGAATTCCTTACTTGCACCTGGGTTCCAAATAAGAATCCA AACAAAGACATTTTAGATAAGATAAATCTAAAGCCAAGGAAACAAAAGAAATGATG ATAAGGAGATCATACCTACCGGCTCATTAGTGTGTGAGCCATCTTGGGAAGACTCT AAAGTCAGGCCATTATATCTGTGATGCCTATGACTTTGAGAAACAGATCTGGTTCACT TACGATGATATGCGGGTGTAGGTATCCAGGAGGCCAGATGCAGGAGGATAGGCGTT GCACCTGGGTACATCTCTTTTACATGCATAATGAGATCTTTGAAGAGATGTTGAAAAG AGAAGAGAATGCCAGCTTAATAGCAAGGAGGTAGAGGAGACCTTCAGAAGGAATAA GAGGAACGTACTCTCTTGTACAGATCTGCCTGACTGTCTCACTCGATACCACTTCC TCCATGGAAGGAAAACGTGAACCTTTATCCAGAGATGAAAATGCAATTAGTCTTAGGC CAAAGGTCAAACAGAAACACTTAATGGGGAGATCTGCATTCTAATCC</p>		
	ORF Start: ATG at 101	ORF Stop: TAA at 2840	
	SEQ ID NO: 340	913 aa	MW at 104046.0kD
NOV122a, CG59746-01 Protein Sequence	<p>MAALFLRGFVQIGNCKTGISKSKEAFIEAVERKKKDRVLVLYFKSGKYSTRFLSDNIQN VVLKSYRGNQNLHLTLQNNGLFIEGLSSTDAEQLKIFLDRVHQNEVQPPVPRPGKG SVFSSTQKEINKTSFHKVDEKSSSKSFEIAKSGGTGVLQRMPLLSKLLTLTCGELSE NQHKRKRMLSSSEMNEEFLKENNSVEYKKSADCSRCSVYNREKQLKLELEENKK LECESSIMNATGNPYLDDIGLLQALTEKMLVFLQQQYSDGYTKWDKLKLFELFP EKICHGLPNLNTCYMNAVLQSLLSIPSFADLLNQSFPWGKIPLNALTMCLARLLFF KDTYNIETIKEMLLNLKKAISAAAEIFHGNAQNDAHEFLAHCLDQLKDNMEKLNTIWK PKSEFGEDNFKQVFPADDPDTSGFSCPVTNFELELLHSIACKACGQVILKTELNNYL SINLPQRIKAHPSSIQTDFDLFFGAELEYKCAKEHKTSVGVHFSFRLPRILIVHLK RYSLENEFCALKKNDQEVIIISKYLVSSHCHNEGTRPPLPLSEDGEITDFQLKVIKMT SGNISVSWPATKESKDILAPHIGSDKESEQKKGTQVFKGASRRQQQYLGKNSKPNEL</p>		

100900030200

Table 122B. Protein Sequence Properties NOV122a	
PSort analysis:	0.7000 probability located in nucleus; 0.4270 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1047 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 16 and 17

5

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV122a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU07888	Polypeptide sequence for human hspG25 - Homo sapiens, 913 aa. [WO200166752-A2, 13-SEP-2001]	1..913 1..913	913/913 (100%) 913/913 (100%)	0.0
AAB75607	Human cancer associated antigen precursor HOM-TES-84/6 SEQ ID NO:6 - Homo sapiens, 912 aa. [WO200100874-A2, 04-JAN-2001]	1..905 1..904	429/920 (46%) 566/920 (60%)	0.0
AAU07869	Polypeptide sequence for mammalian Spg25 - Mammalia, 835 aa. [WO200166752-A2, 13-SEP-2001]	1..904 1..834	335/921 (36%) 504/921 (54%)	e-147
AAG75460	Human colon cancer antigen protein SEQ ID NO:6224 - Homo sapiens, 109 aa. [WO200122920-A2, 05-APR-2001]	810..912 3..107	61/105 (58%) 79/105 (75%)	3e-28
AAB39364	Gene 8 human secreted protein homologous amino acid sequence #113 - Bos taurus, 64 aa. [WO200057903-A2, 05-OCT-2000]	810..871 1..64	39/64 (60%) 48/64 (74%)	5e-15

In a BLAST search of public sequence databases, the NOV122a protein was found to have homology to the proteins shown in the BLASTP data in Table 122D.

Table 122D. Public BLASTP Results for NOV122a				
Protein Accession Number	Protein/Organism/Length	NOV122a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BXU7	Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Homo sapiens (Human), 913 aa.	1..913 1..913	913/913 (100%) 913/913 (100%)	0.0
Q9HBJ7	UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Homo sapiens (Human), 922 aa.	1..905 1..904	429/920 (46%) 566/920 (60%)	0.0
Q9HCH8	KIAA1594 PROTEIN - Homo sapiens (Human), 931 aa (fragment).	50..912 3..929	393/932 (42%) 535/932 (57%)	e-171
Q99MX1	Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Mus musculus (Mouse), 835 aa.	1..904 1..834	335/921 (36%) 504/921 (54%)	e-147
Q9ES63	UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Mus musculus (Mouse), 869 aa.	1..908 1..848	341/933 (36%) 480/933 (50%)	e-131

PFam analysis predicts that the NOV122a protein contains the domains shown in the Table 122E.

Table 122E. Domain Analysis of NOV122a			
Pfam Domain	NOV122a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UCH-1: domain 1 of 1	295..326	21/32 (66%) 29/32 (91%)	8.8e-12
UCH-2: domain 1 of 1	820..885	20/72 (28%) 47/72 (65%)	2.2e-11

Example 123.

The NOV123 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 123A.

Table 123A. NOV123 Sequence Analysis			
	SEQ ID NO: 341	2146 bp	
NOV123a, CG88613-01 DNA Sequence	GAAGGAGCGGGCATGAGGCGCTGCCGTGCCGTGGGAGCCTGAACGAGGCGGAGGCCG GGGCGCTGCCCGCGGCGGCCCGCATGGGACTGGAGGCGCGCGAGGAGGGCGGCGCG GCAGCCGGGACAGCAGCGACCTGGGCCCCGGCGCAGGGGCCCGGCGGGGCGGCCGAG GGGGGCGGGCCCTGGGCCCCGACAGAGGGGTCCAGCCTCCACAGCGAGCCTGAGAGGG CCGGCCTCGGGCCTGCGCCGGGACAGAGAGTCCGCGAGGCAGAATTCGTGACAGACGG ACAGACTGAGCCCCGCGGAGCTGGCCTTGGAGTAGAGACCGAGAGGCCCAAGCAAAAG ACGGAGCCAGACAGGTCCAGCCTCCGGACGCATCTAGAATGGAGCTGGTCAGAGCTGG AGACGACTTGTCTTTGGACGAGACCGGGACAGATGGCCTTTTGGACTGATCCGCACAG GTCCGACCTCCAGTTTCAGCCCCGAGGAGGCCAGCCCTGGACACAGCCAGGGGTTTCAT GGGCCCTGGACAGAGCTGGAACGCGATGGGTACAGACTCAGCCAGAGAGGGTCAAGT CCTGGGCTGATAACCTCTGGACCCACCAGAACAGTTCAGCCTCCAGACTCACCAGAGA AGGAGCCTGTCCCTCAAAAGAGCCAAGTGCTGATGGCTCCTGGAAGAAGTGTATACT GATGGCTCCAGGACACAACAGGATATTGAAGGTCCCTGGACAGGCCATATACTGATG GCTCCAGAAAAACAGGATACTGAAGCAGCCAGGAACAGCCTGGCAGCTGGTGGTTT CCAAATACAAACAGGATACTGATGGCTCCTGGACACAACCTAGCACTGACGGTTCACAG ACAGCACCTGGGACAGACTGCCTCTTGGGAGAGCCTGAGGATGGCCATTAGAGGAAC CAGAGCCTGGAGAATTGCTGACTCACCCTGTACTCTCAGCTGAAGTGTAGCCCCCTGTG CCCTGTGCCCCGCTCATCATTACCCCTGAGACCCCTGAGCCTGAGGCCAGCCAGTG GGACCCCCCTCCCGGGTTGAGGGGGGCGAGCGGCGGCTTCTCCTCTGCCTCTTCTTTG ACGAGTCTGAGGATGACGTGGTGGCCGGGGGCGGAGGTGCCAGGACAGTCCCGAGGACAG GTCTGGGAGCAAAACCTGGAAGAAGCTGAAGACAGTTCTGAAGTATTCACCTTTGTG GTCTCCTTCCGAAAACACTACCTTGGGTCCAGCTTCTTGAGATGCTGGGAACCTTCC AGGCAGGAGAGGATGGTCGGATTCTGAAACGTTTCTGTAGTGTGAGCAGCGCAGCCT GGAGCAGCTGATGAAAGACCCGCTGCGACCTTTCGTGCTGCCTACTATGGCATGGTG CTGCAGGATGGCCAGACCTTCAACCAGATGGAAGACCTCCTGGCTGACTTTGAGGGCC CCTCTATTATGGACTGCAAGATGGGCAGCAGGACCTATCTGGAAGAGGAGCTAGTGAA GGCAGCGGAACGTCCCCGTCCCCGGAAGGACATGTATGAGAAGATGGTGGCTGTGGAC CCTGGGCCCTTACCCCTGAGGAGCATGCCAGGGTGACGTACCAAGCCCCGCTACATA TGCAGTGGAGGGAACCATGAGCTCCACCTTACCTGGGCTTCCGGATCGAGGGCAT CAAGAAGGCAGATGGGACCTGTAACACCAACTTCAAGAAGACGCAGGCACTGGAGCAG GTGACAAAAGTGTGGAGGACTTCGTGGATGGAGACCAGTCTATCTGCAAAAGTACG TGGCATGCCTAGAAGAACTTCGTGAAGCTCTGGAGATCTCCCCCTTCTTCAAGACCCA CGAGGTGGTAGGCAGCTCCCTCCTCTTCGTGCACGACCACACCGGCCTGGCCAAGGTC TGGATGATGACTTTCGCAAGACGGTGGCCTTGCCCGACCAACAGACGCTCAGCCACA GGCTGCCCTGGGCTGAGGGCAACCGTGAGGACGGCTACCTCTGGGGCTGGACAACAT GATCTGCCTCCTGCAGGGGCTGGCACAGAGCTGAGCTGCTCAGCCACCATCAGGTTAA TTGGATGGCGCCAGTCTGGCTGGAGGAGCCTGAGATGCCATGGGAGGCTGAGGTTG		
	ORF Start: ATG at 13	ORF Stop: TGA at 2062	
	SEQ ID NO: 342	683 aa	MW at 75206.8kD
NOV123a, CG88613-01 Protein Sequence	MRRCPCRGSLNEAEAGALPAAARMGLEAPRGRRRQPGQRPFGAGAPAGRPEGGGP WARTEGSSLHSEPERAGLGPA PGTESPQAEFWTDGTEPAAAGLVETERPKQKTEPD RSSLRTHLEWSWSELETCLWTETGTDGLWTDPHRSDLQFQPEEASPWTPQVHGFWT ELETHGSQTQPERVKSADNLWTHQNSSSLQTHPEGACPSKEPSADGSWKELYTDGSR TQQDIEGPWTEPYTDGSQKKQDTEAARKQPGTGGFQIQDQTDGSWTQPSTDGSTAPG TDCLLGEPEDEPLEEPEPELTHLYSHLKCSPVPRLIITPETPEPEAQPVGPPS RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKLKTVLKYSPFVVSFR KHYPPVQLSGHAGNFQAGEDGRILKRFCQCEQRSLEQLMKDPLRFPVPAAYGMVLQDG QTFNQMEDLLADFEGPSIMDKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAP TPEEHAQGAVTKPRYMQWRETMSSTSLGFRIEGIKKADGTCNTNFKKTQALEQVTKV LEDFVDGDHVI LQKYVACLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMD FGKTVLPDHTLSHRLPWAEGNREDGYLWGLDNMICLLQGLAQS		

Further analysis of the NOV123a protein yielded the following properties shown in

5 Table 123B.

Table 123B. Protein Sequence Properties NOV123a	
PSort analysis:	0.5663 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV123a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 123C.

Table 123C. Geneseq Results for NOV123a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV123a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41393	Human polypeptide SEQ ID NO 6324 - Homo sapiens, 687 aa. [WO200153312-A1, 26-JUL-2001]	1..683 5..687	682/683 (99%) 682/683 (99%)	0.0
AAM39607	Human polypeptide SEQ ID NO 2752 - Homo sapiens, 711 aa. [WO200153312-A1, 26-JUL-2001]	12..683 36..711	642/680 (94%) 643/680 (94%)	0.0
AAE04364	Human kinase (PKIN)-5 - Homo sapiens, 798 aa. [WO200146397-A2, 28-JUN-2001]	273..682 380..793	219/432 (50%) 285/432 (65%)	e-117

In a BLAST search of public sequence databases, the NOV123a protein was found to have homology to the proteins shown in the BLASTP data in Table 123D.

Table 123D. Public BLASTP Results for NOV123a				
Protein Accession Number	Protein/Organism/Length	NOV123a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96DU7	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE C - Homo sapiens (Human), 683 aa.	1..683 1..683	683/683 (100%) 683/683 (100%)	0.0

Q9Y475	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE ISOENZYME (EC 2.7.1.127) - Homo sapiens (Human), 604 aa (fragment).	83..683 4..604	601/601 (100%) 601/601 (100%)	0.0
S17682	1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human, 472 aa.	273..682 54..467	219/432 (50%) 285/432 (65%)	e-117
CAB65055	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE B - Homo sapiens (Human), 946 aa.	273..682 528..941	219/432 (50%) 285/432 (65%)	e-117
Q96JS1	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE, ISOFORM B (EC 2.7.1.127) - Homo sapiens (Human), 946 aa.	273..682 528..941	219/432 (50%) 285/432 (65%)	e-117

PFam analysis predicts that the NOV123a protein contains the domains shown in the Table 123E.

Table 123E. Domain Analysis of NOV123a			
Pfam Domain	NOV123a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 124.

The NOV124 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 124A.

Table 124A. NOV124 Sequence Analysis		
	SEQ ID NO: 343	1395 bp
NOV124a, CG59993-01 DNA Sequence	GGTAAGACGACCTCTGGATGCTCACCTGCCCCTCTTCACCTCTCGTCCCCAGCTGTTT CCTCTGCCACCATGAGGAACATTTTCAAGAGGAACAGGAGCCTATTGTGGCTCCTGC CACCACCACGCCACGATGCCCATTTGGACCCGTGGACAACCTCCACTGAGAGTGGGGGT GCTGGGGAGAGCCAGGAGGACATGTTTGCCAACTGAAGGAGAAGTTATTCAATGAGA TAAACAAGATTCCCTTACCACCCTGGGCACTGATCGCCATTGCTGTGGTTGCTGGGCT CCTGCTTCTCAGCTGCTTCTGTCATCTGCAAGAAATGCTGCTGCAAGAAGAAGAAG AACAAAGAAGGAGAAGGGCAAAGGCATGAAGAATGCCATGAACATGAAGGACATGAAAG GGGGTCAGGATGACGACGACGACAGACAGGCTGACTGAGGGGAAGGTGAAGGGGA GGAGGAGAAAGAGCCAGAGAACCTGGGCAAACTGCAGTTTCCCTGGACTATGATTTT CAGGCTAATCAGCTTACTGTGGGCGTTCTGCAGGCTGCTGAACCTGCCCTGGCCTGGACA TGGGAGGCACCTCAGACCCTTATGTCAAGGTCTTCTCCTTCTGACAAGAAGAAGAA ATATGAGACCAAGTCCATCGGAAGACACTGAACCTGCCTTCAATGAAACCTTCACC TTCAAGGTGCCATACCAGGAGCTTGGGGGCAAACTCTGGTGATGGCCATCTATGACT TTGACCGCTTCTCCAACATGACATCATTGGAGAGGTAAGGTGCCTATGAACACAGT GGACCTCGGCCAGCCCATTTAGGAGTGGAGAGACCTGCAAGGCGGGGAAAAGGAGGAG CCGAGAAAGCTGGGCGACATCTGCACCTCCCTGCGCTATGTGCCACGCGCGGGAAGC TCACTGTCTGCATCCTGGAGGCTAAGAACCTCAAGAAGATGGACGTGGGCGGCTTTC AGACCCGTACGTGAAGATCCACCTGATGCAGAAATGGCAAGAGGCTCAAGAAGAAGAAG ACAACCGTGAAGAAGAAGACCCTGAACCCATACTTCAACGAGTCCTTCAGCTTTGAGA	

	TCCCCCTCGAGCAGATTAGAAAGTCCAGGTAGTGGTCACCGTGTGGACTATGACAA GCTGGGCAAGAACGAAGCCATAGGCAAGATCTTCGTGGGCAGCAATGCCACGGGCACA GAGCTGCGGCACATGGTCCGACATGCTGGCCAAACCCCGGAGGCCCATCGCCCAAGTGGC ACTCGCTCAAGCCTGAGGAGGAGGTGGATGCACTCCTGGGCAAGAACAAAGTAGACAGC AGCGGCTGGGACCCACACCTTTCACGGACACTGACAAGATCCAGAGCTATCAATACC TCA		
	ORF Start: ATG at 70	ORF Stop: TAG at 1327	
	SEQ ID NO: 344	419 aa	MW at 46871.8kD
NOV124a, CG59993-01 Protein Sequence	MRNIFKRNQEPIVAPATTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAVVAGLLLLTCCFCICKKCCCKKKKKKKEKKGKGMKNAMNMKDMKGGQD DDDAETGLTEGEGEGEEKEPENLGLKQFSLDYDFQANQLTVGVLQAAELPALDMGGT SDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTFKVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLQGP IEEWRDLQGGEEKEEPEKLGDICTSLRYVPTAGKLTVC I LEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKKTTVKKKTLNPFYNESFSFEIPFE QIQKVQVVTVLDYDKLGKNEAIGKIFVGSNATGTELRHWSMLANPRRPIAQWHSLK PEEEVDALLGKNK		
	SEQ ID NO: 345	1338 bp	
NOV124b, CG59993-02 DNA Sequence	CCACCATGAGGAACATTTTCAAGAGGAACCAGGAGCCTATTGTGGCTCCTGCCACCAC CACCGCCACGATGCCCATTTGACCCGCTGGACAACCTCCACTGAGAGTGGGGGTGTCTGGG GAGAGTCAGGAGGACATGTTTGCCAAACTGAAGGAGAAGTTATTCAATGAGATAAACA AGATTCCCTTACCACCTTGGGCACTGATCGCCATTGCTGTGGTTGTCTGGGCTCCTGCT TCTCACCTGCTGTTTCTGCATCTGCAAGAAATGCTGCTGCAAGAAGAAGAAGAACAAG AAGGAGAAGGGCAAAGGTAAGAAGATGCCATGAACATGAAGGACATGAAGGGGGGTC AGGATGACGACGACGCAGAGACAGGCCTGACTGAGGGGGAAGGTGAAGGGGAGGAGGA GAAAGAGCCAGAGAACCTGGGCAAACTGCAGTTTTCCTTGGACTATGATTTTCAGGCT AATCAGCTTACTGTGGCGTTTCTGCAGGCTGCTGAACCTGCCTGCCCTGGACATGGGAG GCACCTCAGACCCTTATGTCAAGGTCTTCTCTCCTTCTCTGACAAGAAGAAGAAATATGA GACCAAAAGTCATCGGAAGACACTGAACCTGCGTTCAATGAAACCTTCACCTTCAAG GTGCCATACCAGGAGCTTGGGGGCAAAACTCTGGTGATGGCCATCTATGACTTTGACC GCTTCTCCAACATGACATCATTGGAGAGGTAAGGTGCCTATGAACACAGTGGACCT CGGCCAGCCCATTGAGGAGTGGAGAGACCTGCAAGGCGGGGAAAAGGAGGAGCCGGAG AAGCTGGGCGACATCTGCACCTCCCTGCGCTATGTGCCACGGCCGGGAAGCTCACTG TCTGCATCTCGGAGGCTAAGAACCTCAAGAAGATGGACGTGGGCGGCCTTTAGACCC GTACGTGAAGATCCACCTGATGCAGAATGGCAAGAGGCTCAAGAAGAAGAAGACAAC ATGAAGAAGAAGACCTGAACCCATACTTCAACAGATCCTTCAGCTTTGAGATCCCT TCGAGCAGATTAGAAAAGTCCAGGTAGTGGTCACCGTGTCTGGAATGTAGACAAGCTGGG CAAGAACGAAGCCATAGGCAAGATCTTCGTGGGCAGCAATGCCACGGGCACAGAGCTG CGGCACCTGGTCCGACATGCTGGCCAACCCCGGAGGCCCATCGCCAGTGGCACTCGC TCAAGCCTGAGGAGGAGGTGGGTGCACTCCTGGGCAAGAACAAGTAGACAGCAGCGGC TGGGACCCACACCTTTCACGGACACTGACAAGATCCAGAGCTATCAATAAGGTGTAG GCGG		
	ORF Start: ATG at 6	ORF Stop: TAG at 1263	
	SEQ ID NO: 346	419 aa	MW at 46845.9kD
NOV124b, CG59993-02 Protein Sequence	MRNIFKRNQEPIVAPATTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAVVAGLLLLTCCFCICKKCCCKKKKKKKEKKGKGMKNAMNMKDMKGGQD DDDAETGLTEGEGEGEEKEPENLGLKQFSLDYDFQANQLTVGVLQAAELPALDMGGT SDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTFKVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLQGP IEEWRDLQGGEEKEEPEKLGDICTSLRYVPTAGKLTVC I LEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKKTVMKKKTLNPFYNESFSFEIPFE QIQKVQVVTVLDYDKLGKNEAIGKIFVGSNATGTELRHWSMLANPRRPIAQWHSLK PEEEVGALLGKNK		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 124B.

Table 124B. Comparison of NOV124a against NOV124b.		
Protein Sequence	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV124b	1..419 1..419	335/419 (79%) 335/419 (79%)

Further analysis of the NOV124a protein yielded the following properties shown in Table 124C.

Table 124C. Protein Sequence Properties NOV124a	
PSort analysis:	0.8202 probability located in mitochondrial inner membrane; 0.6000 probability located in endoplasmic reticulum (membrane); 0.3500 probability located in nucleus; 0.3034 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV124a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 124D.

Table 124D. Geneseq Results for NOV124a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR97722	Mouse inositol polyphosphate binding protein IP4-BP - Mus musculus, 422 aa. [JP08092290-A, 09-APR-1996]	1..419 1..422	412/422 (97%) 414/422 (97%)	0.0
AAU19715	Human novel extracellular matrix protein, Seq ID No 365 - Homo sapiens, 461 aa. [WO200155368-A1, 02-AUG-2001]	128..405 169..447	141/280 (50%) 201/280 (71%)	2e-80
AAU19714	Human novel extracellular matrix protein, Seq ID No 364 - Homo sapiens, 295 aa. [WO200155368-A1, 02-AUG-2001]	141..409 11..281	140/273 (51%) 193/273 (70%)	3e-74
AAW87702	A human membrane fusion protein designated SYNTAX2 - Homo sapiens, 375 aa. [WO9856813-A2, 17-DEC-1998]	59..407 31..364	146/352 (41%) 220/352 (62%)	4e-73
AAO05534	Human polypeptide SEQ ID NO 19426 - Homo sapiens, 149 aa. [WO200164835-A2, 07-SEP-2001]	33..164 15..149	127/135 (94%) 131/135 (96%)	5e-70

In a BLAST search of public sequence databases, the NOV124a protein was found to have homology to the proteins shown in the BLASTP data in Table 124E.

Table 124E. Public BLASTP Results for NOV124a				
Protein Accession Number	Protein/Organism/Length	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P29101	Synaptotagmin II (SytII) - Rattus norvegicus (Rat), 422 aa.	1..419 1..422	411/422 (97%) 414/422 (97%)	0.0
A55417	synaptotagmin II - mouse, 422 aa.	1..419 1..422	412/422 (97%) 414/422 (97%)	0.0
P46097	Synaptotagmin II (SytII) - Mus musculus (Mouse), 422 aa.	1..419 1..422	411/422 (97%) 413/422 (97%)	0.0
P24506	Synaptotagmin B (Synaptic vesicle protein O-P65-B) - Discopyge ommata (Electric ray), 439 aa.	10..419 27..439	341/413 (82%) 366/413 (88%)	0.0
P46096	Synaptotagmin I (SytI) (p65) - Mus musculus (Mouse), 421 aa.	10..419 8..421	323/418 (77%) 353/418 (84%)	0.0

5 Pfam analysis predicts that the NOV124a protein contains the domains shown in the Table 124F.

Table 124F. Domain Analysis of NOV124a			
Pfam Domain	NOV124a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Adeno_E3_CR2: domain 1 of 1	62..108	16/50 (32%) 26/50 (52%)	6.5
C2: domain 1 of 2	156..242	54/97 (56%) 81/97 (84%)	1.8e-42
C2: domain 2 of 2	287..375	44/97 (45%) 80/97 (82%)	2.9e-39

Example 125.

The NOV125 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 125A.

Table 125A. NOV125 Sequence Analysis			
	SEQ ID NO: 347	3226 bp	
NOV125a, CG59991-01 DNA Sequence	<div>GGACCACTTCTGATGCATCTCTGGGTCCCAACACTATCCACTGCAAGGCCTCGAAACA GGGGGGCCAGATGGGACCCCCATTTAGCACAAAGAGAGACGTCCACACTCTGTGAGCCC AAAGGGAGAAGGCTCAGGCCACGGCAGAGACGGAACAGGAAACGTACGAAAAACA GCCTCAAGTTGCCAGGTCCCTTGCAGGAACAGACAGGCCTGGGGCCGCCACCTGGG CTCAGAGCTTGGGCTGCATGGAGGTGACACATGGGACTACAAGAGTCACTGATGATGACC AAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTGTAAACACTGCTGCTGACTGGC CGGAAATGCAACGTTGGCTGGTGCCTTTTGATTGACACCGGTGGGGCTTCCGGCCTCG CACGGTGGTTCTGCACGGAAGTCAAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATC GTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCTCACTCTTCTTCC TCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTTCATCTCCAG GGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCCGACCAAGAAAGGCTG TTGTTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCTCAACAATGACACAAAGC TCTGCAAAAGACTGGGCTGAGAAGCAGCCTCCGTTACCCCTCATACGTCAGTCTGTGTAG GAAGGTCCTGCTCCCTGAGTCTTCTCTGATCGTCACCGTCAGAGACGTGGGCACAGAG AAGCTCAAGTCAGAGGTCGTGTCTCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGG AACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGG GTTGCGTGCATCATGAACAACCGTGAGTGTCTGACCAAGTGCCAGGTGCCCCGCGTGC GGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGAGAGCGTCGCC CCTTCAACCAACGCTCACAGGCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCC TCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAGAGTTGTCTGAAGCGCTTC TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACC TCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCATCATGAACATCTCT TCTCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGAC TTCTGTGCCGCTTGTACTACGTGTTAGAGGGCTTGGAAATCGAGCCAGCTCTCTGCC CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATAT CCACTCGCTTTGGATGAAGCGTTTCTTGTGTTGGCCTCGTGAGCGAAGACGTAAAGGAG CCACTGGAGGTCTGCTGGGCTGTCCCGTTCCCTGGGGGTGAAGCAGAAGCTTCTGCG ACTGGGTCTCTGTTGGGTGACGAGCTAATGCCACCACCCAGGAGAGACACCTTGA CGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAAC AGCTTCCAAGAAGTGTGGCTTCCGATTAAACAGAACCTGGACTGTATAGCATCTTCTCT TCTGCTCCAGCACTGTCCGTATTTCGGGAAAATTCGGGTGGATGTCAAAGGGATCTT CCCAAGAGATGAGTCCGCTGAGGCATGTCTGTGGTCCCTCTATGGATGCGGGATAAG ACCTTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCACCCACACC TGCGGCAGCTGGACCTGGGCGAGCAGCATCTTGACAGAGCGGGCCATGAAGACCTGTG TGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCGTATGTTTGAAGATGCACAG ATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGAT CCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGC CTTAAACACCCAAAATGTTTGTGAGAGTCTTTGAGGCTGGATTGCTGTGGATTGACC CATGCCTGTTACCTGAAGATCTCCCAATCTTACGACCTCCCCAGCTGAAATCTC TGAGCCTGGCAGGAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTT GAGAGTCTCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC ACGGGTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGTCTGACACACCTGT GCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAATCTACTGTGTCGATCCATGAG GCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGGT GGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACCTATGGCTGACGCACTGAGACC TTAGCATGAACCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTTCATGAGAGA ACCATCTTGTCTATCTCCAGGACCTGGAGTTGGTAAAGTGTCTATCTACCGCCGCGTGC TGTGAGAGTCTGTCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCA CGGACAATGCCCTGGGTGACCGTGGGGTGTGTGCACTGTGCGAGGGACTGAAGCAAAA GAACAGTGTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTCTGATTGCTGT GAGGCACTCTCCTTGGCCCTTCTCTGCAACCGGCATCTGACCACTTAAACCTGGTGC AGAATAACTTCAGTCCCAAGGAATGATGAAGCTGTGTTTCGGCCTTTGCCTGTCCCAC GTCTAACTTACAGATAATTGGGCTGTGGAATGGCAGTACCCTGTGCAAAATAAGGAAG CTGCTGGAGGAAGTGCAGTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT CTTTTGATGAAGATGACCGGTACTGGTGGAAAACTGAAGATACGGAACCTGCCCA CTCACACCCATCTGATGGAGGAACTTTAAACGCTGT</div>		
	ORF Start: ATG at 69	ORF Stop: TGA at 3168	
	SEQ ID NO: 348	1033 aa	MW at 116310.7kD
NOV125a, CG59991-01 Protein Sequence	<div>MGPPFSTRETSLCEPKGRRLRPRQRNRQENVTKNSLKLPGPLQEQTGLGPPHLGSEL GLHGDDTWDYKSHVMTKFAEEEDVRRSFENTAADWPENMTLAGAFSDRWGFRPRTVV LHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESVTEFISREWP DSQAPVTEIMSRPERLLFIIDGFDLGSVLNNDTKLCKDWAEEKQPPFTLIRSLRLKVL LPESFLIVTVRDVGTGKLVSEVSPRYLLVRGISGEQRIHLLBERGIGEHQKTLQGLRA IMNRELDDQCQVPAVGS LICVALQLQDVVGESVAPFNQTLTGLHAAVFVHQLTPRGV VRRCLNLEERVVLKRFRCMAVEGVVNRKSVFDDGDDLMLVQGLGESELRALFHMNILLPD SHCEEYTFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSL WMKRFLEGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATT PGDTLDFAH CLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPLYLRKIRVDVKGIFPRD ESAECAPVVPLWMRDKTLIEQWEDFCSMLGTHPLRLQLDLGSSILTERAMKTLCAKL</div>		

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	RHPTCKIQTLMFNAQITPGVQHLWRIVMANRNLRLSLNLGGTHLKEEDVRMACEALKH PKCLLESRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPKSDALRVS QCALQKLILEDGKITATGCQSLASALVSNRSLTHLCLSNNSLGNLGVNLLCRSMRLPH CSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSC HLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSV LTRLGLKACGLTSDCCEALSALSCNRHLTSLNLVQNNFSPKGMMLKCSAFACPTSNL QIIGLWKWQYPVQIRKLEEVQLLKPRVVIDGSWHSFDEDDRYWKN
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Further analysis of the NOV125a protein yielded the following properties shown in Table 125B.

Table 125B. Protein Sequence Properties NOV125a	
PSort analysis:	0.7600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV125a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 125C.

Table 125C. Geneseq Results for NOV125a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV125a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE07514	Human PYRIN-1 protein - Homo sapiens, 1034 aa. [WO200161005-A2, 23-AUG-2001]	103..934 207..1003	276/843 (32%) 445/843 (52%)	e-126
AAE07513	Human nucleotide binding site 1 (NBS-1) protein - Homo sapiens, 1033 aa. [WO200161005-A2, 23-AUG-2001]	114..935 180..990	281/839 (33%) 431/839 (50%)	e-120
AAU07878	Polypeptide sequence for mammalian Spg65 - Mammalia, 748 aa. [WO200166752-A2, 13-SEP-2001]	207..963 9..748	218/766 (28%) 380/766 (49%)	7e-95
AAE06758	Human G-protein coupled receptor-8 (GCREC-8) protein - Homo sapiens, 1473 aa. [WO200157085-A2, 09-AUG-2001]	21..764 219..959	235/772 (30%) 380/772 (48%)	3e-88
AAB62571	Human CARD-7 polypeptide -	21..764 219..959	235/772 (30%) 380/772 (48%)	3e-88

	[WO200130813-A1, 03-MAY-2001]			
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In a BLAST search of public sequence databases, the NOV125a protein was found to have homology to the proteins shown in the BLASTP data in Table 125D.

Table 125D. Public BLASTP Results for NOV125a				
Protein Accession Number	Protein/Organism/Length	NOV125a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JLR2	MATERNAL-ANTIGEN-THAT-EMBRYOS-REQUIRE PROTEIN - Mus musculus (Mouse), 1111 aa.	24..1033 104..1111	548/1019 (53%) 716/1019 (69%)	0.0
Q9R1M5	MATER PROTEIN - Mus musculus (Mouse), 1111 aa.	24..1033 104..1111	547/1019 (53%) 716/1019 (69%)	0.0
AAL35293	NALP4 - Homo sapiens (Human), 994 aa.	63..958 94..981	291/907 (32%) 473/907 (52%)	e-133
Q96MN2	CDNA FLJ32126 FIS, CLONE PEBLM2000112, WEAKLY SIMILAR TO HOMO SAPIENS NUCLEOTIDE-BINDING SITE PROTEIN 1 MRNA - Homo sapiens (Human), 919 aa.	63..958 19..906	291/907 (32%) 473/907 (52%)	e-133
AAL12497	CRYOPYRIN - Homo sapiens (Human), 1034 aa.	103..934 207..1003	276/843 (32%) 445/843 (52%)	e-125

5 PFam analysis predicts that the NOV125a protein contains the domains shown in the Table 125E.

Table 125E. Domain Analysis of NOV125a			
Pfam Domain	NOV125a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRR: domain 1 of 6	671..695	6/25 (24%) 16/25 (64%)	1.6e+02
LRR: domain 2 of 6	728..752	7/27 (26%) 17/27 (63%)	2.3e+02

LRR: domain 3 of 6	785..809	7/26 (27%) 19/26 (73%)	1.6e+02
LRR: domain 4 of 6	814..836	6/25 (24%) 14/25 (56%)	4.3e+02
LRR: domain 5 of 6	899..923	8/26 (31%) 20/26 (77%)	27
LRR: domain 6 of 6	956..977	7/25 (28%) 16/25 (64%)	2.9e+02

Example 126.

The NOV126 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 126A.

Table 126A. NOV126 Sequence Analysis			
	SEQ ID NO: 349		2310 bp
NOV126a, CG59987-01 DNA Sequence	CCGCGCCTCAGTCCGCCGTCCGCCCTCCGCGCCCGCGCCGCTAGCATGACCGACGCGC TGTTCGCCCGGCCCCCCAGCCGCTGGAGAAGGAGAACGACGGCTACTTTTCGGAAGGG CTGTAATCCCCTTGACAAAACCGGCCGGAGTAAATTGCAGAATCAAAGAGCTGCTTTG AATCAGCAGATCCTGAAAGCCGTGCGGATGAGGACCGGAGCGGAAAACCTTCTGAAAG TGGCCACAAACTCAAAGGTGCGGGAGCAAGTGCGGCTGGAGCTGAGCTTTCGTCAACT AGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGGCTGAACATCTCGGTGGGCGTCTAT CAGAACACAGAGGAGGCATTTACGATTCCCCTGATTCTCTTGGCTGAAGGAAACGA AAGACGTCGACTTTGCAGTCGTCTCAAGGATTTTATCCTGGAACATTACAGTGAAGA TGGCTATTTATATGAAGATGAAATTGCAGATCTTATGGATCTGAGACAAGCTTGTGCG ACGCTAGCCGGGATGAGGCCGGGGTGGAAGTCTGCTGATGACATACTTTCATCCAGCTGG GCTTTGTCTGAGAGTCGATTCTTCCC GCCACACGGCAGATGGGACTCCTGTTCACTTG GTATGACTCTCTCACCGGGGTTCCGGTCAGCCAGCAGAACCTGCTGCTGGAGAGAGGCC AGTGTCTCTGTCAACACTGGGGCCCTCTACACCCAGATTGGGACCCGGTGTGATCGGC AGACGCAAGGCTGGGCTGGAGAGTGCCATAGATGCCTTTCAGAGAGCCGAGGGGTTTT AAATTACCTGAAAGACACATTTACCCATACTCCAAGTTACGACATGAGCCCTGCCATG CTCAGCGTGCTCGTCAAATGATGCTTGCAAGCCCAAGAAAGCGTGTGTGAGAAAA TCAGCCTTCTCTGGGATCCGGAATGAATCTTTCATGCTGGTGAAGGTGGCTCAGGAGGC TGCTAAGGTGGGAGAGGTCTACCAACAGCTACACGACGACCATGCTGCTGGAGCGCGGGT AAAGAGAACATCCCCTACTCTGGGCCAGCTTAGCCTGCGTGAAGGCCACCACTACG CGGCCCTGGCCCACTACTTCACTGCCATCCTCTCATCGACCACAGGTGAAGCCAGG CACGGATCTGGACCACAGGAGAAGTGCCTGTCCCAGCTCTACGACCACATGCCAGAG GGGCTGACACCTTGGCCCACTGAAGAATGATCAGCAGCGCCGACAGCTGGGGAAGT CCCACTTGCGCAGAGCCATGGCTCATCAGAGGAGTCGGTGGGAGGCGAGCCCTCTG CAAGAAGCTGCGGAGCATTGAGGTGCTACAGAAGGTGCTGTGTGCCGACAGGAACGC TCCCGGCTCACGTACGCCACAGCACAGGAGGAGGATGACCTGCTGAACCTGATCGACG CCCCCAGAGTGTTGTTGCTAAAACTGAGCAAGAGGTTGACATTATATGCCCCAGTTT TCCAGCTGACAGTCACGGACTTCTTCCAGAAGCTGGGCCCTTATCTGTGCTGTGCGGT ACAAGCGGTGGACGCCTCCTCGAAGCATCCGCTTCACTGCAGAAGAAGGGGACTTGG GGTTCACTTGAAGAGGGAACGCCCCCGTTTCAAGTTCACTTCTGGATCCTTACTGCTC TGCTTCGGTGGCAGGAGCCCGGAAGGAGATTATATTGTCTCCATTAGCTTGTGGAT TGTAAGTGGCTGACGCTGAGTGAGGTTATGAAGCTGCTGAAGAGCTTTGGCGAGGACG AGATCGAGATGAAAGTCGTGAGCCCTCTGGACTCCACATCATCCATGCATAATAAGAG TGCCACATACTCCGTGGGAATGCAGAAAACGTACTCCATGATCTGCTTAGCCATTGAT GATGACGACAAAACGATAAAAACCAAGAAAATCTCCAAGAAGCTTTCCTTCTGAGTT GGGGACCAACAAGAACAGACAGAAGTCAGCCAGCACCTTGTGCCCTCCATCCGTGCGG GGCTGCACGGCCTCAGGTCAAGAAGAAGCTGCCCTCCCCTTACGCCCTTCTCAACTCA GACAGTTCTTGGTACTAATGTGAGGAAACAAACATGTTTCAGGCCCGGAACATTTCCGG TGCTGACTCGGCCTTAAACGTTTGTGCCATAATGGAATAATCTATCTATCTGTTCTC AAATCCTGTTTTTCTCATAGTGTAACCTCACATTTGATGTGTTTTATGAAGGAAAGT AACCAAGAAACCTCTAGGAATTAGTGAAAAAAGAACTTTTTTGAGGTG		
	ORF Start: ATG at 46		ORF Stop: TAA at 2104
	SEQ ID NO: 350		686 aa MW at 76812.3kD
NOV126a, CG59987-01 Protein Sequence	MTDALLPAAPQPLEKENDGYFRKGCNPLAQTRSKLQNQRAALNQIILKAVRMRGTAE NLLKVATNSKVRQVRLSLFVNSDLQMLKEELEGLNIVGVYQNTTEAFTIPLIPLG LKETKDVFDAVVLKDFILEHYSYEDGYLYEDEIADLMDLRQACRTPSRDEAGVELLMTY		

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	FIQLGFVESRFFPPTRQMGLLFTWYDSLTVGPVVSQNNLLEKASVLFNTGALYTOIGT RCDRQTQAGLESIDAFAQRAAGVLNLYLKDTFTHTPSYDMS PAMLSVLVKMMLAQAQES VFEKISLPGIRNEFFMLVKVAQEAAKVGEVYQQLHAAMSQAPVKENIPYSWASLACVK AHHYAALAHYFTAILLIDHQVKPGTDLHDHKEKCLSQLYDHMEGLTPLATLKNQDQRR QLGKSHLRRAMAHHEESVREASLCKKLRSIEVLQKVLCAAQERSRLTYAQHQEEDDLL NLIDAPRVLLKLSKRLTLYCPSSPADSHGLLPEAGPLSVLSANKRWTTPRSIRFTA EGDLGFTLRGNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCKWLTLSEVMKLLKS FGEDEIEMKVVSLLDSTSSMHNKSATYSVGMQKTYSMICLAIDDDDKDTKKISKKL SFLSWGNTKNRQKSASTLCLPSVGAARPQVKKKLPSPFSLNSDSSWY		
	SEQ ID NO: 351	2109 bp	
NOV126b, CG59987-02 DNA Sequence	CGCCGCTAGCATGACCGACGCGCTGTTGCCCGCGGCCCCCAGCCGCTGGAGAAGGAG AACGACGGCTACTTTCGGAAGGGCTGTAATCCCCTTGCAACAACCGCGCGGAGTAAAT TGCAGAATCAAAGAGCTGCTTTGAATCAGCAGATCTGAAAGCCGTGCGGATGAGGAC CGGAGCGGAAAACCTTCTGAAAGTGGCCACAACTCAAAGGTGCGGGAGCAAGTGGCG CTGGAGCTGAGCTTCGTCAACTCAGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGGC TGAACATCTCGGTGGGCGTCTATCAGAACACAGAGGAGGCATTTACGATTCCCCTGAT TCCTCTTGGCCTGAAGGAAACGAAAGACGTCGACTTTGCGAGTCGTCCTCAAGGATTTT ATCTCTGGAACATTACAGTGAAGATGGCTATTATATGAAGATGAAATTCGAGATCTTA TGGATCTGAGACAAGCTTGTGCGACGCTAGCCGGATGAGGCCGGGTGGAAGTCTGCT GATGACATACTTCATCCAGCTGGGCTTTGTGCGAGAGTCGATTCTTCCCGCCACACGG CAGATGGGACTCCTGTTACCTGGTATGACTCTCTCACCGGGGTTCCGGTCAGCCAGC AGAACTCTGCTGTGGAGAAGGCCAGTGTCTGTTCACACTGGGGCCCTCTACACCCA GATTGGGACCCGCTGCGATCGGCAGACGCGAGGCTGGGCTGGAGAGTGCCATAGATGCC TTTCAGAGAGCCGCGAGGGGTTTTAAATTACCTGAAAGACACATTTACCCATACTCCAA GTTACGACATGAGCCCTGCCATGCTCAGCGTGTCTCGTCAAAATGATGCTTGCAAGC CCAAGAAAGCGTGTGTGAGAAAATCAGCCTTCTCGGATCCGGAATGAATTCTTCATG CTGGTGAAGGTGGCTCAGGAGGCTGCTAAGGTGGGAGAGGTTACCAACAGCTACACG CAGCCATGAGCCAGGCGCGGTGAAAGAGAACATCCCTACTCTCTGGGCCAGCTTAGC CTGCGTGAAGGCCACCACTACGCGGCCCTGGCCCACTACTTCACTGCCATCTCTCTC ATCGACACCAAGGTGAAGCCAGGCACGGATCTGGACCAACAGGAGAAGTGCTGTGCC AGCTCTACGACCACATGCCAGAGGGGCTGACACCCTTGGCCACAGCTGAAGAATGATCA GCAGCGCCGACAGCTGGGGAAGTCCCCTTGCGCAGAGCCATGGCTCATCACGAGGAG TCGGTGGGGAGGCAAGCCTCTGCAAGAAGCTGCGGAGCATTTAGGTGCTACAGAAGG TGCTGTGTGCCGACAGGAACGCTCCCGGCTCAGTACGCCAGCACCAGGAGGAGGA TGACCTGTGAACCTGATCGACGCCCCAGTGTTGTTGCTAAAACCTGAGCAAGAGGTT GACATTATATTGCCCGAGTTCTCCAAGCTGACAGTCACGGACTTCTTCCAGAAAGCTGG GCCCTTATCTGTGTTTTCGGCTAACAAGCGGTGGACGCTCTCTCGAAGCATCCGCTT CACTGCAGAAGAAGGGGACTTGGGGTTACCTTGAGAGGGAACGCCCGCGTTACAGTT CACTTCTGGATCCTTACTGCTCTGCCTCGGTGGCAGGAGCCCGGGAAGGAGATTATA TTGTCTCCATTAGCTTGTGGATTGTAAGTGGCTGACGCTGAGTGAGGTTATGAAGCT GCTGAAGAGCTTTGGCGAGGACGAGATCGAGATGAAAGTCGTGAGCCTCTCTGGACTCC ACATCATCCATGCATAATAAGAGTGCCACATACTCCGTGGGAATGTAGAAAACGTA CCATGATCTGCTTAGCCATTGATGATGACGACAAAACGATGATAAAACCAAGAAATCTC CAAGAAGCTTTCTCTCTGAGTTGGGGCACCAACAAGAACAGACAGAAGTCAGCCAGC ACCTTGTGCTCTCCATCGGTGCGGGCTGCACGGCCTCAGGTCAAGAAGAAGCTGCCCT CCCCCTTACGCTTCTCAACTCAGACAGTCTTGGTACTAATGTGAGGAAACAAACAT GTTACAGGCCCCGAACATTTC		
	ORF Start: ATG at 11	ORF Stop: TAG at 1844	
	SEQ ID NO: 352	611 aa	MW at 68613.9kD
NOV126b, CG59987-02 Protein Sequence	MTDALLPAAPQPLEKENDGYFRKGCNPLAQTRSKLQNRALNQILKAVRMRTGAE NLLKVATNSKVRQVRLELSFVNSDLQMLKEELEGLNISVGVIYQNTTEAFTIPLIPLG LKETKDVFVAVLKDFILEHYSYEDGYLYEDEIADLMDLRQACRTPSRDEAGVELLMY FIQLGFVESRFFPPTRQMGLLFTWYDSLTVGPVVSQNNLLEKASVLFNTGALYTOIGT RCDRQTQAGLESIDAFAQRAAGVLNLYLKDTFTHTPSYDMS PAMLSVLVKMMLAQAQES VFEKISLPGIRNEFFMLVKVAQEAAKVGEVYQQLHAAMSQAPVKENIPYSWASLACVK AHHYAALAHYFTAILLIDHQVKPGTDLHDHKEKCLSQLYDHMEGLTPLATLKNQDQRR QLGKSHLRRAMAHHEESVREASLCKKLRSIEVLQKVLCAAQERSRLTYAQHQEEDDLL NLIDAPSVVAKTEQEVDIILPQFSKLTVDFFQKLGPLSVFSANKRWTTPRSIRFTA EGDLGFTLRGNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCKWLTLSEVMKLLKS FGEDEIEMKVVSLLDSTSSMHNKSATYSVGM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 126B.

Table 126B. Comparison of NOV126a against NOV126b.		
Protein Sequence	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV126b	1..611 1..611	585/612 (95%) 590/612 (95%)

Further analysis of the NOV126a protein yielded the following properties shown in Table 126C.

Table 126C. Protein Sequence Properties NOV126a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

- 5 A search of the NOV126a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 126D.

Table 126D. Geneseq Results for NOV126a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU10192	Human prostate specific protein PSL22 - Homo sapiens, 686 aa. [WO200172962-A2, 04-OCT-2001]	1..686 1..686	660/687 (96%) 665/687 (96%)	0.0
AAB68561	Human GTP-binding associated protein #61 - Homo sapiens, 666 aa. [WO200105970-A2, 25-JAN-2001]	27..686 7..666	626/661 (94%) 633/661 (95%)	0.0
AAG64579	Human transcription termination factor binding protein 54 - Homo sapiens, 488 aa. [CN1297918-A, 06-JUN-2001]	201..686 3..488	458/487 (94%) 464/487 (95%)	0.0
AAB29661	Human histidine domain-protein tyrosine phosphatase, SEQ ID NO:2	110..357 7..253	82/252 (32%) 135/252 (53%)	3e-28

	[WO200063392-A1, 26-OCT-2000]			
AAU00869	Human cancer related protein 5 - Homo sapiens, 257 aa. [WO200118014-A1, 15-MAR-2001]	409..597 8..196	70/189 (37%) 102/189 (53%)	2e-27

In a BLAST search of public sequence databases, the NOV126a protein was found to have homology to the proteins shown in the BLASTP data in Table 126E.

Table 126E. Public BLASTP Results for NOV126a				
Protein Accession Number	Protein/Organism/Length	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RU1	RHOPHILIN-LIKE PROTEIN - Homo sapiens (Human), 685 aa.	1..686 1..685	627/688 (91%) 640/688 (92%)	0.0
Q9DBN2	I300002E07RIK PROTEIN - Mus musculus (Mouse), 686 aa.	1..686 1..686	573/687 (83%) 616/687 (89%)	0.0
Q61085	GTP-RHO binding protein 1 (Rhopilin) - Mus musculus (Mouse), 643 aa.	16..596 20..580	273/583 (46%) 361/583 (61%)	e-135
Q9XYY9	RHOPHILIN - Drosophila melanogaster (Fruit fly), 718 aa.	21..615 31..674	248/654 (37%) 363/654 (54%)	e-110
Q96PV9	KIAA1929 PROTEIN - Homo sapiens (Human), 410 aa (fragment).	23..366 17..362	178/346 (51%) 241/346 (69%)	1e-93

5 PFam analysis predicts that the NOV126a protein contains the domains shown in the Table 126F.

Table 126F. Domain Analysis of NOV126a			
Pfam Domain	NOV126a Match Region	Identities/ Similarities for the Matched Region	Expect Value
HR1: domain 1 of 1	38..110	19/87 (22%) 53/87 (61%)	1.2e-05
BRO1: domain 1 of 1	111..263	60/172 (35%) 125/172 (73%)	3.8e-56

PDZ: domain 1 of 1	516..593	20/84 (24%) 53/84 (63%)	0.46
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Example 127.

The NOV127 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 127A.

Table 127A. NOV127 Sequence Analysis		
	SEQ ID NO: 353	3351 bp
NOV127a, CG59971-01 DNA Sequence	<p><u>CGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTGTTGTGGAAGCTCGCGGGGT</u> TGCTGCGGGAGTCCGGTGATGTGGTCCTGTCTGGCTGTAGCACCCCTGAGCCTGTGAC TCCCACACTGCAACAGCTGAACACGTATTTAGCTGCACCTGGGGCCATGGGGCCCT GGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCCCCTGTTATTCTTC AGCTTCAGTTTCTCTCGATGTGCTGCAGAAAAACACTTCACTCAAGCTGGTCCATGT TGCTGGTCTGGCCCCACAGGGCCATCAAGATTTCCCTTCAAATCCCTTCGGCAC CTGGAGCTCCGAGGTGTTCCCTCCACTGTCTGCATGGCCTCCGAGGCATCTACTCCC AGCTGGAGACCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGTCTCTCTCAGC CTGCGGCGGCGACTTCTGCTCTGCCCTCCCTGGCTGGCTCTGCTTTCTGCCAACTTC AGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGTT TCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAAGGATTCTGATGGATTGTG TGAGCTCCACCATCTGGACATCTCTATAATCGCTGCATTTGGTGCCAAGATGGGA CCCTCAGGGGCTGCTCTGGGGGTCTGATACTGCGAGGCAATGAGCTTCGGAGCCTCG CAGGCCTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTGGCATAACAACCTGCTGGA AGGACACCGGGAGCTGTCAACACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTG GAGGGGAACCTCTTTGGTTCCACCCTGAGCACCAGCAGCCACTGCCCAGTACTTGT CACCCCGGGCCAGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCTACT GACAGATTTTCAGCAGACTCACACATCCTTGGGGCTCAGCCCATGGGCCACCTTTG CCCTGGCCAGTGGGGAGTACTCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCC TCTCCTCAGGGGTGTGTGACCCAGCCCTGCTTCATAAGGTTAAGAGCCGAGTCCG TGTGAGGCGGGCAAGCATCTCTGAACCCAGTGATACGGACCCGAGGCCCGAACTCTG AACCCCTCTCCGGCTGGTTGGTTCTGTCAGCAGCACCCGGAGCTGGAGCTCATGAGCA GCTTCCGGGAACGGTTCCGGCCGCAACTGGCTGCAGTACAGGAGTCACTGGAGCCCTC CGGAAACCTCTGCCGGCCACCCCACTACTTCTGCACCCAGTGCACCTCCAGCCAGC TCCCAGGGCCCGACACTGCACCCAGACCTTCAACCCCGCAGGAGGAAGCCAGAGGCC CCCAGGAGTCACCAAGAAAATGTCAGAGGAGGTCAGGGCCGAGCCACAGGAGGAGGA AGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAGGGGGAGATGGTGGAAACAGGGAGAA GAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGACCAGAAGGAAGTGAAGCGGAAC TCTGTCCGCCCTTGTGGTGTGTCCCCTGGAGGGCCCTGAGGGCGTACGGGGCAGGGA ATGCTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTGGAACCTCAAGCAGCTCGC ACCTTGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAGATAGAGCCGAGGGCCC AGGCCCAGGGTCCCCCTTGTCTGCGCAGGGCTCAGATCTGCTCCCTGGGTGAGTTTCA CCTCAGTCTGCGCTTCTCTACATCTGCCCTGACCGGCAGTTGCGTCTGCTATTGTGTG CTGGAGCCTGATGCCACGCACTGTCCAGGAGCTGCTTGGCGTGTGACCCAGTCA CCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGTGGGTAGATTCCA GTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCAGGATGGGATTAGACAGT GAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGTGTCTCTAACT GTGGTAGTGACCACTGGTTCTCCTCGCTGTGTCTCGGGGAACGCCCTTCTGTGGCTGCG GAAACAGGGAGAGCAGTCTCTGGCTCCTTCTCCGTCTGCCAGCCCTGTCTGCCACCT CCTGGCCATGGTGACCACCTTGACAGGGCCAAGAACAGCCACCTCAGGCACCGAGCA CCCGTGACCATGGTAGTTGGAGCCTCAGTCCC GCCCTGAGCGCTGTGGCCTCCCGCTC TGTGGACCACCGACTCCGGCTCTTCTTGATGTTGAGGTGTTAGCGATGCCAGGAG GAGTTCAGTGCTGCTCAAGGTCCCAGTGGCATTGGCAGGCCACTGGGGAGTTCA TGTGCTTGTGGTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGGAGAT GAGTGAGCCTCCAGCTAGCTGGCTGCAGCTGACCTGGCTGTTCCCTGCGAGGATCTG AGTGGCATAGAGCTGGGCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGCAGCTGGGG CGGGCCGCTGTGTGCTGCTGCCCCGAGATGCCAGGCATTGCCGGGCCCTGCTGTGGCTG GCTCCTTGGTGTCTTGCACTCTGCCCCCTGCTGGAGGAACCTGTGTCACTGCCACA GAGGAGGAGGTCAACCCCAAGCACCGGCTCTGGCCATTGCTGGAAAAAGACTCATCT TGGAGGCTCGCCAGTTCTTCTACCTTCCGGCGTCTCTGGTTGAAGGTGAAGCCTCTGT GCAGCTGATGCTTCCCTCCACCTGCTCGTATCCCTGTTGTGCTGACTCCGTCACCCCTG TTCCTGTTAGATGAGGATGCTGCAGGCTCCCCGGCAGAGCCCTCTCTCCAGCAGCAT CTGGCGAAGCCTCTGAAAGGTGCTCCCTCGGGCCGGGCCCTGCTGTGGCTGTGAG GGAGCAGCAGCCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCTGAG GACTTGCGGCTGCTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTCC GTGTGGTGTGTGACGAGCAGCTGACAGCCCTGCTTGGCTGGATGCCGGGAACCATGGGA GGAGCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGA TGAGGGTCCCACGCTGACCTTGGCCCTGACCTCAGGAGCCACGCT</p>	
	ORF Start: ATG at	ORF Stop: TGA at 3307

[illegible]

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	CTGTTAGATGAGGATGCTGCAGGGTCCCCGGCAGAGCCCTCTCCTCCAGCAGCATCTG GCGAAGCCTCTGAGAAGGTGCCTCCCTCGGGGCCGGGCCCTGCTGTGCGTGTGAGGGA GCAGCAGCCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCCCTGAGGAC TTGCGGCTGCTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTCCGTG TGGTGTGTCAGGAGCAGCTGACAGCCCTGCTTGCTGGATCCGGGAACCATGGGAGGA GCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA GGGTCCACGCTGACCTTGGCCCTGACCTCAGGAGCCACGCT		
	ORF Start: ATG at 13	ORF Stop: TGA at 3304	
	SEQ ID NO: 356	1097 aa	MW at 121064.1kD
NOV127b, CG59971-02 Protein Sequence	MTAQQRDSSLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHLPWGPQGQ FVALPSHPADSPVILQQLFDVLQKTLCLKLVHAGPGTGPikiFFFKSLRHELR GVPLHCLHGLRGIYSQLETICSRSLQALEELLSACGGDFCSALPWLALLSANFSYNA LTALDSSLRLLSALRFLNLSHNQVQDCQGFMDLCELHHLDI SYNRLHLVPRMGPSGA ALGVLILRGNELRSLPGLEQLRNLRLDLAYNLLLEGHRELSPLWLLAELRKLYLEGNP LWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQQTHTSLGLSPMGPPLPWPV GSTPETSGGPDLSLSSGGVVTQPLLHKVKSRRVRRASISEPSDTPPEPRTLNPSP AGWVQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGP DTAPRPSPPQEEARGPQESPOKMSEEVRAEPQEEEEKEGKEEKEGEMVEQEEEEAG EEEEEEQDQKEVEAEELCRPLLVCLEGPVGVRGECFLRVTSAHLEFEVELQAARTLER LELQSLEAAEIEPEAQQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDA HAAVQELLAVLTPVTNVAREQLGEARDLLGRFQCLRCGHEFKPEEPRMGLDSEEGWR PLPQKTESPAVCPNCGSDHVLLAVSRGTPNRRKQGEQSLAPSPASPVCHPGHGD HLDRAKNSPQPAPSTRDHGSWSLSPAPERCGLRSDVHRLRLFLDVEVFSDAQEEFQCC LKVPVALAGHTGEFMCVVVSDRRLLYLLKVTGEMSEPPASWLQTLAVPLQDLSGIEL GLAGQSLRLEWAAGAGRCVLLPRDARHCRAFLEELLGVLQSLPPAWRNCVSATEEVT PQHRLWPLLEKDSSLEARQFFYLRAFLVEGEASVQLMLPSTCLVSLLLTPSTLFLLE DAAGSPAEPSPPAASGEASEKVPSPGPGPAVRVREQQLSSSLSSVLLYRSAPEDLRL FYDEVSRLESFVALRVVCQEQLTALLAWIREPWEELFSIGLRTVIEALALDR		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 127B.

Table 127B. Comparison of NOV127a against NOV127b.		
Protein Sequence	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV127b	1..1098	891/1098 (81%)
	1..1097	891/1098 (81%)

Further analysis of the NOV127a protein yielded the following properties shown in Table 127C.

Table 127C. Protein Sequence Properties NOV127a	
PSort analysis:	0.5163 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.2442 probability located in mitochondrial inner membrane; 0.2442 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV127a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 127D.

Table 127D. Geneseq Results for NOV127a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM39827	Human polypeptide SEQ ID NO 2972 - Homo sapiens, 169 aa. [WO200153312-A1, 26-JUL-2001]	375..528 14..167	140/154 (90%) 145/154 (93%)	3e-78
AAM41613	Human polypeptide SEQ ID NO 6544 - Homo sapiens, 184 aa. [WO200153312-A1, 26-JUL-2001]	375..528 29..182	140/154 (90%) 145/154 (93%)	4e-78
AAU19764	Human novel extracellular matrix protein, Seq ID No 414 - Homo sapiens, 211 aa. [WO200155368-A1, 02-AUG-2001]	444..647 13..209	157/207 (75%) 160/207 (76%)	2e-75
ABB19833	Protein #1832 encoded by probe for measuring heart cell gene expression - Homo sapiens, 127 aa. [WO200157274-A2, 09-AUG-2001]	409..535 1..127	127/127 (100%) 127/127 (100%)	2e-70
AAM67606	Human bone marrow expressed probe encoded protein SEQ ID NO: 27912 - Homo sapiens, 127 aa. [WO200157276-A2, 09-AUG-2001]	409..535 1..127	127/127 (100%) 127/127 (100%)	2e-70

In a BLAST search of public sequence databases, the NOV127a protein was found to have homology to the proteins shown in the BLASTP data in Table 127E.

Table 127E. Public BLASTP Results for NOV127a				
Protein Accession Number	Protein/Organism/Length	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL49726	LKB1-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1099 aa.	1..1098 12..1099	1077/1098 (98%) 1078/1098 (98%)	0.0

Q96PY9	KIAA1898 PROTEIN - Homo sapiens (Human), 1013 aa (fragment).	76..1098 1..1013	1003/1023 (98%) 1003/1023 (98%)	0.0
Q96CN3	SIMILAR TO RIKEN CDNA 1200014D22 GENE - Homo sapiens (Human), 804 aa (fragment).	288..1098 4..804	793/811 (97%) 793/811 (97%)	0.0
Q9DBT7	1200014D22RIK PROTEIN - Mus musculus (Mouse), 1072 aa.	1..1098 1..1072	816/1098 (74%) 895/1098 (81%)	0.0
Q9VMK9	CG9044 PROTEIN - Drosophila melanogaster (Fruit fly), 1289 aa.	12..433 8..463	139/459 (30%) 220/459 (47%)	6e-38

PFam analysis predicts that the NOV127a protein contains the domains shown in the Table 127F.

Table 127F. Domain Analysis of NOV127a			
Pfam Domain	NOV127a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRR: domain 1 of 5	164..186	7/25 (28%) 15/25 (60%)	2.5e+02
LRR: domain 2 of 5	187..209	6/25 (24%) 16/25 (64%)	2.5e+02
LRR: domain 3 of 5	210..231	8/25 (32%) 13/25 (52%)	83
LRR: domain 4 of 5	233..254	9/25 (36%) 17/25 (68%)	16
LRR: domain 5 of 5	255..279	10/27 (37%) 19/27 (70%)	22
Pkinase_C: domain 1 of 1	620..629	5/11 (45%) 9/11 (82%)	8.9
rubredoxin: domain 1 of 2	669..686	5/18 (28%) 13/18 (72%)	4.6
rubredoxin: domain 2 of 2	708..713	5/6 (83%) 6/6 (100%)	1.2e+03

Example B: Sequencing Methodology and Identification of NOVX Clones

1. **GeneCalling™ Technology:** This is a proprietary method of performing differential gene expression profiling between two or more samples developed at CuraGen and described by Shimkets, et al., "Gene expression analysis by transcript profiling coupled to a gene database query" *Nature Biotechnology* 17:198-803 (1999). cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then digested with up to as many as 120 pairs of restriction enzymes and pairs of linker-adaptors specific for each pair of restriction enzymes were ligated to the appropriate end. The restriction digestion generates a mixture of unique cDNA gene fragments. Limited PCR amplification is performed with primers homologous to the linker adapter sequence where one primer is biotinylated and the other is fluorescently labeled. The doubly labeled material is isolated and the fluorescently labeled single strand is resolved by capillary gel electrophoresis. A computer algorithm compares the electropherograms from an experimental and control group for each of the restriction digestions. This and additional sequence-derived information is used to predict the identity of each differentially expressed gene fragment using a variety of genetic databases. The identity of the gene fragment is confirmed by additional, gene-specific competitive PCR or by isolation and sequencing of the gene fragment.
2. **SeqCalling™ Technology:** cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included

in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

3. PathCalling™ Technology:

The NOVX nucleic acid sequences are derived by laboratory screening of cDNA library by the two-hybrid approach. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, are sequenced. In silico prediction was based on sequences available in CuraGen Corporation's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory screening was performed using the methods summarized below:

cDNA libraries were derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then directionally cloned into the appropriate two-hybrid vector (Gal4-activation domain (Gal4-AD) fusion). Such cDNA libraries as well as commercially available cDNA libraries from Clontech (Palo Alto, CA) were then transferred from E.coli into a CuraGen Corporation proprietary yeast strain (disclosed in U. S. Patents 6,057,101 and 6,083,693, incorporated herein by reference in their entirety).

Gal4-binding domain (Gal4-BD) fusions of a CuraGen Corporation proprietary library of human sequences was used to screen multiple Gal4-AD fusion cDNA libraries resulting in the selection of yeast hybrid diploids in each of which the Gal4-AD fusion contains an individual cDNA. Each sample was amplified using the polymerase chain reaction (PCR) using non-specific primers at the cDNA insert boundaries. Such PCR product was sequenced; sequence traces were evaluated manually and edited for

corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Physical clone: the cDNA fragment derived by the screening procedure, covering the entire open reading frame is, as a recombinant DNA, cloned into pACT2 plasmid (Clontech) used to make the cDNA library. The recombinant plasmid is inserted into the host and selected by the yeast hybrid diploid generated during the screening procedure by the mating of both CuraGen Corporation proprietary yeast strains N106' and YULH (U. S. Patents 6,057,101 and 6,083,693).

4. **RACE:** Techniques based on the polymerase chain reaction such as rapid amplification of cDNA ends (RACE), were used to isolate or complete the predicted sequence of the cDNA of the invention. Usually multiple clones were sequenced from one or more human samples to derive the sequences for fragments. Various human tissue samples from different donors were used for the RACE reaction. The sequences derived from these procedures were included in the SeqCalling Assembly process described in preceding paragraphs.

5. **Exon Linking:** The NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. **Table B1** shows the sequences of the PCR primers used for obtaining different clones. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated

homology of the predicted exons to closely related human sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal
 5 kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The PCR product derived from exon linking was cloned into the pCR2.1 vector from Invitrogen. The resulting bacterial
 10 clone has an insert covering the entire open reading frame cloned into the pCR2.1 vector. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were
 15 evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

6. Physical Clone:

Exons were predicted by homology and the intron/exon boundaries were
 20 determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent
 25 inconsistencies thereby obtaining the sequences encoding the full-length protein.

The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clones used for expression and screening purposes.

30

Example C: Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines
 35 and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on an

Applied Biosystems ABI PRISM® 7700 or an ABI PRISM® 7900 HT Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on metabolic diseases), AI_comprehensive_panel (containing normal tissue and samples from autoimmune diseases), Panel CNSD.01 (containing central nervous system samples from normal and diseased brains) and CNS_neurodegeneration_panel (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 μ l) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (Applied Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions.

In other cases, non-normalized RNA samples were converted to single strand cDNA (sscDNA) using Superscript II (Invitrogen Corporation; Catalog No. 18064-147) and random hexamers according to the manufacturer's instructions. Reactions containing up to 10 μ g of total RNA were performed in a volume of 20 μ l and incubated for 60 minutes at 42°C. This reaction can be scaled up to 50 μ g of total RNA in a final volume of 100 μ l. sscDNA samples are then normalized to reference nucleic acids as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions.

Probes and primers were designed for each assay according to Applied Biosystems Primer Express Software package (version I for Apple Computer's Macintosh Power PC)

or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60°C, primer optimal T_m = 59°C, maximum primer difference = 2°C, probe does not have 5'G, probe T_m must be 10°C greater than primer T_m , amplicon size 75bp to 100bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900nM each, and probe, 200nM.

PCR conditions: When working with RNA samples, normalized RNA from each tissue and each cell line was spotted in each well of either a 96 well or a 384-well PCR plate (Applied Biosystems). PCR cocktails included either a single gene specific probe and primers set, or two multiplexed probe and primers sets (a set specific for the target clone and another gene-specific set multiplexed with the target probe). PCR reactions were set up using TaqMan® One-Step RT-PCR Master Mix (Applied Biosystems, Catalog No. 4313803) following manufacturer's instructions. Reverse transcription was performed at 48°C for 30 minutes followed by amplification/PCR cycles as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

When working with sscDNA samples, normalized sscDNA was used as described previously for RNA samples. PCR reactions containing one or two sets of probe and primers were set up as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions. PCR amplification was performed as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were analyzed and processed as described previously.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on these panels are comprised of samples derived from all major organ systems from single adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var = small cell variant,
non-s = non-sm = non-small,
squam = squamous,
pl. eff = pl effusion = pleural effusion,
glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

General_screening_panel_v1.4

The plates for Panel 1.4 include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in Panel 1.4 are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS

cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in Panel 1.4 are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on

5 Panel 1.4 are comprised of pools of samples derived from all major organ systems from 2 to 5 different adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland,

10 spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose. Abbreviations are as described for Panels 1, 1.1, 1.2, and 1.3D.

Panels 2D and 2.2

The plates for Panels 2D and 2.2 generally include 2 control wells and 94 test

15 samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor.

20 These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologist at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding

25 the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of disease and

30 were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

Panel 3D

The plates of Panel 3D are comprised of 94 cDNA samples and two control samples. Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1.3D are of the most common cell lines used in the scientific literature.

Panels 4D, 4R, and 4.1D

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4R) or cDNA (Panels 4D/4.1D) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) was employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5ng/ml, TNF alpha at approximately 5-10ng/ml, IFN gamma at approximately 20-50ng/ml, IL-4 at approximately 5-10ng/ml, IL-9 at approximately 5-10ng/ml, IL-13 at approximately

5-10ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20ng/ml PMA and 1-2μg/ml ionomycin, IL-12 at 5-10ng/ml, IFN gamma at 20-50ng/ml and IL-18 at 5-10ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5μg/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol (5.5×10^{-5} M) (Gibco), and 10mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco), 50ng/ml GM-CSF and 5ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10μg/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. CD45RO beads were then used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5µg/ml anti-CD28 (Pharmingen) and 3µg/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco). To activate the cells, we used PWM at 5µg/ml or anti-CD40 (Pharmingen) at approximately 10µg/ml and IL-4 at 5-10ng/ml. Cells were harvested for RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10µg/ml anti-CD28 (Pharmingen) and 2µg/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10^5 - 10^6 cells/ml in DMEM 5% FCS

(Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10mM Hepes (Gibco) and IL-2 (4ng/ml). IL-12 (5ng/ml) and anti-IL4 (1µg/ml) were used to direct to Th1, while IL-4 (5ng/ml) and anti-IFN gamma (1µg/ml) were used to direct to Th2 and IL-10 at 5ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10mM Hepes (Gibco) and IL-2 (1ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1µg/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1mM dbcAMP at 5×10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10ng/ml and ionomycin at 1µg/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5ng/ml IL-4, 5ng/ml IL-9, 5ng/ml IL-13 and 25ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane

(Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15ml Falcon Tube. An equal volume of isopropanol was added and left at -20°C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300µl of RNase-free water and 35µl buffer (Promega) 5µl DTT, 7µl RNasin and 8µl DNase were added. The tube was incubated at 37°C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80°C.

AI_comprehensive panel_v1.0

The plates for AI_comprehensive panel_v1.0 include two control wells and 89 test samples comprised of cDNA isolated from surgical and postmortem human tissues obtained from the Backus Hospital and Clinomics (Frederick, MD). Total RNA was extracted from tissue samples from the Backus Hospital in the Facility at CuraGen. Total RNA from other tissues was obtained from Clinomics.

Joint tissues including synovial fluid, synovium, bone and cartilage were obtained from patients undergoing total knee or hip replacement surgery at the Backus Hospital. Tissue samples were immediately snap frozen in liquid nitrogen to ensure that isolated RNA was of optimal quality and not degraded. Additional samples of osteoarthritis and rheumatoid arthritis joint tissues were obtained from Clinomics. Normal control tissues were supplied by Clinomics and were obtained during autopsy of trauma victims.

Surgical specimens of psoriatic tissues and adjacent matched tissues were provided as total RNA by Clinomics. Two male and two female patients were selected between the ages of 25 and 47. None of the patients were taking prescription drugs at the time samples were isolated.

Surgical specimens of diseased colon from patients with ulcerative colitis and Crohns disease and adjacent matched tissues were obtained from Clinomics. Bowel tissue from three female and three male Crohn's patients between the ages of 41-69 were used. Two patients were not on prescription medication while the others were taking dexamethasone, phenobarbital, or tylenol. Ulcerative colitis tissue was from three male and

four female patients. Four of the patients were taking lebrid and two were on phenobarbital.

Total RNA from post mortem lung tissue from trauma victims with no disease or with emphysema, asthma or COPD was purchased from Clinomics. Emphysema patients
5 ranged in age from 40-70 and all were smokers, this age range was chosen to focus on patients with cigarette-linked emphysema and to avoid those patients with alpha-1 anti-trypsin deficiencies. Asthma patients ranged in age from 36-75, and excluded smokers to prevent those patients that could also have COPD. COPD patients ranged in age from 35-
10 80 and included both smokers and non-smokers. Most patients were taking corticosteroids, and bronchodilators.

In the labels employed to identify tissues in the AI_comprehensive panel_v1.0 panel, the following abbreviations are used:

AI = Autoimmunity
Syn = Synovial
15 Normal = No apparent disease
Rep22 /Rep20 = individual patients
RA = Rheumatoid arthritis
Backus = From Backus Hospital
OA = Osteoarthritis
20 (SS) (BA) (MF) = Individual patients
Adj = Adjacent tissue
Match control = adjacent tissues
-M = Male
-F = Female
25 COPD = Chronic obstructive pulmonary disease

Panels 5D and 5I

The plates for Panel 5D and 5I include two control wells and a variety of cDNAs isolated from human tissues and cell lines with an emphasis on metabolic diseases. Metabolic tissues were obtained from patients enrolled in the Gestational Diabetes study.
30 Cells were obtained during different stages in the differentiation of adipocytes from human mesenchymal stem cells. Human pancreatic islets were also obtained.

In the Gestational Diabetes study subjects are young (18 - 40 years), otherwise healthy women with and without gestational diabetes undergoing routine (elective) Caesarean section. After delivery of the infant, when the surgical incisions were being

repaired/closed, the obstetrician removed a small sample (<1 cc) of the exposed metabolic tissues during the closure of each surgical level. The biopsy material was rinsed in sterile saline, blotted and fast frozen within 5 minutes from the time of removal. The tissue was then flash frozen in liquid nitrogen and stored, individually, in sterile screw-top tubes and kept on dry ice for shipment to or to be picked up by CuraGen. The metabolic tissues of interest include uterine wall (smooth muscle), visceral adipose, skeletal muscle (rectus) and subcutaneous adipose. Patient descriptions are as follows:

10	Patient 2	Diabetic Hispanic, overweight, not on insulin
	Patient 7-9	Nondiabetic Caucasian and obese (BMI>30)
	Patient 10	Diabetic Hispanic, overweight, on insulin
	Patient 11	Nondiabetic African American and overweight
	Patient 12	Diabetic Hispanic on insulin

Adipocyte differentiation was induced in donor progenitor cells obtained from Osirus (a division of Clonetics/BioWhittaker) in triplicate, except for Donor 3U which had only two replicates. Scientists at Clonetics isolated, grew and differentiated human mesenchymal stem cells (HuMSCs) for CuraGen based on the published protocol found in Mark F. Pittenger, et al., Multilineage Potential of Adult Human Mesenchymal Stem Cells Science Apr 2 1999: 143-147. Clonetics provided Trizol lysates or frozen pellets suitable for mRNA isolation and ds cDNA production. A general description of each donor is as follows:

Donor 2 and 3 U: Mesenchymal Stem cells, Undifferentiated Adipose
 Donor 2 and 3 AM: Adipose, AdiposeMidway Differentiated
 Donor 2 and 3 AD: Adipose, Adipose Differentiated

Human cell lines were generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: kidney proximal convoluted tubule, uterine smooth muscle cells, small intestine, liver HepG2 cancer cells, heart primary stromal cells, and adrenal cortical adenoma cells. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. All samples were processed at CuraGen to produce single stranded cDNA.

Panel 5I contains all samples previously described with the addition of pancreatic islets from a 58 year old female patient obtained from the Diabetes Research Institute at the

University of Miami School of Medicine. Islet tissue was processed to total RNA at an outside source and delivered to CuraGen for addition to panel 5I.

In the labels employed to identify tissues in the 5D and 5I panels, the following abbreviations are used:

- 5 GO Adipose = Greater Omentum Adipose
- SK = Skeletal Muscle
- UT = Uterus
- PL = Placenta
- AD = Adipose Differentiated
- 10 AM = Adipose Midway Differentiated
- U = Undifferentiated Stem Cells

Panel CNSD.01

- The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the
- 15 Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

- Disease diagnoses are taken from patient records. The panel contains two brains
- 20 from each of the following diagnoses: Alzheimer's disease, Parkinson's disease, Huntington's disease, Progressive Supranuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus pallidus, substantia nigra, Brodman Area 4 (primary motor strip), Brodman Area 7 (parietal cortex), Brodman Area 9 (prefrontal cortex), and Brodman area
- 25 17 (occipital cortex). Not all brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus pallidus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to
- 30 be free of any pathology consistent with neurodegeneration.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

- 5 PSP = Progressive supranuclear palsy
 Sub Nigra = Substantia nigra
 Glob Palladus= Globus palladus
 Temp Pole = Temporal pole
 Cing Gyr = Cingulate gyrus
 BA 4 = Brodman Area 4

Panel CNS_Neurodegeneration_V1.0

10 The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

15 Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and controls with no dementia but evidence of severe Alzheimer's like
20 pathology, (specifically senile plaque load rated as level 3 on a scale of 0-3; 0 = no evidence of plaques, 3 = severe AD senile plaque load). Within each of these brains, the following regions are represented: hippocampus, temporal cortex (Brodman Area 21), parietal cortex (Brodman area 7), and occipital cortex (Brodman area 17). These regions were chosen to encompass all levels of neurodegeneration in AD. The hippocampus is a
25 region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the parietal cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within AD patients. Not all brain regions are represented in all cases.

30 In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology upon autopsy

Control = Control brains; patient not demented, showing no neuropathology
Control (Path) = Control brains; pateint not demented but showing sever AD-like pathology
SupTemporal Ctx = Superior Temporal Cortex
Inf Temporal Ctx = Inferior Temporal Cortex

5

A. CG58522-01: HUMAN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA

Expression of gene CG58522-01 was assessed using the primer-probe set Ag3365, described in Table AA. Results of the RTQ-PCR runs are shown in Table AB.

10 Table AA. Probe Name Ag3365

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cagaatgaaccaaggagactca-3'	22	3	357
Probe	TET-5'-ctactccgcatgcggcagaagacatt-3'-TAMRA	26	35	358
Reverse	5'-cacatccatctgtcatctcctt-3'	22	62	359

Table AB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3365, Run 216709759	Tissue Name	Rel. Exp.(%) Ag3365, Run 216709759
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	10.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca.	0.0	Colon ca. Colo-205	0.0

OVCAR-3			
Ovarian ca. SK-OV-3	4.9	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	7.9	Stomach Pool	0.0
Ovarian ca. OVCAR-8	26.8	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	1.7	Lymph Node Pool	16.5
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	3.3	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	4.5	CNS cancer (glio) SNB-19	6.2
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	25.7
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	100.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	4.8
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.8
Liver	0.0	Brain (Thalamus) Pool	3.6
Fetal Liver	0.0	Brain (whole)	6.9
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0

Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3365 - Significant expression of this gene is seen only in the lung cancer cell line NCI-H23 (CT=33.1). Therefore, expression of this gene may be used to distinguish this sample from the other samples on this panel.

Panel 4D Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

B. CG58520-01: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1

Expression of gene CG58520-01 was assessed using the primer-probe set Ag3364, described in Table BA.

Table BA. Probe Name Ag3364

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - ttcttctgcggagtcaaagtag - 3'	22	43	360
Probe	TET-5' - ttggtcttcttgttactgacctgca - 3' - TAMRA	26	75	361
Reverse	5' - tcactctgccttatcaacgtttc - 3'	22	106	362

CNS_neurodegeneration_v1.0 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel CNS_1 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

C. CG58520-03: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR)

- 5 Expression of gene CG58520-03 was assessed using the primer-probe set Ag5092, described in Table CA.

Table CA. Probe Name Ag5092

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gaacattcctgtccactgga-3'	20	625	363
Probe	TET-5'-atTTTcaagcgatggataccctaaaa-3'- TAMRA	26	645	364
Reverse	5'-cacttctacggagggtttt-3'	20	692	365

CNS_neurodegeneration_v1.0 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

- 10 **General_screening_panel_v1.5 Summary:** Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

D. CG58518-01: GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 -

- 15 Expression of gene CG58518-01 was assessed using the primer-probe sets Ag3363, Ag1130, Ag1198, Ag1253 and Ag1603, described in Tables DA, DB, DC, DD and DE. Results of the RTQ-PCR runs are shown in Tables DF, DG and DH.

Table DA. Probe Name Ag3363

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggttttccagttagtctcctt-3'	22	14	366
Probe	TET-5'-cacctacatctggatcatattgaaacca-3'- TAMRA	28	36	367
Reverse	5'-ttgatgttagaagcagcacaaa-3'	22	68	368

Hs688(B).T		NCI-N87	
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	16.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	6.8
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	6.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	8.5
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	10.9
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0

Lung ca. NCI-H146	77.9	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	100.0	CNS cancer (glio) SF-295	11.4
Lung ca. A549	10.1	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	34.4	Brain (fetal)	0.0
Lung ca. NCI-H460	30.6	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	5.1
Fetal Liver	0.0	Brain (whole)	50.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	3.0	Adrenal Gland	0.0
Fetal Kidney	8.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Tissue Name	Rel. Exp.(%) Ag1130, Run 125117140	Rel. Exp.(%) Ag1130, Run 126566764	Rel. Exp.(%) Ag1198, Run 129140506	Tissue Name	Rel. Exp.(%) Ag1130, Run 125117140	Rel. Exp.(%) Ag1130, Run 126566764	Rel. Exp.(%) Ag1198, Run 129140506
Endothelial cells	0.0	0.0	0.0	Renal ca. 786-0	0.0	0.0	0.0
Heart (Fetal)	0.0	0.0	0.0	Renal ca. A498	7.3	4.7	0.0
Pancreas	0.0	0.0	0.0	Renal ca. RXF 393	0.0	0.0	0.0
Pancreatic ca. CAPAN 2	9.0	0.0	0.0	Renal ca. ACHN	0.0	0.0	0.0
Adrenal Gland	0.0	2.6	0.0	Renal ca. UO-31	3.9	0.0	0.0
Thyroid	0.0	0.0	0.0	Renal ca. TK-10	0.0	0.0	0.0
Salivary gland	0.0	0.0	0.0	Liver	26.6	0.0	0.0

Pituitary gland	0.0	0.0	0.0	Liver (fetal)	25.3	0.0	0.0
Brain (fetal)	0.0	0.0	0.0	Liver ca. (hepatoblast) HepG2	0.0	0.0	0.0
Brain (whole)	2.6	20.0	0.0	Lung	0.0	0.0	0.0
Brain (amygdala)	1.3	32.1	0.0	Lung (fetal)	0.0	0.0	0.0
Brain (cerebellum)	1.5	3.8	0.0	Lung ca. (small cell) LX-1	3.4	0.0	0.0
Brain (hippocampus)	0.0	27.0	0.0	Lung ca. (small cell) NCI-H69	28.5	74.2	0.0
Brain (thalamus)	9.9	22.5	9.8	Lung ca. (s.cell var.) SHP-77	3.8	9.7	0.0
Cerebral Cortex	0.0	0.0	0.0	Lung ca. (large cell) NCI-H460	8.8	4.1	5.3
Spinal cord	4.4	0.0	0.0	Lung ca. (non-sm. cell) A549	51.4	9.5	7.2
glio/astro U87-MG	0.0	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	0.0	0.0	0.0
glio/astro U-118-MG	0.0	0.0	0.0	Lung ca. (non-s.cell) HOP-62	8.4	2.7	9.6
astrocytoma SW1783	2.9	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0	0.0
neuro*; metast SK-N-AS	0.0	0.0	0.0	Lung ca. (squamous) SW 900	3.2	8.7	0.0
astrocytoma SF-539	5.1	0.0	0.0	Lung ca. (squamous) NCI-H596	2.3	15.9	0.0
astrocytoma	2.3	0.0	0.0	Mammary	0.0	0.0	0.0

a SNB-75				gland			
glioma SNB-19	6.3	20.7	9.0	Breast ca.* (pl.ef) MCF-7	0.0	0.0	0.0
glioma U251	1.4	0.0	1.8	Breast ca.* (pl.ef) MDA- MB-231	0.0	0.0	0.0
glioma SF- 295	0.0	0.0	0.0	Breast ca.* (pl. ef) T47D	14.1	37.4	0.0
Heart	0.0	0.0	0.0	Breast ca. BT-549	12.5	21.0	12.3
Skeletal Muscle	2.3	0.0	0.0	Breast ca. MDA-N	0.0	0.0	0.0
Bone marrow	0.0	0.0	0.0	Ovary	0.0	0.0	0.0
Thymus	0.0	0.0	0.0	Ovarian ca. OVCAR- 3	0.0	0.0	0.0
Spleen	2.2	0.0	0.0	Ovarian ca. OVCAR- 4	0.0	0.0	0.0
Lymph node	0.0	0.0	0.0	Ovarian ca. OVCAR- 5	66.9	35.4	4.4
Colorectal Tissue	11.3	27.7	21.8	Ovarian ca. OVCAR- 8	2.7	0.0	0.0
Stomach	0.0	0.0	0.0	Ovarian ca. IGROV-1	6.0	0.0	0.0
Small intestine	5.4	0.0	0.0	Ovarian ca. (ascites) SK-OV-3	30.8	0.0	0.0
Colon ca. SW480	3.2	0.0	0.0	Uterus	0.0	0.0	0.0
Colon ca.* SW620 (SW480	0.0	0.0	0.0	Placenta	0.0	0.0	0.0

met)							
Colon ca. HT29	1.9	14.4	0.0	Prostate	6.9	0.0	0.0
Colon ca. HCT-116	0.0	0.0	0.0	Prostate ca.* (bone met) PC-3	100.0	0.0	0.0
Colon ca. CaCo-2	0.0	0.0	0.0	Testis	54.7	100.0	36.9
Colon ca. Tissue (ODO3866)	72.2	75.8	100.0	Melanom a Hs688(A). T	4.2	0.0	0.0
Colon ca. HCC-2998	5.3	4.8	0.0	Melanom a* (met) Hs688(B). T	2.7	34.2	13.3
Gastric ca.* (liver met) NCI-N87	50.3	0.0	0.0	Melanom a UACC- 62	0.0	0.0	0.0
Bladder	6.0	22.1	0.0	Melanom a M14	31.4	36.3	20.2
Trachea	0.0	0.0	0.0	Melanom a LOX IMVI	0.0	0.0	0.0
Kidney	2.0	0.0	0.0	Melanom a* (met) SK-MEL- 5	2.4	0.0	0.0
Kidney (fetal)	1.1	2.5	0.0				

Table DH. Panel 4R

Tissue Name	Rel. Exp.(%) Ag1198, Run 142014937	Tissue Name	Rel. Exp.(%) Ag1198, Run 142014937
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	2.5	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC	0.0

		TNFalpha + IL-1beta	
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1 _anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	16.4
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL- 1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell)	0.0	Lung fibroblast IL-13	0.0

ionomycin			
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 1	100.0
Monocytes rest	0.0	IBD Colitis 2	0.0
Monocytes LPS	0.0	IBD Crohn's	0.0
Macrophages rest	0.0	Colon	0.0
Macrophages LPS	0.0	Lung	0.0
HUVEC none	0.0	Thymus	0.0
HUVEC starved	0.0	Kidney	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3363 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3363 - Significant expression is seen in lung cancer cell line NCI-H146 (CT=34.5) and lung cancer cell line SHP-77 (CT=34.2).

- 5 Therefore, expression of this can be used to distinguish these samples from the rest of the samples on this panel.

- 10 **Panel 1.2 Summary:** Ag1130/Ag1198 - Three different runs using the same primer sequences yield similar results. Significant expression of this gene is seen in testis and a colon cancer sample. Therefore, expression of this gene can be used to differentiate these samples from other samples on these panels. Results from a third experiment using the probe and primer set Ag1253 show low/undetectable levels of expression in all the samples on this panel.

Panel 1.3D Summary: Ag1253 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

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Expression of gene CG58516-01 was assessed using the primer-probe set Ag3362, described in Table EA. Results of the RTO-PCR runs are shown in Tables EB and EC.

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcgggcaggacctttact-3'	19	1474	381
Probe	TET-5'-tcctacagctaattctgcagggcaca-3'-TAMRA	26	1498	382
Reverse	5'-tacgctttactcccgtaaagtca-3'	22	1543	383

15

Tissue Name	Rel. Exp.(%) Ag3362, Run 210153738	Tissue Name	Rel. Exp.(%) Ag3362, Run 210153738
AD 1 Hippo	9.9	Control (Path) 3 Temporal Ctx	0.0
AD 2 Hippo	33.2	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	4.3	AD 1 Occipital Ctx	2.0
AD 4 Hippo	16.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	96.6	AD 3 Occipital Ctx	5.4

AD 6 Hippo	43.2	AD 4 Occipital Ctx	24.7
Control 2 Hippo	29.1	AD 5 Occipital Ctx	24.5
Control 4 Hippo	16.6	AD 6 Occipital Ctx	31.9
Control (Path) 3 Hippo	3.8	Control 1 Occipital Ctx	0.9
AD 1 Temporal Ctx	7.1	Control 2 Occipital Ctx	89.5
AD 2 Temporal Ctx	23.2	Control 3 Occipital Ctx	12.6
AD 3 Temporal Ctx	5.6	Control 4 Occipital Ctx	6.3
AD 4 Temporal Ctx	20.0	Control (Path) 1 Occipital Ctx	65.1
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	15.8
AD 5 Sup Temporal Ctx	43.8	Control (Path) 3 Occipital Ctx	2.0
AD 6 Inf Temporal Ctx	30.8	Control (Path) 4 Occipital Ctx	11.6
AD 6 Sup Temporal Ctx	69.7	Control 1 Parietal Ctx	2.8
Control 1 Temporal Ctx	9.0	Control 2 Parietal Ctx	39.2
Control 2 Temporal Ctx	59.0	Control 3 Parietal Ctx	23.5
Control 3 Temporal Ctx	11.7	Control (Path) 1 Parietal Ctx	69.7
Control 4 Temporal Ctx	8.2	Control (Path) 2 Parietal Ctx	14.9
Control (Path) 1 Temporal Ctx	56.3	Control (Path) 3 Parietal Ctx	0.9
Control (Path) 2 Temporal Ctx	34.2	Control (Path) 4 Parietal Ctx	38.7

Table EC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3362, Run 216523482	Tissue Name	Rel. Exp.(%) Ag3362, Run 216523482
Adipose	6.3	Renal ca. TK-10	44.1
Melanoma* Hs688(A).T	17.6	Bladder	9.4

Melanoma* Hs688(B).T	18.3	Gastric ca. (liver met.) NCI-N87	21.6
Melanoma* M14	17.1	Gastric ca. KATO III	17.6
Melanoma* LOXIMVI	13.6	Colon ca. SW-948	5.8
Melanoma* SK- MEL-5	19.6	Colon ca. SW480	34.6
Squamous cell carcinoma SCC-4	14.6	Colon ca.* (SW480 met) SW620	14.2
Testis Pool	4.0	Colon ca. HT29	7.2
Prostate ca.* (bone met) PC-3	90.8	Colon ca. HCT-116	14.3
Prostate Pool	4.0	Colon ca. CaCo-2	19.8
Placenta	11.4	Colon cancer tissue	3.6
Uterus Pool	2.1	Colon ca. SW1116	9.4
Ovarian ca. OVCAR-3	17.4	Colon ca. Colo-205	8.8
Ovarian ca. SK- OV-3	47.0	Colon ca. SW-48	13.2
Ovarian ca. OVCAR-4	14.7	Colon Pool	5.7
Ovarian ca. OVCAR-5	31.6	Small Intestine Pool	10.2
Ovarian ca. IGROV-1	12.9	Stomach Pool	6.2
Ovarian ca. OVCAR-8	6.7	Bone Marrow Pool	1.3
Ovary	12.5	Fetal Heart	1.1
Breast ca. MCF-7	75.8	Heart Pool	3.4
Breast ca. MDA- MB-231	30.4	Lymph Node Pool	8.7
Breast ca. BT 549	65.5	Fetal Skeletal Muscle	2.3
Breast ca. T47D	100.0	Skeletal Muscle Pool	9.4
Breast ca. MDA-N	33.4	Spleen Pool	4.6
Breast Pool	4.6	Thymus Pool	7.3
Trachea	7.7	CNS cancer (glio/astro) U87-MG	33.9
Lung	4.9	CNS cancer (glio/astro) U-118-MG	27.2
Fetal Lung	7.1	CNS cancer (neuro;met) SK-N-AS	16.0
Lung ca. NCI-N417	9.3	CNS cancer (astro) SF- 539	14.3
Lung ca. LX-1	15.8	CNS cancer (astro) SNB-75	60.7

Lung ca. NCI-H146	4.9	CNS cancer (glio) SNB-19	13.8
Lung ca. SHP-77	16.5	CNS cancer (glio) SF-295	28.5
Lung ca. A549	27.2	Brain (Amygdala) Pool	5.3
Lung ca. NCI-H526	4.1	Brain (cerebellum)	5.0
Lung ca. NCI-H23	15.0	Brain (fetal)	16.4
Lung ca. NCI-H460	9.5	Brain (Hippocampus) Pool	5.5
Lung ca. HOP-62	7.6	Cerebral Cortex Pool	8.7
Lung ca. NCI-H522	18.2	Brain (Substantia nigra) Pool	8.3
Liver	0.0	Brain (Thalamus) Pool	6.3
Fetal Liver	7.3	Brain (whole)	7.0
Liver ca. HepG2	29.5	Spinal Cord Pool	5.6
Kidney Pool	17.7	Adrenal Gland	6.3
Fetal Kidney	4.6	Pituitary gland Pool	0.8
Renal ca. 786-0	17.2	Salivary Gland	5.6
Renal ca. A498	5.1	Thyroid (female)	9.7
Renal ca. ACHN	17.3	Pancreatic ca. CAPAN2	11.7
Renal ca. UO-31	11.1	Pancreas Pool	9.2

CNS_neurodegeneration_v1.0 Summary: Ag3362 Highest expression of the CG58516-01 gene is seen in the occipital cortex of a control patient and the temporal cortex of an Alzheimer's patient. While the CG58516-01 gene does not appear to be preferentially expressed in Alzheimer's disease, this panel confirms expression of the CG58516-01 gene at moderate/high levels in the brain in an additional set of individuals. Please see Panel 1.4 for discussion of potential utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3362 The CG58516-01 gene is widely expressed in this panel, with highest expression in the breast cancer cell line T47D (CT=29). Significant expression is also seen in cell lines derived from prostate, breast and ovarian cancers. In general, expression of the CG58516-01 gene appears to be greater in the cancer cell lines than in normal tissue. Thus, the expression of this gene could be used to distinguish these cell line types from others in the panel.

Among tissues involved in central nervous system function, this gene is expressed at low but significant levels in all brain regions examined. This gene encodes a protein with a putative zinc-finger motif. Since these proteins are known to interact with nucleic acids,

this suggests that this gene product may play a potential role in transcription. Thus, therapeutic modulation of the CG58516-01 gene product may be used to regulate the transcription of disease-related proteins such as ataxin, huntingtin, or various apoptosis cascade proteins.

- 5 Among tissues with metabolic function, this gene is expressed at low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, skeletal muscle, heart, and fetal liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and
- 10 diabetes.

References:

1. Zhu W, Chan EK, Li J, Hemmerich P, Tan EM. (2001) Transcription activating property of autoantigen SG2NA and modulating effect of WD-40 repeats. Exp Cell Res. 269(2):312-21

- 15 **Panel 4D Summary:** Ag3362 Results from one experiment with the CG58516-01 gene are not included because the amp plot corresponding to the run indicates that there were problems with the experiment.

F. CG58473-01: PROTEIN KINASE

- Expression of gene CG58473-01 was assessed using the primer-probe set Ag3357, described in Table FA. Results of the RTQ-PCR runs are shown in Tables FB and FC.
- 20

Table FA. Probe Name Ag3357

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcaagggtggccctaaaattc-3'	21	853	384
Probe	TET-5'-ccaggacctcatctccaagctgctta-3'-TAMRA	26	897	385
Reverse	5'-agccgttctgaggggttat-3'	19	926	386

Table FB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%)	Tissue Name	Rel. Exp.(%)
-------------	--------------	-------------	--------------

	Ag3357, Run 216523477		Ag3357, Run 216523477
Adipose	0.0	Renal ca. TK-10	13.2
Melanoma* Hs688(A).T	0.0	Bladder	7.2
Melanoma* Hs688(B).T	1.1	Gastric ca. (liver met.) NCI-N87	5.4
Melanoma* M14	50.0	Gastric ca. KATO III	49.0
Melanoma* LOXIMVI	33.0	Colon ca. SW-948	14.9
Melanoma* SK- MEL-5	24.7	Colon ca. SW480	95.9
Squamous cell carcinoma SCC-4	11.6	Colon ca.* (SW480 met) SW620	53.6
Testis Pool	8.2	Colon ca. HT29	10.3
Prostate ca.* (bone met) PC-3	3.2	Colon ca. HCT-116	76.3
Prostate Pool	0.0	Colon ca. CaCo-2	14.1
Placenta	2.4	Colon cancer tissue	6.3
Uterus Pool	0.0	Colon ca. SW1116	18.6
Ovarian ca. OVCAR-3	51.1	Colon ca. Colo-205	24.3
Ovarian ca. SK- OV-3	53.2	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	10.4	Colon Pool	4.6
Ovarian ca. OVCAR-5	12.3	Small Intestine Pool	1.7
Ovarian ca. IGROV-1	10.1	Stomach Pool	1.2
Ovarian ca. OVCAR-8	13.4	Bone Marrow Pool	1.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	20.3	Heart Pool	0.0
Breast ca. MDA- MB-231	65.1	Lymph Node Pool	1.4
Breast ca. BT 549	100.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	34.2	Skeletal Muscle Pool	1.6
Breast ca. MDA-N	36.3	Spleen Pool	3.4
Breast Pool	1.3	Thymus Pool	4.7
Trachea	0.0	CNS cancer (glio/astro) U87-MG	7.8
Lung	0.0	CNS cancer (glio/astro) U-118-MG	54.0

Fetal Lung	5.0	CNS cancer (neuro;met) SK-N-AS	7.9
Lung ca. NCI-N417	17.9	CNS cancer (astro) SF-539	22.4
Lung ca. LX-1	28.5	CNS cancer (astro) SNB-75	19.2
Lung ca. NCI-H146	74.7	CNS cancer (glio) SNB-19	14.6
Lung ca. SHP-77	40.6	CNS cancer (glio) SF-295	3.0
Lung ca. A549	64.6	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	23.8	Brain (cerebellum)	0.0
Lung ca. NCI-H23	63.7	Brain (fetal)	0.0
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	2.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	34.4	Brain (Substantia nigra) Pool	2.6
Liver	0.0	Brain (Thalamus) Pool	9.3
Fetal Liver	0.0	Brain (whole)	2.5
Liver ca. HepG2	11.4	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	3.1	Pituitary gland Pool	1.4
Renal ca. 786-0	20.0	Salivary Gland	0.0
Renal ca. A498	3.6	Thyroid (female)	0.0
Renal ca. ACHN	18.9	Pancreatic ca. CAPAN2	20.4
Renal ca. UO-31	10.4	Pancreas Pool	1.3

Table FC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3357, Run 165231196	Tissue Name	Rel. Exp.(%) Ag3357, Run 165231196
Secondary Th1 act	9.0	HUVEC IL-1beta	9.5
Secondary Th2 act	43.2	HUVEC IFN gamma	6.3
Secondary Tr1 act	46.0	HUVEC TNF alpha + IFN gamma	7.3
Secondary Th1 rest	6.7	HUVEC TNF alpha + IL4	25.3
Secondary Th2 rest	12.2	HUVEC IL-11	13.1
Secondary Tr1 rest	1.9	Lung Microvascular EC none	3.3
Primary Th1 act	6.1	Lung Microvascular EC	7.1

		TNFalpha + IL-1beta	
Primary Th2 act	21.8	Microvascular Dermal EC none	10.9
Primary Tr1 act	33.0	Microvascular Dermal EC TNFalpha + IL-1beta	7.3
Primary Th1 rest	28.1	Bronchial epithelium TNFalpha + IL1beta	1.9
Primary Th2 rest	12.1	Small airway epithelium none	3.6
Primary Tr1 rest	29.7	Small airway epithelium TNFalpha + IL-1beta	36.3
CD45RA CD4 lymphocyte act	28.5	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	39.8	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	18.6	Astrocytes rest	1.4
Secondary CD8 lymphocyte rest	26.8	Astrocytes TNFalpha + IL-1beta	1.2
Secondary CD8 lymphocyte act	19.2	KU-812 (Basophil) rest	18.2
CD4 lymphocyte none	10.6	KU-812 (Basophil) PMA/ionomycin	30.4
2ry Th1/Th2/Tr1 _anti- CD95 CH11	15.6	CCD1106 (Keratinocytes) none	18.3
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.7
LAK cells IL-2	42.6	Liver cirrhosis	25.7
LAK cells IL-2+IL-12	24.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	24.8	NCI-H292 none	7.8
LAK cells IL-2+ IL-18	40.3	NCI-H292 IL-4	26.4
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	29.7
NK Cells IL-2 rest	23.5	NCI-H292 IL-13	20.7
Two Way MLR 3 day	13.7	NCI-H292 IFN gamma	27.9
Two Way MLR 5 day	13.2	HPAEC none	8.6
Two Way MLR 7 day	11.7	HPAEC TNF alpha + IL- 1 beta	2.4
PBMC rest	0.0	Lung fibroblast none	5.5
PBMC PWM	52.1	Lung fibroblast TNF alpha + IL-1 beta	2.2
PBMC PHA-L	14.6	Lung fibroblast IL-4	0.0
Ramos (B cell) none	16.5	Lung fibroblast IL-9	0.0
Ramos (B cell)	14.7	Lung fibroblast IL-13	0.0

ionomycin			
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	10.4	Dermal fibroblast CCD1070 rest	40.1
EOL-1 dbcAMP	9.9	Dermal fibroblast CCD1070 TNF alpha	43.8
EOL-1 dbcAMP PMA/ionomycin	13.2	Dermal fibroblast CCD1070 IL-1 beta	23.5
Dendritic cells none	4.7	Dermal fibroblast IFN gamma	3.7
Dendritic cells LPS	1.1	Dermal fibroblast IL-4	4.6
Dendritic cells anti-CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	28.1
Macrophages rest	4.3	Lung	59.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	28.3	Kidney	10.0
HUVEC starved	25.3		

CNS_neurodegeneration_v1.0 Summary: Ag3357 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3357 This gene is primarily expressed in cancer cell lines, with highest expression in a breast cancer cell line BT 549(CT=32.8).

- 5 This gene is expressed in the following cell lines but not the corresponding healthy tissue: gastric, brain, colon, lung, breast, ovarian cancer and melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.
- 10 **Panel 4D Summary:** Ag3357 Highest expression of the CG58473-01 gene is seen in pokeweed mitogen-activated purified peripheral blood B lymphocytes (CT=33.2). In addition, no expression of the transcript is seen in PBMC that contain normal B cells, but the transcript is induced when PBMC are treated with the B cell selective pokeweed mitogen. The transcript is not seen in the B cell lymphoma cell line Ramos regardless of
- 15 stimulation. Thus, the putative protein encoded by this gene could potentially be used diagnostically to identify activated B cells. Therefore, therapeutics that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the

symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

5 **G. CG58470-01: UDP-N-ACETYLHEXOSAMINE PYROPHOSPHORYLASE**

Expression of gene CG58470-01 was assessed using the primer-probe set Ag5940, described in Table GA.

Table GA. Probe Name Ag5940

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atatacctgaagctacaacagtttagct-3'	26	422	387
Probe	TET-5'-tggaacaaatgcattattccatattacg-3'-TAMRA	29	459	388
Reverse	5'-gagtgaactcgctgggtcatg-3'	20	489	389

- 10 **General_screening_panel_v1.5 Summary:** Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 5 Islet Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

H. CG58593-01: UBIQUITIN-52

- 15 Expression of gene CG58593-01 was assessed using the primer-probe set Ag3421, described in Table HA.

Table HA. Probe Name Ag3421

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atctgctgcaagtgcattatgc-3'	20	291	390
Probe	TET-5'-cggtgctatcaactgccacaagaaga-3'-TAMRA	26	323	391
Reverse	5'-tgaccttcttctctgggggtac-3'	20	371	392

CNS_neurodegeneration_v1.0 Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

- 5 **Panel 4D Summary:** Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

I. CG57871-01: TOUSLED-LIKE KINASE

Expression of gene CG57871-01 was assessed using the primer-probe set Ag3351, described in Table IA. Results of the RTQ-PCR runs are shown in Tables IB and IC.

10 **Table IA.** Probe Name Ag3351

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gacccctcactgcaacattcttt-3'	22	346	393
Probe	TET-5'-aatcccttaccgcgacgagtagaaca-3'-TAMRA	26	372	394
Reverse	5'-gcactgccatctaaaccataga-3'	22	403	395

Table IB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3351, Run 210141594	Tissue Name	Rel. Exp.(%) Ag3351, Run 210141594
AD 1 Hippo	10.4	Control (Path) 3 Temporal Ctx	3.0
AD 2 Hippo	33.4	Control (Path) 4 Temporal Ctx	65.1
AD 3 Hippo	5.5	AD 1 Occipital Ctx	20.2
AD 4 Hippo	8.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	3.8
AD 6 Hippo	33.4	AD 4 Occipital Ctx	45.1
Control 2 Hippo	29.9	AD 5 Occipital Ctx	15.2
Control 4 Hippo	6.7	AD 6 Occipital Ctx	46.7

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Control (Path) 3 Hippo	3.7	Control 1 Occipital Ctx	2.7
AD 1 Temporal Ctx	16.8	Control 2 Occipital Ctx	52.5
AD 2 Temporal Ctx	45.1	Control 3 Occipital Ctx	45.4
AD 3 Temporal Ctx	6.9	Control 4 Occipital Ctx	6.3
AD 4 Temporal Ctx	54.0	Control (Path) 1 Occipital Ctx	79.0
AD 5 Inf Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	34.4
AD 5 Sup Temporal Ctx	13.0	Control (Path) 3 Occipital Ctx	0.8
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	40.6
AD 6 Sup Temporal Ctx	56.6	Control 1 Parietal Ctx	6.9
Control 1 Temporal Ctx	6.2	Control 2 Parietal Ctx	48.0
Control 2 Temporal Ctx	29.3	Control 3 Parietal Ctx	26.1
Control 3 Temporal Ctx	32.8	Control (Path) 1 Parietal Ctx	73.7
Control 4 Temporal Ctx	13.9	Control (Path) 2 Parietal Ctx	57.4
Control (Path) 1 Temporal Ctx	79.6	Control (Path) 3 Parietal Ctx	3.4
Control (Path) 2 Temporal Ctx	97.3	Control (Path) 4 Parietal Ctx	78.5

Table IC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3351, Run 165222896	Tissue Name	Rel. Exp.(%) Ag3351, Run 165222896
Secondary Th1 act	16.5	HUVEC IL-1beta	15.4
Secondary Th2 act	26.4	HUVEC IFN gamma	13.5
Secondary Tr1 act	23.3	HUVEC TNF alpha + IFN gamma	17.0
Secondary Th1 rest	6.0	HUVEC TNF alpha + IL4	11.0
Secondary Th2 rest	10.7	HUVEC IL-11	5.4
Secondary Tr1 rest	2.1	Lung Microvascular EC none	12.4

Primary Th1 act	19.2	Lung Microvascular EC TNFalpha + IL-1beta	9.6
Primary Th2 act	17.6	Microvascular Dermal EC none	14.7
Primary Tr1 act	36.1	Microvascular Dermal EC TNFalpha + IL-1beta	14.8
Primary Th1 rest	55.5	Bronchial epithelium TNFalpha + IL1beta	14.1
Primary Th2 rest	43.8	Small airway epithelium none	7.7
Primary Tr1 rest	15.9	Small airway epithelium TNFalpha + IL-1beta	50.3
CD45RA CD4 lymphocyte act	13.0	Coronary artery SMC rest	15.6
CD45RO CD4 lymphocyte act	21.0	Coronary artery SMC TNFalpha + IL-1beta	6.1
CD8 lymphocyte act	12.9	Astrocytes rest	11.5
Secondary CD8 lymphocyte rest	14.9	Astrocytes TNFalpha + IL-1beta	11.8
Secondary CD8 lymphocyte act	14.8	KU-812 (Basophil) rest	19.2
CD4 lymphocyte none	10.7	KU-812 (Basophil) PMA/ionomycin	54.0
2ry Th1/Th2/Tr1 _anti- CD95 CH11	12.7	CCD1106 (Keratinocytes) none	12.2
LAK cells rest	17.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.0
LAK cells IL-2	22.4	Liver cirrhosis	7.4
LAK cells IL-2+IL-12	20.4	Lupus kidney	3.4
LAK cells IL-2+IFN gamma	37.9	NCI-H292 none	47.6
LAK cells IL-2+ IL-18	18.6	NCI-H292 IL-4	42.3
LAK cells PMA/ionomycin	10.5	NCI-H292 IL-9	30.4
NK Cells IL-2 rest	17.8	NCI-H292 IL-13	15.7
Two Way MLR 3 day	33.2	NCI-H292 IFN gamma	25.5
Two Way MLR 5 day	10.6	HPAEC none	13.5
Two Way MLR 7 day	9.9	HPAEC TNF alpha + IL- 1 beta	17.7
PBMC rest	12.8	Lung fibroblast none	11.5
PBMC PWM	63.3	Lung fibroblast TNF alpha + IL-1 beta	12.4
PBMC PHA-L	18.0	Lung fibroblast IL-4	31.2
Ramos (B cell) none	14.0	Lung fibroblast IL-9	22.2

Ramos (B cell) ionomycin	77.9	Lung fibroblast IL-13	27.4
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	44.8
B lymphocytes CD40L and IL-4	30.8	Dermal fibroblast CCD1070 rest	33.7
EOL-1 dbcAMP	11.3	Dermal fibroblast CCD1070 TNF alpha	50.0
EOL-1 dbcAMP PMA/ionomycin	13.7	Dermal fibroblast CCD1070 IL-1 beta	13.4
Dendritic cells none	14.7	Dermal fibroblast IFN gamma	14.3
Dendritic cells LPS	19.8	Dermal fibroblast IL-4	25.7
Dendritic cells anti-CD40	14.2	IBD Colitis 2	2.0
Monocytes rest	22.5	IBD Crohn's	3.2
Monocytes LPS	32.8	Colon	26.8
Macrophages rest	31.0	Lung	14.6
Macrophages LPS	30.8	Thymus	28.7
HUVEC none	18.3	Kidney	45.4
HUVEC starved	45.7		

- CNS_neurodegeneration_v1.0 Summary:** Ag3351 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. While no differential expression of this gene is detected between Alzheimer's diseased postmortem brains and those of non-demented controls, the widespread expression of this gene in the brain suggests that therapeutic modulation of the expression or function of this gene may be effective in the treatment of neurologic disorders such as Parkinson's disease, epilepsy, stroke and multiple sclerosis.

General_screening_panel_v1.4 Summary: Ag3351 - Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

- Panel 4D Summary:** Ag3351 The CG57871-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This

		Ctx	
Control (Path) 3 Hippo	8.4	Control 1 Occipital Ctx	4.2
AD 1 Temporal Ctx	17.6	Control 2 Occipital Ctx	65.5
AD 2 Temporal Ctx	25.3	Control 3 Occipital Ctx	13.4
AD 3 Temporal Ctx	4.9	Control 4 Occipital Ctx	6.4
AD 4 Temporal Ctx	17.4	Control (Path) 1 Occipital Ctx	78.5
AD 5 Inf Temporal Ctx	81.8	Control (Path) 2 Occipital Ctx	9.4
AD 5 Sup Temporal Ctx	42.9	Control (Path) 3 Occipital Ctx	3.2
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	9.9
AD 6 Sup Temporal Ctx	53.6	Control 1 Parietal Ctx	6.0
Control 1 Temporal Ctx	5.7	Control 2 Parietal Ctx	37.1
Control 2 Temporal Ctx	34.6	Control 3 Parietal Ctx	16.5
Control 3 Temporal Ctx	10.2	Control (Path) 1 Parietal Ctx	67.4
Control 4 Temporal Ctx	7.1	Control (Path) 2 Parietal Ctx	18.7
Control (Path) 1 Temporal Ctx	41.5	Control (Path) 3 Parietal Ctx	3.3
Control (Path) 2 Temporal Ctx	29.5	Control (Path) 4 Parietal Ctx	34.4

Table JC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3380, Run 217043276	Tissue Name	Rel. Exp.(%) Ag3380, Run 217043276
Adipose	9.0	Renal ca. TK-10	25.5
Melanoma* Hs688(A).T	18.9	Bladder	15.9
Melanoma* Hs688(B).T	16.8	Gastric ca. (liver met.) NCI-N87	52.5
Melanoma* M14	14.9	Gastric ca. KATO III	34.6
Melanoma* LOXIMVI	21.6	Colon ca. SW-948	4.9

Melanoma* SK-MEL-5	27.0	Colon ca. SW480	82.4
Squamous cell carcinoma SCC-4	28.7	Colon ca.* (SW480 met) SW620	20.6
Testis Pool	5.1	Colon ca. HT29	9.2
Prostate ca.* (bone met) PC-3	59.9	Colon ca. HCT-116	20.6
Prostate Pool	8.6	Colon ca. CaCo-2	22.8
Placenta	3.9	Colon cancer tissue	10.1
Uterus Pool	1.9	Colon ca. SW1116	6.2
Ovarian ca. OVCAR-3	32.5	Colon ca. Colo-205	4.9
Ovarian ca. SK-OV-3	57.4	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	14.7	Colon Pool	11.4
Ovarian ca. OVCAR-5	59.5	Small Intestine Pool	9.8
Ovarian ca. IGROV-1	13.1	Stomach Pool	7.4
Ovarian ca. OVCAR-8	19.2	Bone Marrow Pool	4.2
Ovary	5.9	Fetal Heart	6.3
Breast ca. MCF-7	35.1	Heart Pool	4.9
Breast ca. MDA-MB-231	58.2	Lymph Node Pool	11.4
Breast ca. BT 549	26.8	Fetal Skeletal Muscle	3.3
Breast ca. T47D	100.0	Skeletal Muscle Pool	8.1
Breast ca. MDA-N	8.7	Spleen Pool	5.6
Breast Pool	10.4	Thymus Pool	6.3
Trachea	5.5	CNS cancer (glio/astro) U87-MG	39.2
Lung	3.8	CNS cancer (glio/astro) U-118-MG	54.7
Fetal Lung	11.8	CNS cancer (neuro;met) SK-N-AS	19.6
Lung ca. NCI-N417	3.2	CNS cancer (astro) SF-539	12.2
Lung ca. LX-1	20.7	CNS cancer (astro) SNB-75	29.7
Lung ca. NCI-H146	3.8	CNS cancer (glio) SNB-19	13.4
Lung ca. SHP-77	17.9	CNS cancer (glio) SF-295	28.9
Lung ca. A549	30.6	Brain (Amygdala) Pool	11.8

Lung ca. NCI-H526	3.6	Brain (cerebellum)	6.0
Lung ca. NCI-H23	29.3	Brain (fetal)	8.4
Lung ca. NCI-H460	14.8	Brain (Hippocampus) Pool	14.5
Lung ca. HOP-62	19.5	Cerebral Cortex Pool	16.2
Lung ca. NCI-H522	28.7	Brain (Substantia nigra) Pool	16.0
Liver	0.4	Brain (Thalamus) Pool	22.7
Fetal Liver	11.9	Brain (whole)	5.9
Liver ca. HepG2	12.9	Spinal Cord Pool	16.0
Kidney Pool	18.4	Adrenal Gland	5.1
Fetal Kidney	22.8	Pituitary gland Pool	3.8
Renal ca. 786-0	28.5	Salivary Gland	2.1
Renal ca. A498	5.0	Thyroid (female)	8.2
Renal ca. ACHN	22.4	Pancreatic ca. CAPAN2	51.4
Renal ca. UO-31	36.9	Pancreas Pool	12.3

Table JD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3380, Run 165296532	Tissue Name	Rel. Exp.(%) Ag3380, Run 165296532
Secondary Th1 act	13.1	HUVEC IL-1beta	15.0
Secondary Th2 act	14.6	HUVEC IFN gamma	19.6
Secondary Tr1 act	15.2	HUVEC TNF alpha + IFN gamma	28.3
Secondary Th1 rest	4.6	HUVEC TNF alpha + IL4	26.1
Secondary Th2 rest	4.7	HUVEC IL-11	7.8
Secondary Tr1 rest	8.0	Lung Microvascular EC none	25.5
Primary Th1 act	14.9	Lung Microvascular EC TNFalpha + IL-1beta	19.5
Primary Th2 act	13.2	Microvascular Dermal EC none	37.9
Primary Tr1 act	20.7	Microvascular Dermal EC TNFalpha + IL-1beta	24.8
Primary Th1 rest	35.6	Bronchial epithelium TNFalpha + IL1beta	37.1
Primary Th2 rest	24.0	Small airway epithelium none	15.0
Primary Tr1 rest	16.2	Small airway epithelium TNFalpha + IL-1beta	100.0

CD45RO CD4 lymphocyte act	23.3	Coronary artery SMC rest	30.1
CD45RO CD4 lymphocyte act	18.2	Coronary artery SMC TNFalpha + IL-1beta	13.6
CD8 lymphocyte act	7.4	Astrocytes rest	22.5
Secondary CD8 lymphocyte rest	13.4	Astrocytes TNFalpha + IL-1beta	21.2
Secondary CD8 lymphocyte act	4.4	KU-812 (Basophil) rest	17.9
CD4 lymphocyte none	8.0	KU-812 (Basophil) PMA/ionomycin	68.3
2ry Th1/Th2/Tr1_anti-CD95 CH11	10.7	CCD1106 (Keratinocytes) none	22.1
LAK cells rest	13.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.2
LAK cells IL-2	12.9	Liver cirrhosis	3.1
LAK cells IL-2+IL-12	13.2	Lupus kidney	2.9
LAK cells IL-2+IFN gamma	15.6	NCI-H292 none	48.6
LAK cells IL-2+ IL-18	17.0	NCI-H292 IL-4	66.9
LAK cells PMA/ionomycin	9.5	NCI-H292 IL-9	59.5
NK Cells IL-2 rest	7.0	NCI-H292 IL-13	36.6
Two Way MLR 3 day	15.2	NCI-H292 IFN gamma	42.6
Two Way MLR 5 day	7.0	HPAEC none	14.3
Two Way MLR 7 day	9.6	HPAEC TNF alpha + IL-1 beta	25.9
PBMC rest	6.4	Lung fibroblast none	12.5
PBMC PWM	60.7	Lung fibroblast TNF alpha + IL-1 beta	11.0
PBMC PHA-L	18.8	Lung fibroblast IL-4	25.9
Ramos (B cell) none	31.9	Lung fibroblast IL-9	20.6
Ramos (B cell) ionomycin	94.0	Lung fibroblast IL-13	18.8
B lymphocytes PWM	42.9	Lung fibroblast IFN gamma	23.3
B lymphocytes CD40L and IL-4	24.7	Dermal fibroblast CCD1070 rest	59.5
EOL-1 dbcAMP	12.9	Dermal fibroblast CCD1070 TNF alpha	64.2
EOL-1 dbcAMP PMA/ionomycin	10.4	Dermal fibroblast CCD1070 IL-1 beta	32.8
Dendritic cells none	19.6	Dermal fibroblast IFN gamma	10.7

Dendritic cells LPS	10.7	Dermal fibroblast IL-4	21.6
Dendritic cells anti-CD40	18.8	IBD Colitis 2	2.0
Monocytes rest	15.0	IBD Crohn's	3.6
Monocytes LPS	13.8	Colon	36.9
Macrophages rest	25.3	Lung	19.3
Macrophages LPS	8.1	Thymus	72.2
HUVEC none	19.9	Kidney	24.5
HUVEC starved	35.8		

CNS_neurodegeneration_v1.0 Summary: Ag3380 This panel does not show differential expression of the CG58590-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

- 5 **General_screening_panel_v1.4 Summary:** Ag3380 - This gene is expressed at low to moderate levels in all samples on this pattern. The highest level of expression is seen in breast cancer cell line T47D (CT=27.8). Based on expression in this panel, this gene may be involved in brain, colon, renal, lung, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these
- 10 cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

- This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and fetal liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis,
- 15 and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes. Furthermore, this gene is more highly expressed in fetal (CT=30.9) liver when compared to expression in the adult (CT>35) and may be useful for the differentiation of the fetal and adult sources of this tissue.

- In addition, this gene is expressed at moderate levels in the all regions of the CNS
- 20 examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3380 - This gene is expressed from moderate to low levels across all of the samples on this panel. The highest expression is seen in small airway epithelium treated with TNFalpha and IL-1beta (CT=28.7). Interestingly, expression is much lower in untreated small airway epithelium (CT=31.5). There is also a significant difference
 5 between mononuclear cells treated with PWM (CT=29.5) and untreated cells (CT=32.7). Therefore, expression of this gene can be used to differentiate treated and untreated samples.

Expression of this gene is detected at a moderate level (CT=30.2) in normal colon (similar levels for colon are seen on panel 1.4 (CT=30.9), but is significantly lower in the
 10 IBD Colitis 2 (CT=34.4) and IBD Crohn's (CT=33.5) samples. Therefore, therapies designed with the protein encoded for by this gene may potentially modulate colon function and play a role in the identification and treatment of inflammatory or autoimmune diseases which effect the colon including Crohn's disease and ulcerative colitis.

15 **K. CG58572-01 and CG58572-02: GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE**

Expression of gene CG58572-01 and full length clone CG58572-02 was assessed using the primer-probe set Ag3375, described in Table KA. Results of the RTQ-PCR runs are shown in Tables KB, KC and KD.

Table KA. Probe Name Ag3375

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - aagaagtggactggagtcagaa - 3'	22	58	399
Probe	TET- 5' - tacatctttctccagccatttcccca - 3' - TAMRA	26	86	400
Reverse	5' - agcagtacaaagaggcctcaa - 3'	21	135	401

20 Table KB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3375, Run 210154239	Tissue Name	Rel. Exp.(%) Ag3375, Run 210154239
AD 1 Hippo	17.1	Control (Path) 3 Temporal Ctx	4.8
AD 2 Hippo	19.3	Control (Path) 4 Temporal Ctx	27.5
AD 3 Hippo	7.4	AD 1 Occipital Ctx	11.5

AD 4 Hippo	4.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	72.2	AD 3 Occipital Ctx	5.9
AD 6 Hippo	53.6	AD 4 Occipital Ctx	12.7
Control 2 Hippo	20.3	AD 5 Occipital Ctx	26.6
Control 4 Hippo	6.8	AD 6 Occipital Ctx	19.8
Control (Path) 3 Hippo	5.5	Control 1 Occipital Ctx	3.2
AD 1 Temporal Ctx	11.6	Control 2 Occipital Ctx	36.1
AD 2 Temporal Ctx	23.8	Control 3 Occipital Ctx	7.4
AD 3 Temporal Ctx	5.5	Control 4 Occipital Ctx	4.1
AD 4 Temporal Ctx	16.5	Control (Path) 1 Occipital Ctx	66.0
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	8.2
AD 5 Sup Temporal Ctx	55.9	Control (Path) 3 Occipital Ctx	1.9
AD 6 Inf Temporal Ctx	37.9	Control (Path) 4 Occipital Ctx	12.2
AD 6 Sup Temporal Ctx	59.5	Control 1 Parietal Ctx	2.4
Control 1 Temporal Ctx	3.5	Control 2 Parietal Ctx	31.6
Control 2 Temporal Ctx	25.3	Control 3 Parietal Ctx	11.7
Control 3 Temporal Ctx	8.2	Control (Path) 1 Parietal Ctx	49.7
Control 3 Temporal Ctx	4.0	Control (Path) 2 Parietal Ctx	15.4
Control (Path) 1 Temporal Ctx	52.9	Control (Path) 3 Parietal Ctx	4.2
Control (Path) 2 Temporal Ctx	26.6	Control (Path) 4 Parietal Ctx	32.5

Table KC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3375, Run 165674233	Tissue Name	Rel. Exp.(%) Ag3375, Run 165674233
Liver adenocarcinoma	51.8	Kidney (fetal)	9.7
Pancreas	9.3	Renal ca. 786-0	19.6
Pancreatic ca. CAPAN	52.1	Renal ca. A498	26.2

2			
Adrenal gland	8.9	Renal ca. RXF 393	15.7
Thyroid	6.3	Renal ca. ACHN	8.2
Salivary gland	18.3	Renal ca. UO-31	35.4
Pituitary gland	15.1	Renal ca. TK-10	9.8
Brain (fetal)	15.5	Liver	20.4
Brain (whole)	34.6	Liver (fetal)	16.5
Brain (amygdala)	16.0	Liver ca. (hepatoblast) HepG2	49.0
Brain (cerebellum)	34.2	Lung	4.5
Brain (hippocampus)	12.1	Lung (fetal)	5.4
Brain (substantia nigra)	12.8	Lung ca. (small cell) LX-1	32.3
Brain (thalamus)	17.9	Lung ca. (small cell) NCI-H69	17.3
Cerebral Cortex	10.4	Lung ca. (s.cell var.) SHP-77	30.1
Spinal cord	13.3	Lung ca. (large cell)NCI-H460	66.4
glio/astro U87-MG	14.8	Lung ca. (non-sm. cell) A549	19.1
glio/astro U-118-MG	95.3	Lung ca. (non-s.cell) NCI-H23	13.8
Astrocytoma SW1783	42.0	Lung ca. (non-s.cell) HOP-62	18.7
neuro*; met SK-N-AS	47.0	Lung ca. (non-s.cl) NCI-H522	19.5
Astrocytoma SF-539	11.4	Lung ca. (squam.) SW 900	9.9
Astrocytoma SNB-75	15.6	Lung ca. (squam.) NCI-H596	19.6
glioma SNB-19	11.8	Mammary gland	14.6
glioma U251	40.9	Breast ca.* (pl.ef) MCF-7	81.2
glioma SF-295	10.1	Breast ca.* (pl.ef) MDA-MB-231	91.4
Heart (fetal)	1.3	Breast ca.* (pl.ef) T47D	35.4
Heart	4.7	Breast ca. BT-549	97.9
Skeletal muscle (fetal)	1.2	Breast ca. MDA-N	14.8
Skeletal muscle	38.7	Ovary	1.6
Bone marrow	4.6	Ovarian ca. OVCAR-3	39.2
Thymus	2.7	Ovarian ca.	23.0

		OVCAR-4	
Spleen	7.9	Ovarian ca. OVCAR-5	13.8
Lymph node	13.0	Ovarian ca. OVCAR-8	8.5
Colorectal	3.3	Ovarian ca. IGROV-1	5.6
Stomach	27.7	Ovarian ca.* (ascites) SK-OV-3	44.8
Small intestine	19.3	Uterus	19.5
Colon ca. SW480	16.5	Placenta	2.6
Colon ca.* SW620(SW480 met)	29.1	Prostate	15.6
Colon ca. HT29	13.8	Prostate ca.* (bone met)PC-3	56.6
Colon ca. HCT-116	27.7	Testis	40.6
Colon ca. CaCo-2	17.4	Melanoma Hs688(A).T	5.5
Colon ca. tissue(ODO3866)	26.4	Melanoma* (met) Hs688(B).T	8.9
Colon ca. HCC-2998	32.1	Melanoma UACC-62	17.8
Gastric ca.* (liver met) NCI-N87	100.0	Melanoma M14	27.7
Bladder	28.7	Melanoma LOX IMVI	6.6
Trachea	9.4	Melanoma* (met) SK-MEL-5	13.0
Kidney	9.0	Adipose	8.0

Table KD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3375, Run 165296547	Tissue Name	Rel. Exp.(%) Ag3375, Run 165296547
Secondary Th1 act	14.6	HUVEC IL-1beta	24.5
Secondary Th2 act	13.0	HUVEC IFN gamma	24.5
Secondary Tr1 act	17.3	HUVEC TNF alpha + IFN gamma	24.0
Secondary Th1 rest	0.9	HUVEC TNF alpha + IL4	23.2
Secondary Th2 rest	1.5	HUVEC IL-11	12.1
Secondary Tr1 rest	2.9	Lung Microvascular EC none	21.3
Primary Th1 act	16.0	Lung Microvascular EC	24.1

		TNFalpha + IL-1beta	
Primary Th2 act	12.1	Microvascular Dermal EC none	27.4
Primary Tr1 act	25.0	Microvascular Dermal EC TNFalpha + IL-1beta	24.0
Primary Th1 rest	10.4	Bronchial epithelium TNFalpha + IL1beta	20.3
Primary Th2 rest	6.1	Small airway epithelium none	11.3
Primary Tr1 rest	9.0	Small airway epithelium TNFalpha + IL-1beta	54.0
CD45RA CD4 lymphocyte act	14.6	Coronary artery SMC rest	23.5
CD45RO CD4 lymphocyte act	13.6	Coronary artery SMC TNFalpha + IL-1beta	12.0
CD8 lymphocyte act	14.2	Astrocytes rest	5.3
Secondary CD8 lymphocyte rest	14.4	Astrocytes TNFalpha + IL-1beta	5.4
Secondary CD8 lymphocyte act	5.8	KU-812 (Basophil) rest	19.5
CD4 lymphocyte none	2.4	KU-812 (Basophil) PMA/ionomycin	56.3
2ry Th1/Th2/Tr1 _anti- CD95 CH11	2.6	CCD1106 (Keratinocytes) none	26.6
LAK cells rest	5.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.8
LAK cells IL-2	10.7	Liver cirrhosis	2.6
LAK cells IL-2+IL-12	12.5	Lupus kidney	0.8
LAK cells IL-2+IFN gamma	20.2	NCI-H292 none	28.7
LAK cells IL-2+ IL-18	16.6	NCI-H292 IL-4	54.7
LAK cells PMA/ionomycin	12.5	NCI-H292 IL-9	45.7
NK Cells IL-2 rest	7.1	NCI-H292 IL-13	24.3
Two Way MLR 3 day	6.8	NCI-H292 IFN gamma	33.2
Two Way MLR 5 day	8.9	HPAEC none	17.8
Two Way MLR 7 day	6.0	HPAEC TNF alpha + IL- 1 beta	30.1
PBMC rest	0.8	Lung fibroblast none	10.2
PBMC PWM	42.3	Lung fibroblast TNF alpha + IL-1 beta	6.3
PBMC PHA-L	11.6	Lung fibroblast IL-4	27.2
Ramos (B cell) none	30.6	Lung fibroblast IL-9	26.8
Ramos (B cell)	100.0	Lung fibroblast IL-13	21.8

ionomycin			
B lymphocytes PWM	77.4	Lung fibroblast IFN gamma	29.5
B lymphocytes CD40L and IL-4	12.2	Dermal fibroblast CCD1070 rest	42.3
EOL-1 dbcAMP	13.0	Dermal fibroblast CCD1070 TNF alpha	51.4
EOL-1 dbcAMP PMA/ionomycin	6.9	Dermal fibroblast CCD1070 IL-1 beta	22.5
Dendritic cells none	4.5	Dermal fibroblast IFN gamma	11.1
Dendritic cells LPS	3.8	Dermal fibroblast IL-4	19.5
Dendritic cells anti-CD40	2.9	IBD Colitis 2	0.7
Monocytes rest	2.2	IBD Crohn's	0.9
Monocytes LPS	1.3	Colon	7.6
Macrophages rest	6.6	Lung	6.2
Macrophages LPS	2.7	Thymus	9.4
HUVEC none	17.4	Kidney	4.2
HUVEC starved	37.4		

CNS_neurodegeneration_v1.0 Summary: Ag3375 This panel does not show differential expression of the CG58572-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

- 5 **Panel 1.3D Summary:** Ag3375 - This gene is expressed at moderate to low levels in all samples on this panel, with the highest expression in gastric cancer cell line NCI-N87 (CT=28.8). Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the
- 10 presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene might be of use in the treatment of these cancers.

- This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis,
- 15 and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3375 The CG58572-01 gene is ubiquitously expressed on this panel, with highest expression in the B cell line Ramos treated with ionomycin (CT=26.2). Significant levels of expression are also seen in pokeweed mitogen-activated B lymphocytes. Therefore, therapies that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

Interestingly, there is a difference between the levels of expression in resting and activated secondary T cells. The level in activated secondary T cells (CT=28.7-29.2) appears to be higher than in resting T cells (CT=31.3-33.1). Therefore, therapeutics designed with the protein encoded by this transcript could be important in the regulation of T cell function.

L. CG58564-01 and CG58564-02: PROTEIN TYROSINE PHOSPHATASE -

Expression of gene CG58564-01 and full length clone CG58564-02 was assessed using the primer-probe sets Ag3023 and Ag3373, described in Tables LA and LB. Results of the RTQ-PCR runs are shown in Tables LC, LD, LE and LF.

Table LA. Probe Name Ag3023

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - ctaatgctggatttgtccatca - 3'	22	492	402
Probe	TET-5' - tcaggaatatgaagccatctacctagca - 3' - TAMRA	28	517	403
Reverse	5' - tggagtgggtgacatcatctgta - 3'	22	555	404

Table LB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-atttgatccatcaacttcaggaa-3'	22	502	405
Probe	TET-5'-tgaagccatctacctagcaaaattaaca-3'-TAMRA	28	526	406
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	555	407

Table LC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	60.7	57.8	AD 3 Occipital Ctx	14.7	15.0
AD 6 Hippo	80.7	72.2	AD 4 Occipital Ctx	35.4	22.4
Control 2 Hippo	35.8	38.4	AD 5 Occipital Ctx	3.9	30.4
Control 4 Hippo	16.5	11.7	AD 6 Occipital Ctx	46.0	37.4
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal	9.5	13.2	Control 4	13.3	13.3

Ctx			Occipital Ctx		
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 Sup Temporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
Control 3 Temporal Ctx	20.3	20.0	Control (Path) 1 Parietal Ctx	74.7	64.2
Control 4 Temporal Ctx	9.7	9.9	Control (Path) 2 Parietal Ctx	28.9	59.9
Control (Path) 1 Temporal Ctx	59.9	68.3	Control (Path) 3 Parietal Ctx	10.2	9.0
Control (Path) 2 Temporal Ctx	40.3	41.2	Control (Path) 4 Parietal Ctx	44.8	43.8

Table LD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3

Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK-MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK-OV-3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV-1	10.9	Stomach Pool	9.9
Ovarian ca. OVCAR-8	9.2	Bone Marrow Pool	11.6
Ovary	9.7	Fetal Heart	20.7
Breast ca. MCF-7	37.6	Heart Pool	10.6
Breast ca. MDA-MB-231	37.1	Lymph Node Pool	17.9
Breast ca. BT 549	62.4	Fetal Skeletal Muscle	12.3
Breast ca. T47D	61.1	Skeletal Muscle Pool	16.0
Breast ca. MDA-N	10.0	Spleen Pool	11.6
Breast Pool	17.3	Thymus Pool	12.2
Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF-539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3

Lung ca. SHP-77	18.6	CNS cancer (glio) SF-295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table LE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931	Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931
Liver adenocarcinoma	51.1	Kidney (fetal)	26.2
Pancreas	6.1	Renal ca. 786-0	34.2
Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6
Adrenal gland	3.8	Renal ca. RXF 393	17.2
Thyroid	3.0	Renal ca. ACHN	13.5
Salivary gland	3.9	Renal ca. UO-31	0.0
Pituitary gland	3.6	Renal ca. TK-10	23.0
Brain (fetal)	8.1	Liver	11.7
Brain (whole)	8.5	Liver (fetal)	8.0
Brain (amygdala)	6.7	Liver ca. (hepatoblast) HepG2	26.2
Brain (cerebellum)	15.2	Lung	3.1
Brain (hippocampus)	5.4	Lung (fetal)	11.0
Brain (substantia nigra)	9.0	Lung ca. (small cell) LX-1	12.9
Brain (thalamus)	4.2	Lung ca. (small cell)	9.9

		NCI-H69	
Cerebral Cortex	2.0	Lung ca. (s.cell var.) SHP-77	67.8
Spinal cord	6.9	Lung ca. (large cell)NCI-H460	3.4
glio/astro U87-MG	28.5	Lung ca. (non-sm. cell) A549	45.1
glio/astro U-118-MG	46.7	Lung ca. (non-s.cell) NCI-H23	22.7
astrocytoma SW1783	40.6	Lung ca. (non-s.cell) HOP-62	25.7
neuro*; met SK-N-AS	27.2	Lung ca. (non-s.cl) NCI-H522	38.2
astrocytoma SF-539	29.7	Lung ca. (squam.) SW 900	27.4
astrocytoma SNB-75	35.1	Lung ca. (squam.) NCI-H596	29.9
glioma SNB-19	15.6	Mammary gland	5.1
glioma U251	37.9	Breast ca.* (pl.ef) MCF-7	47.0
glioma SF-295	18.4	Breast ca.* (pl.ef) MDA-MB-231	22.7
Heart (fetal)	2.9	Breast ca.* (pl.ef) T47D	86.5
Heart	12.9	Breast ca. BT-549	15.9
Skeletal muscle (fetal)	3.4	Breast ca. MDA-N	10.4
Skeletal muscle	36.3	Ovary	2.9
Bone marrow	4.5	Ovarian ca. OVCAR-3	26.1
Thymus	14.3	Ovarian ca. OVCAR-4	16.3
Spleen	8.7	Ovarian ca. OVCAR-5	83.5
Lymph node	11.8	Ovarian ca. OVCAR-8	9.3
Colorectal	10.4	Ovarian ca. IGROV- 1	12.0
Stomach	7.8	Ovarian ca.* (ascites) SK-OV-3	100.0
Small intestine	5.1	Uterus	4.9
Colon ca. SW480	19.3	Placenta	1.3
Colon ca.* SW620(SW480 met)	42.9	Prostate	3.9
Colon ca. HT29	9.9	Prostate ca.* (bone met)PC-3	78.5

Colon ca. HCT-116	26.2	Testis	9.7
Colon ca. CaCo-2	41.5	Melanoma Hs688(A).T	5.9
Colon ca. tissue(ODO3866)	6.3	Melanoma* (met) Hs688(B).T	14.2
Colon ca. HCC-2998	16.0	Melanoma UACC-62	14.0
Gastric ca.* (liver met) NCI-N87	18.8	Melanoma M14	5.7
Bladder	30.6	Melanoma LOX IMVI	8.8
Trachea	3.2	Melanoma* (met) SK-MEL-5	14.7
Kidney	9.6	Adipose	18.9

Table LF. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617	Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617
Secondary Th1 act	18.6	17.9	HUVEC IL-1beta	20.3	18.6
Secondary Th2 act	24.3	28.5	HUVEC IFN gamma	25.3	22.7
Secondary Tr1 act	22.8	21.8	HUVEC TNF alpha + IFN gamma	16.3	18.0
Secondary Th1 rest	7.5	6.8	HUVEC TNF alpha + IL4	18.2	13.4
Secondary Th2 rest	11.6	9.5	HUVEC IL-11	13.7	9.9
Secondary Tr1 rest	12.1	10.7	Lung Microvascular EC none	25.7	21.6
Primary Th1 act	20.7	16.5	Lung Microvascular EC TNFalpha + IL-1beta	26.2	18.3
Primary Th2 act	20.2	19.3	Microvascular Dermal EC none	27.5	21.3
Primary Tr1 act	23.3	27.7	Microvascular Dermal EC TNFalpha + IL-1beta	20.7	19.9
Primary Th1 rest	51.1	51.4	Bronchial epithelium	13.0	16.3

			TNFalpha + IL1beta		
Primary Th2 rest	26.2	29.5	Small airway epithelium none	8.1	8.5
Primary Tr1 rest	23.7	26.1	Small airway epithelium TNFalpha + IL-1beta	50.3	39.8
CD45RA CD4 lymphocyte act	14.6	11.0	Coronary artery SMC rest	20.2	18.9
CD45RO CD4 lymphocyte act	25.2	22.4	Coronary artery SMC TNFalpha + IL-1beta	12.0	9.8
CD8 lymphocyte act	20.4	15.8	Astrocytes rest	10.4	11.1
Secondary CD8 lymphocyte rest	16.5	19.9	Astrocytes TNFalpha + IL-1beta	11.7	9.8
Secondary CD8 lymphocyte act	13.2	9.3	KU-812 (Basophil) rest	47.6	38.2
CD4 lymphocyte none	17.1	11.6	KU-812 (Basophil) PMA/ionomycin	94.0	92.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	18.3	16.6	CCD1106 (Keratinocytes) none	19.9	13.2
LAK cells rest	25.5	16.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.0	4.8
LAK cells IL-2	27.2	22.5	Liver cirrhosis	3.1	2.7
LAK cells IL-2+IL-12	27.2	19.3	Lupus kidney	2.1	1.7
LAK cells IL-2+IFN gamma	36.3	34.4	NCI-H292 none	30.1	18.9
LAK cells IL-2+IL-18	35.1	29.7	NCI-H292 IL-4	33.9	34.6
LAK cells PMA/ionomycin	12.4	11.0	NCI-H292 IL-9	40.1	29.1
NK Cells IL-2 rest	20.0	15.0	NCI-H292 IL-13	16.2	14.2
Two Way MLR 3 day	24.0	16.7	NCI-H292 IFN gamma	16.6	18.4
Two Way MLR 5 day	12.9	10.1	HPAEC none	13.6	13.5
Two Way MLR 7 day	11.4	9.5	HPAEC TNF alpha + IL-1 beta	25.3	25.3

PBMC rest	13.7	10.5	Lung fibroblast none	11.4	14.2
PBMC PWM	69.3	66.4	Lung fibroblast TNF alpha + IL-1 beta	6.1	7.2
PBMC PHA-L	22.8	17.7	Lung fibroblast IL-4	28.5	29.1
Ramos (B cell) none	24.1	19.3	Lung fibroblast IL-9	23.0	23.3
Ramos (B cell) ionomycin	100.0	100.0	Lung fibroblast IL-13	20.6	18.9
B lymphocytes PWM	71.7	74.2	Lung fibroblast IFN gamma	39.0	32.5
B lymphocytes CD40L and IL-4	29.1	28.7	Dermal fibroblast CCD1070 rest	33.9	31.0
EOL-1 dbcAMP	12.1	10.5	Dermal fibroblast CCD1070 TNF alpha	76.8	62.0
EOL-1 dbcAMP PMA/ionomycin	14.5	10.9	Dermal fibroblast CCD1070 IL-1 beta	20.3	13.9
Dendritic cells none	13.2	14.8	Dermal fibroblast IFN gamma	14.2	9.5
Dendritic cells LPS	11.7	8.3	Dermal fibroblast IL-4	26.4	20.4
Dendritic cells anti-CD40	17.7	12.7	IBD Colitis 2	2.6	2.2
Monocytes rest	16.7	17.6	IBD Crohn's	2.0	1.9
Monocytes LPS	6.4	5.0	Colon	11.9	10.5
Macrophages rest	23.5	22.8	Lung	13.3	11.2
Macrophages LPS	9.9	7.1	Thymus	14.4	12.9
HUVEC none	20.6	17.9	Kidney	27.5	19.6
HUVEC starved	43.5	38.4			

CNS_neurodegeneration_v1.0 Summary: Ag3023/Ag3373 This panel does not show differential expression of the CG58564-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

- 5 **General_screening_panel_v1.4 Summary:** Ag3373 Highest expression of the CG58564-01 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung,

breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

- 5 Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

- 10 In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

- 15 **Panel 1.3D Summary:** Ag3023 The CG58564-01 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and
20 ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

- 25 Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a phosphatase that is also expressed at low to moderate levels across the CNS. Some phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways.

Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

References:

1. Wiessner C. The dual specificity phosphatase PAC-1 is transcriptionally induced
5 in the rat brain following transient forebrain ischemia. Brain Res Mol Brain Res 1995
Feb;28(2):353-6

2. Boschert U, Muda M, Camps M, Dickinson R, Arkinstall S. Induction of the
dual specificity phosphatase PAC1 in rat brain following seizure activity. Neuroreport 1997
Sep 29;8(14):3077-80

10 **Panel 4D Summary:** Ag3023/Ag3373 The CG585864-01 gene is expressed at high to
moderate levels in a wide range of cell types and tissues of significance in the immune
response in health and disease. Highest expression of this gene is seen in ionomycin treated
Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule
15 drug or antibody therapeutic may modulate the functions of cells of the immune system as
well as resident tissue cells and lead to improvement of the symptoms of patients suffering
from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory
bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid
arthritis.

M. CG58564-03: Dual specificity phosphatase

20 Expression of gene CG58564-03 was assessed using the primer-probe sets Ag3023,
Ag3373 and Ag5847, described in Tables MA, MB and MC. Results of the RTQ-PCR runs
are shown in Tables MD, ME, MF, MG and MH.

Table MA. Probe Name Ag3023

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctaagtctggatttgcctca-3'	22	261	408
Probe	TET-5'-tcaggaatatgaagccatctacctagca- 3'-TAMRA	28	230	409
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	198	410

Table MB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atttgtccatcaacttcaggaa-3'	22	251	411
Probe	TET-5'-tgaagccatctacctagcaaaattaaca-3'-TAMRA	28	221	412
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	198	413

Table MC. Probe Name Ag5847

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cattccaaatgtttctgtagt-3'	21	335	414
Probe	TET-5'-ttcatagcagatgaatatgggcctaagaac-3'-TAMRA	30	371	415
Reverse	5'-ccacagtgcaaggaagac-3'	18	457	416

Table MD. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	60.7	57.8	AD 3 Occipital Ctx	14.7	15.0
AD 6 Hippo	80.7	72.2	AD 4 Occipital Ctx	35.4	22.4
Control 2 Hippo	35.8	38.4	AD 5 Occipital Ctx	3.9	30.4
Control 4	16.5	11.7	AD 6	46.0	37.4

Hippo			Occipital Ctx		
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal Ctx	9.5	13.2	Control 4 Occipital Ctx	13.3	13.3
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 Sup Temporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
Control 3 Temporal Ctx	20.3	20.0	Control (Path) 1 Parietal Ctx	74.7	64.2
Control 4 Temporal Ctx	9.7	9.9	Control (Path) 2 Parietal Ctx	28.9	59.9
Control (Path) 1 Temporal Ctx	59.9	68.3	Control (Path) 3 Parietal Ctx	10.2	9.0
Control (Path) 2 Temporal Ctx	40.3	41.2	Control (Path) 4	44.8	43.8

			Parietal Ctx		
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Table ME. General screening panel v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3
Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK- MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK- OV-3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV-1	10.9	Stomach Pool	9.9
Ovarian ca. OVCAR-8	9.2	Bone Marrow Pool	11.6
Ovary	9.7	Fetal Heart	20.7
Breast ca. MCF-7	37.6	Heart Pool	10.6
Breast ca. MDA- MB-231	37.1	Lymph Node Pool	17.9
Breast ca. BT 549	62.4	Fetal Skeletal Muscle	12.3
Breast ca. T47D	61.1	Skeletal Muscle Pool	16.0
Breast ca. MDA-N	10.0	Spleen Pool	11.6

Breast Pool	17.3	Thymus Pool	12.2
Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF-539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3
Lung ca. SHP-77	18.6	CNS cancer (glio) SF-295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table MF. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5847, Run 247590257	Tissue Name	Rel. Exp.(%) Ag5847, Run 247590257
Adipose	0.1	Renal ca. TK-10	0.2
Melanoma* Hs688(A).T	0.1	Bladder	0.1
Melanoma* Hs688(B).T	0.1	Gastric ca. (liver met.) NCI-N87	0.2

Melanoma* M14	0.1	Gastric ca. KATO III	0.1
Melanoma* LOXIMVI	0.1	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	0.1	Colon ca. SW480	0.2
Squamous cell carcinoma SCC-4	0.2	Colon ca.* (SW480 met) SW620	1.8
Testis Pool	0.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.6	Colon ca. HCT-116	0.2
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.2	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.1	Colon Pool	0.1
Ovarian ca. OVCAR-5	0.2	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.1	Bone Marrow Pool	0.0
Ovary	0.1	Fetal Heart	0.1
Breast ca. MCF-7	0.3	Heart Pool	0.0
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	0.1
Breast ca. BT 549	0.2	Fetal Skeletal Muscle	0.1
Breast ca. T47D	0.2	Skeletal Muscle Pool	0.1
Breast ca. MDA-N	0.1	Spleen Pool	0.1
Breast Pool	0.0	Thymus Pool	0.1
Trachea	0.1	CNS cancer (glio/astro) U87-MG	0.2
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.5
Fetal Lung	0.2	CNS cancer (neuro;met) SK-N-AS	0.2
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.1
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.2
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.1

Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	0.2
Lung ca. A549	0.2	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.1	Brain (fetal)	0.1
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.1	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.1	Brain (whole)	0.0
Liver ca. HepG2	0.1	Spinal Cord Pool	0.0
Kidney Pool	0.1	Adrenal Gland	0.0
Fetal Kidney	0.1	Pituitary gland Pool	0.0
Renal ca. 786-0	0.2	Salivary Gland	100.0
Renal ca. A498	0.1	Thyroid (female)	0.0
Renal ca. ACHN	0.1	Pancreatic ca. CAPAN2	0.1
Renal ca. UO-31	0.1	Pancreas Pool	0.0

Table MG. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931	Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931
Liver adenocarcinoma	51.1	Kidney (fetal)	26.2
Pancreas	6.1	Renal ca. 786-0	34.2
Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6
Adrenal gland	3.8	Renal ca. RXF 393	17.2
Thyroid	3.0	Renal ca. ACHN	13.5
Salivary gland	3.9	Renal ca. UO-31	0.0
Pituitary gland	3.6	Renal ca. TK-10	23.0
Brain (fetal)	8.1	Liver	11.7
Brain (whole)	8.5	Liver (fetal)	8.0
Brain (amygdala)	6.7	Liver ca. (hepatoblast) HepG2	26.2
Brain (cerebellum)	15.2	Lung	3.1
Brain (hippocampus)	5.4	Lung (fetal)	11.0
Brain (substantia nigra)	9.0	Lung ca. (small cell) LX-1	12.9
Brain (thalamus)	4.2	Lung ca. (small cell)	9.9

		NCI-H69	
Cerebral Cortex	2.0	Lung ca. (s.cell var.) SHP-77	67.8
Spinal cord	6.9	Lung ca. (large cell)NCI-H460	3.4
Glio/astro U87-MG	28.5	Lung ca. (non-sm. cell) A549	45.1
Glio/astro U-118-MG	46.7	Lung ca. (non-s.cell) NCI-H23	22.7
astrocytoma SW1783	40.6	Lung ca. (non-s.cell) HOP-62	25.7
neuro*; met SK-N-AS	27.2	Lung ca. (non-s.cl) NCI-H522	38.2
astrocytoma SF-539	29.7	Lung ca. (squam.) SW 900	27.4
astrocytoma SNB-75	35.1	Lung ca. (squam.) NCI-H596	29.9
glioma SNB-19	15.6	Mammary gland	5.1
glioma U251	37.9	Breast ca.* (pl.ef) MCF-7	47.0
glioma SF-295	18.4	Breast ca.* (pl.ef) MDA-MB-231	22.7
Heart (fetal)	2.9	Breast ca.* (pl.ef) T47D	86.5
Heart	12.9	Breast ca. BT-549	15.9
Skeletal muscle (fetal)	3.4	Breast ca. MDA-N	10.4
Skeletal muscle	36.3	Ovary	2.9
Bone marrow	4.5	Ovarian ca. OVCAR-3	26.1
Thymus	14.3	Ovarian ca. OVCAR-4	16.3
Spleen	8.7	Ovarian ca. OVCAR-5	83.5
Lymph node	11.8	Ovarian ca. OVCAR-8	9.3
Colorectal	10.4	Ovarian ca. IGROV- 1	12.0
Stomach	7.8	Ovarian ca.* (ascites) SK-OV-3	100.0
Small intestine	5.1	Uterus	4.9
Colon ca. SW480	19.3	Placenta	1.3
Colon ca.* SW620(SW480 met)	42.9	Prostate	3.9
Colon ca. HT29	9.9	Prostate ca.* (bone met)PC-3	78.5

Colon ca. HCT-116	26.2	Testis	9.7
Colon ca. CaCo-2	41.5	Melanoma Hs688(A).T	5.9
Colon ca. tissue(ODO3866)	6.3	Melanoma* (met) Hs688(B).T	14.2
Colon ca. HCC-2998	16.0	Melanoma UACC-62	14.0
Gastric ca.* (liver met) NCI-N87	18.8	Melanoma M14	5.7
Bladder	30.6	Melanoma LOX IMVI	8.8
Trachea	3.2	Melanoma* (met) SK-MEL-5	14.7
Kidney	9.6	Adipose	18.9

Table MH. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617	Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617
Secondary Th1 act	18.6	17.9	HUVEC IL-1beta	20.3	18.6
Secondary Th2 act	24.3	28.5	HUVEC IFN gamma	25.3	22.7
Secondary Tr1 act	22.8	21.8	HUVEC TNF alpha + IFN gamma	16.3	18.0
Secondary Th1 rest	7.5	6.8	HUVEC TNF alpha + IL4	18.2	13.4
Secondary Th2 rest	11.6	9.5	HUVEC IL-11	13.7	9.9
Secondary Tr1 rest	12.1	10.7	Lung Microvascular EC none	25.7	21.6
Primary Th1 act	20.7	16.5	Lung Microvascular EC TNFalpha + IL-1beta	26.2	18.3
Primary Th2 act	20.2	19.3	Microvascular Dermal EC none	27.5	21.3
Primary Tr1 act	23.3	27.7	Microvascular Dermal EC TNFalpha + IL-1beta	20.7	19.9
Primary Th1 rest	51.1	51.4	Bronchial epithelium	13.0	16.3

			TNFalpha + IL1beta		
Primary Th2 rest	26.2	29.5	Small airway epithelium none	8.1	8.5
Primary Tr1 rest	23.7	26.1	Small airway epithelium TNFalpha + IL-1beta	50.3	39.8
CD45RA CD4 lymphocyte act	14.6	11.0	Coronary artery SMC rest	20.2	18.9
CD45RO CD4 lymphocyte act	25.2	22.4	Coronary artery SMC TNFalpha + IL-1beta	12.0	9.8
CD8 lymphocyte act	20.4	15.8	Astrocytes rest	10.4	11.1
Secondary CD8 lymphocyte rest	16.5	19.9	Astrocytes TNFalpha + IL-1beta	11.7	9.8
Secondary CD8 lymphocyte act	13.2	9.3	KU-812 (Basophil) rest	47.6	38.2
CD4 lymphocyte none	17.1	11.6	KU-812 (Basophil) PMA/ionomycin	94.0	92.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	18.3	16.6	CCD1106 (Keratinocytes) none	19.9	13.2
LAK cells rest	25.5	16.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.0	4.8
LAK cells IL-2	27.2	22.5	Liver cirrhosis	3.1	2.7
LAK cells IL-2+IL-12	27.2	19.3	Lupus kidney	2.1	1.7
LAK cells IL-2+IFN gamma	36.3	34.4	NCI-H292 none	30.1	18.9
LAK cells IL-2+IL-18	35.1	29.7	NCI-H292 IL-4	33.9	34.6
LAK cells PMA/ionomycin	12.4	11.0	NCI-H292 IL-9	40.1	29.1
NK Cells IL-2 rest	20.0	15.0	NCI-H292 IL-13	16.2	14.2
Two Way MLR 3 day	24.0	16.7	NCI-H292 IFN gamma	16.6	18.4
Two Way MLR 5 day	12.9	10.1	HPAEC none	13.6	13.5
Two Way MLR 7 day	11.4	9.5	HPAEC TNF alpha + IL-1 beta	25.3	25.3

PBMC rest	13.7	10.5	Lung fibroblast none	11.4	14.2
PBMC PWM	69.3	66.4	Lung fibroblast TNF alpha + IL-1 beta	6.1	7.2
PBMC PHA-L	22.8	17.7	Lung fibroblast IL-4	28.5	29.1
Ramos (B cell) none	24.1	19.3	Lung fibroblast IL-9	23.0	23.3
Ramos (B cell) ionomycin	100.0	100.0	Lung fibroblast IL-13	20.6	18.9
B lymphocytes PWM	71.7	74.2	Lung fibroblast IFN gamma	39.0	32.5
B lymphocytes CD40L and IL-4	29.1	28.7	Dermal fibroblast CCD1070 rest	33.9	31.0
EOL-1 dbcAMP	12.1	10.5	Dermal fibroblast CCD1070 TNF alpha	76.8	62.0
EOL-1 dbcAMP PMA/ionomycin	14.5	10.9	Dermal fibroblast CCD1070 IL-1 beta	20.3	13.9
Dendritic cells none	13.2	14.8	Dermal fibroblast IFN gamma	14.2	9.5
Dendritic cells LPS	11.7	8.3	Dermal fibroblast IL-4	26.4	20.4
Dendritic cells anti-CD40	17.7	12.7	IBD Colitis 2	2.6	2.2
Monocytes rest	16.7	17.6	IBD Crohn's	2.0	1.9
Monocytes LPS	6.4	5.0	Colon	11.9	10.5
Macrophages rest	23.5	22.8	Lung	13.3	11.2
Macrophages LPS	9.9	7.1	Thymus	14.4	12.9
HUVEC none	20.6	17.9	Kidney	27.5	19.6
HUVEC starved	43.5	38.4			

- CNS_neurodegeneration_v1.0 Summary:** Ag3023/Ag3373 This panel does not show differential expression of the CG56804-03 gene, a splice variant of CG56804-01, in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system. Ag5847 - This primer pair recognizes only the splice variant CG58564-03. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG56804-03 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.5 Summary: Ag5847 - This primer pair, specific to this splice variant, CG58564-03. Expression of this variant is highest in salivary gland (CT=28.6). Therefore, expression of this gene can be used to differentiate this sample from others on the panel.

Panel 1.3D Summary: Ag3023 The CG56804-03 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a dual specificity phosphatase that is also expressed at low to moderate levels across the CNS. Dual-specificity phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

Panel 4.1D Summary: Ag5847 - This primer pair recognizes a splice variant of CG58564-03. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3023/Ag3373 The CG56804-03 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

N. CG58564-04: Dual specificity phosphatase

Expression of gene CG58564-04, a splice variant of CG58564-01, was assessed using the primer-probe sets Ag3023, Ag3373 and Ag5844, described in Tables NA, NB and NC. Results of the RTQ-PCR runs are shown in Tables ND, NE, NF and NG.

Table NA. Probe Name Ag3023

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctaagtctggatttgtccatca-3'	22	190	417
Probe	TET-5'-tcaggaatatgaagccatctacctagca-3'-TAMRA	28	159	418
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	127	419

Table NB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atttgtccatcaacttcaggaa-3'	22	180	420
Probe	TET-5'-tgaagccatctacctagcaaaaattaaca-3'-TAMRA	28	150	421
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	127	422

Table NC. Probe Name Ag5844

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccttagtctaaataactgctg-3'	21	377	423
Probe	TET-5'-agtttgcttcaatatatttgcgtatgcata-3'-TAMRA	30	415	424
Reverse	5'-aggagtggacctaccctat-3'	19	552	425

Table ND. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	60.7	57.8	AD 3	14.7	15.0

			Occipital Ctx		
AD 6 Hippo	80.7	72.2	AD 4 Occipital Ctx	35.4	22.4
Control 2 Hippo	35.8	38.4	AD 5 Occipital Ctx	3.9	30.4
Control 4 Hippo	16.5	11.7	AD 6 Occipital Ctx	46.0	37.4
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal Ctx	9.5	13.2	Control 4 Occipital Ctx	13.3	13.3
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 Sup Temporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
Control 3 Temporal Ctx	20.3	20.0	Control (Path) 1	74.7	64.2

			Parietal Ctx		
Control 4 Temporal Ctx	9.7	9.9	Control (Path) 2 Parietal Ctx	28.9	59.9
Control (Path) 1 Temporal Ctx	59.9	68.3	Control (Path) 3 Parietal Ctx	10.2	9.0
Control (Path) 2 Temporal Ctx	40.3	41.2	Control (Path) 4 Parietal Ctx	44.8	43.8

Table NE. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3
Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK- MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK- OV-3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV-1	10.9	Stomach Pool	9.9
Ovarian ca.	9.2	Bone Marrow Pool	11.6

OVCAR-8			
Ovary	9.7	Fetal Heart	20.7
Breast ca. MCF-7	37.6	Heart Pool	10.6
Breast ca. MDA-MB-231	37.1	Lymph Node Pool	17.9
Breast ca. BT 549	62.4	Fetal Skeletal Muscle	12.3
Breast ca. T47D	61.1	Skeletal Muscle Pool	16.0
Breast ca. MDA-N	10.0	Spleen Pool	11.6
Breast Pool	17.3	Thymus Pool	12.2
Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF-539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3
Lung ca. SHP-77	18.6	CNS cancer (glio) SF-295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table NF. Panel 1.3D

SECRET

Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931	Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931
Liver adenocarcinoma	51.1	Kidney (fetal)	26.2
Pancreas	6.1	Renal ca. 786-0	34.2
Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6
Adrenal gland	3.8	Renal ca. RXF 393	17.2
Thyroid	3.0	Renal ca. ACHN	13.5
Salivary gland	3.9	Renal ca. UO-31	0.0
Pituitary gland	3.6	Renal ca. TK-10	23.0
Brain (fetal)	8.1	Liver	11.7
Brain (whole)	8.5	Liver (fetal)	8.0
Brain (amygdala)	6.7	Liver ca. (hepatoblast) HepG2	26.2
Brain (cerebellum)	15.2	Lung	3.1
Brain (hippocampus)	5.4	Lung (fetal)	11.0
Brain (substantia nigra)	9.0	Lung ca. (small cell) LX-1	12.9
Brain (thalamus)	4.2	Lung ca. (small cell) NCI-H69	9.9
Cerebral Cortex	2.0	Lung ca. (s.cell var.) SHP-77	67.8
Spinal cord	6.9	Lung ca. (large cell)NCI-H460	3.4
Glio/astro U87-MG	28.5	Lung ca. (non-sm. cell) A549	45.1
Glio/astro U-118-MG	46.7	Lung ca. (non-s.cell) NCI-H23	22.7
astrocytoma SW1783	40.6	Lung ca. (non-s.cell) HOP-62	25.7
neuro*; met SK-N-AS	27.2	Lung ca. (non-s.cl) NCI-H522	38.2
astrocytoma SF-539	29.7	Lung ca. (squam.) SW 900	27.4
astrocytoma SNB-75	35.1	Lung ca. (squam.) NCI-H596	29.9
glioma SNB-19	15.6	Mammary gland	5.1
glioma U251	37.9	Breast ca.* (pl.ef) MCF-7	47.0
glioma SF-295	18.4	Breast ca.* (pl.ef) MDA-MB-231	22.7
Heart (fetal)	2.9	Breast ca.* (pl.ef) T47D	86.5
Heart	12.9	Breast ca. BT-549	15.9

Skeletal muscle (fetal)	3.4	Breast ca. MDA-N	10.4
Skeletal muscle	36.3	Ovary	2.9
Bone marrow	4.5	Ovarian ca. OVCAR-3	26.1
Thymus	14.3	Ovarian ca. OVCAR-4	16.3
Spleen	8.7	Ovarian ca. OVCAR-5	83.5
Lymph node	11.8	Ovarian ca. OVCAR-8	9.3
Colorectal	10.4	Ovarian ca. IGROV-1	12.0
Stomach	7.8	Ovarian ca.* (ascites) SK-OV-3	100.0
Small intestine	5.1	Uterus	4.9
Colon ca. SW480	19.3	Placenta	1.3
Colon ca.* SW620(SW480 met)	42.9	Prostate	3.9
Colon ca. HT29	9.9	Prostate ca.* (bone met)PC-3	78.5
Colon ca. HCT-116	26.2	Testis	9.7
Colon ca. CaCo-2	41.5	Melanoma Hs688(A).T	5.9
Colon ca. tissue(ODO3866)	6.3	Melanoma* (met) Hs688(B).T	14.2
Colon ca. HCC-2998	16.0	Melanoma UACC-62	14.0
Gastric ca.* (liver met) NCI-N87	18.8	Melanoma M14	5.7
Bladder	30.6	Melanoma LOX IMVI	8.8
Trachea	3.2	Melanoma* (met) SK-MEL-5	14.7
Kidney	9.6	Adipose	18.9

Table NG. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617	Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617
Secondary Th1 act	18.6	17.9	HUVEC IL-1beta	20.3	18.6
Secondary Th2 act	24.3	28.5	HUVEC IFN gamma	25.3	22.7

Secondary Tr1 act	22.8	21.8	HUVEC TNF alpha + IFN gamma	16.3	18.0
Secondary Th1 rest	7.5	6.8	HUVEC TNF alpha + IL4	18.2	13.4
Secondary Th2 rest	11.6	9.5	HUVEC IL-11	13.7	9.9
Secondary Tr1 rest	12.1	10.7	Lung Microvascular EC none	25.7	21.6
Primary Th1 act	20.7	16.5	Lung Microvascular EC TNFalpha + IL- 1beta	26.2	18.3
Primary Th2 act	20.2	19.3	Microvascular Dermal EC none	27.5	21.3
Primary Tr1 act	23.3	27.7	Microvascular Dermal EC TNFalpha + IL- 1beta	20.7	19.9
Primary Th1 rest	51.1	51.4	Bronchial epithelium TNFalpha + IL1beta	13.0	16.3
Primary Th2 rest	26.2	29.5	Small airway epithelium none	8.1	8.5
Primary Tr1 rest	23.7	26.1	Small airway epithelium TNFalpha + IL- 1beta	50.3	39.8
CD45RA CD4 lymphocyte act	14.6	11.0	Coronary artery SMC rest	20.2	18.9
CD45RO CD4 lymphocyte act	25.2	22.4	Coronary artery SMC TNFalpha + IL-1beta	12.0	9.8
CD8 lymphocyte act	20.4	15.8	Astrocytes rest	10.4	11.1
Secondary CD8 lymphocyte rest	16.5	19.9	Astrocytes TNFalpha + IL- 1beta	11.7	9.8
Secondary CD8 lymphocyte act	13.2	9.3	KU-812 (Basophil) rest	47.6	38.2
CD4 lymphocyte none	17.1	11.6	KU-812 (Basophil) PMA/ionomycin	94.0	92.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	18.3	16.6	CCD1106 (Keratinocytes) none	19.9	13.2

LAK cells rest	25.5	16.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.0	4.8
LAK cells IL-2	27.2	22.5	Liver cirrhosis	3.1	2.7
LAK cells IL-2+IL-12	27.2	19.3	Lupus kidney	2.1	1.7
LAK cells IL-2+IFN gamma	36.3	34.4	NCI-H292 none	30.1	18.9
LAK cells IL-2+IL-18	35.1	29.7	NCI-H292 IL-4	33.9	34.6
LAK cells PMA/ionomycin	12.4	11.0	NCI-H292 IL-9	40.1	29.1
NK Cells IL-2 rest	20.0	15.0	NCI-H292 IL-13	16.2	14.2
Two Way MLR 3 day	24.0	16.7	NCI-H292 IFN gamma	16.6	18.4
Two Way MLR 5 day	12.9	10.1	HPAEC none	13.6	13.5
Two Way MLR 7 day	11.4	9.5	HPAEC TNF alpha + IL-1 beta	25.3	25.3
PBMC rest	13.7	10.5	Lung fibroblast none	11.4	14.2
PBMC PWM	69.3	66.4	Lung fibroblast TNF alpha + IL-1 beta	6.1	7.2
PBMC PHA-L	22.8	17.7	Lung fibroblast IL-4	28.5	29.1
Ramos (B cell) none	24.1	19.3	Lung fibroblast IL-9	23.0	23.3
Ramos (B cell) ionomycin	100.0	100.0	Lung fibroblast IL-13	20.6	18.9
B lymphocytes PWM	71.7	74.2	Lung fibroblast IFN gamma	39.0	32.5
B lymphocytes CD40L and IL-4	29.1	28.7	Dermal fibroblast CCD1070 rest	33.9	31.0
EOL-1 dbcAMP	12.1	10.5	Dermal fibroblast CCD1070 TNF alpha	76.8	62.0
EOL-1 dbcAMP PMA/ionomycin	14.5	10.9	Dermal fibroblast CCD1070 IL-1 beta	20.3	13.9
Dendritic cells none	13.2	14.8	Dermal fibroblast IFN gamma	14.2	9.5
Dendritic cells LPS	11.7	8.3	Dermal fibroblast IL-4	26.4	20.4
Dendritic cells	17.7	12.7	IBD Colitis 2	2.6	2.2

anti-CD40					
Monocytes rest	16.7	17.6	IBD Crohn's	2.0	1.9
Monocytes LPS	6.4	5.0	Colon	11.9	10.5
Macrophages rest	23.5	22.8	Lung	13.3	11.2
Macrophages LPS	9.9	7.1	Thymus	14.4	12.9
HUVEC none	20.6	17.9	Kidney	27.5	19.6
HUVEC starved	43.5	38.4			

CNS_neurodegeneration_v1.0 Summary: Ag3023/Ag3373 This panel does not show differential expression of the CG56804-04 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system. Ag5847 - This primer pair recognizes a splice variant of CG58564-01 designated CG58564-04. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG56804-04 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.5 Summary: Ag5844 - This primer pair recognizes a splice variant of CG58564-01. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 1.3D Summary: Ag3023 The CG56804-04 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a dual specificity phosphatase that is also expressed at low to moderate levels across the CNS. Dual-specificity phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

Panel 4.1D Summary: Ag5844 - This primer pair recognizes a splice variant of CG58564-01. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3023/Ag3373 The CG56804-04 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies,

[illegible]

O. CG57819-01: RPGR-INTERACTING PROTEIN-1

Expression of gene CG57819-01 was assessed using the primer-probe set Ag3338,
5 described in Table OA. Results of the RTQ-PCR runs are shown in Tables OB and OC.

Table OA. Probe Name Ag3338

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cccattcagcactgaaacag-3'	20	3021	426
Probe	TET-5'-tcctgtaaatgacaaagaatcctctgaaca-3'-TAMRA	30	3055	427
Reverse	5'-tgcttcactgacttcagaacct-3'	22	3085	428

Table OB. General screening panel v1.4

Tissue Name	Rel. Exp.(%) Ag3338, Run 215773746	Tissue Name	Rel. Exp.(%) Ag3338, Run 215773746
Adipose	1.1	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.0	Bladder	1.1
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.2	Colon ca. SW480	0.4
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	100.0	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.2
Prostate Pool	1.0	Colon ca. CaCo-2	1.0
Placenta	0.0	Colon cancer tissue	0.9
Uterus Pool	0.0	Colon ca. SW1116	0.2
Ovarian ca. OVCAR-3	0.9	Colon ca. Colo-205	0.2
Ovarian ca. SK- OV-3	0.0	Colon ca. SW-48	0.0

Ovarian ca. OVCAR-4	1.2	Colon Pool	0.5
Ovarian ca. OVCAR-5	3.5	Small Intestine Pool	0.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.2
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.9	Fetal Heart	0.8
Breast ca. MCF-7	1.9	Heart Pool	1.1
Breast ca. MDA-MB-231	1.2	Lymph Node Pool	1.4
Breast ca. BT 549	0.2	Fetal Skeletal Muscle	0.2
Breast ca. T47D	6.7	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	1.4
Breast Pool	0.5	Thymus Pool	0.0
Trachea	0.9	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.2	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.4	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.8	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.5	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	0.2
Lung ca. A549	1.5	Brain (Amygdala) Pool	0.7
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.6
Lung ca. NCI-H23	1.5	Brain (fetal)	0.9
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.7
Lung ca. HOP-62	3.0	Cerebral Cortex Pool	0.2
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.7
Liver	0.4	Brain (Thalamus) Pool	1.3
Fetal Liver	0.5	Brain (whole)	0.0
Liver ca. HepG2	0.2	Spinal Cord Pool	0.9
Kidney Pool	0.9	Adrenal Gland	0.0
Fetal Kidney	0.6	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0

Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	3.4
Renal ca. UO-31	0.0	Pancreas Pool	0.8

Tissue Name	Rel. Exp.(%) Ag3338, Run 165221737	Tissue Name	Rel. Exp.(%) Ag3338, Run 165221737
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	6.9
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	2.6
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	1.9
Primary Tr1 act	0.0	Microsvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	4.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	4.6	CCD1106	0.0

		(Keratinocytes) TNFalpha + IL-1beta	
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	2.4
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	4.5
LAK cells PMA/ionomycin	3.1	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	14.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	3.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	4.7	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	13.9	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	6.0	IBD Colitis 2	0.0
Monocytes rest	100.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	15.2
Macrophages rest	1.3	Lung	4.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	3.1
HUVEC starved	0.0		

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General_screening_panel_v1.4 Summary: Ag3338 - Expression of this gene is highest in testis (CT=29.4). Therefore, expression of this gene could be used to distinguish this sample from others on the panel.

There is also low expression in pancreatic cancer cell line CAPAN2, lung cancer
5 cell line HOP-62, breast cancer cell line T47D, and ovarian cancer cell line OVCAR-5.
Thus, expression of this gene could be used to differentiate these samples from other
samples on this panel.

Panel 4D Summary: Ag3338 - Significant expression of this gene is seen only in resting monocytes (CT=32.3) Therefore, expression of this gene can be used to differentiate
10 between this sample and others on this panel.

P. CG57789-01 and CG57789-02: RAS-LIKE PROTEIN RRP22-like

Expression of gene CG57789-01 and variant CG57789-02 was assessed using the primer-probe set Ag3333, described in Table PA. Results of the RTQ-PCR runs are shown in Tables PB, PC and PD.

15 Table PA. Probe Name Ag3333

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tcgactttccacccatcag-3'	19	181	429
Probe	TET-5'-cttcctgtcaatacgtctcaggagt-3'-TAMRA	26	203	430
Reverse	5'-aggatgtaggcgtggacact-3'	20	258	431

Table PB. CNS neurodegeneration v1.0

Tissue Name	Rel. Exp.(%) Ag3333, Run 210146459	Tissue Name	Rel. Exp.(%) Ag3333, Run 210146459
AD 1 Hippo	22.2	Control (Path) 3 Temporal Ctx	7.5
AD 2 Hippo	18.8	Control (Path) 4 Temporal Ctx	21.6
AD 3 Hippo	17.9	AD 1 Occipital Ctx	29.7
AD 4 Hippo	8.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	100.0	AD 3 Occipital Ctx	15.8
AD 6 Hippo	42.9	AD 4 Occipital Ctx	24.7

Control 2 Hippo	25.9	AD 5 Occipital Ctx	90.1
Control 4 Hippo	12.1	AD 6 Occipital Ctx	16.3
Control (Path) 3 Hippo	13.4	Control 1 Occipital Ctx	4.2
AD 1 Temporal Ctx	21.3	Control 2 Occipital Ctx	74.7
AD 2 Temporal Ctx	29.1	Control 3 Occipital Ctx	14.5
AD 3 Temporal Ctx	13.3	Control 4 Occipital Ctx	4.5
AD 4 Temporal Ctx	15.8	Control (Path) 1 Occipital Ctx	47.3
AD 5 Inf Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	13.5
AD 5 Sup Temporal Ctx	43.2	Control (Path) 3 Occipital Ctx	4.1
AD 6 Inf Temporal Ctx	26.4	Control (Path) 4 Occipital Ctx	14.6
AD 6 Sup Temporal Ctx	31.6	Control 1 Parietal Ctx	7.6
Control 1 Temporal Ctx	5.8	Control 2 Parietal Ctx	39.2
Control 2 Temporal Ctx	51.8	Control 3 Parietal Ctx	21.9
Control 3 Temporal Ctx	14.5	Control (Path) 1 Parietal Ctx	56.3
Control 3 Temporal Ctx	8.1	Control (Path) 2 Parietal Ctx	20.2
Control (Path) 1 Temporal Ctx	39.2	Control (Path) 3 Parietal Ctx	6.2
Control (Path) 2 Temporal Ctx	40.9	Control (Path) 4 Parietal Ctx	24.5

Tissue Name	Rel. Exp.(%) Ag3333, Run 216516940	Tissue Name	Rel. Exp.(%) Ag3333, Run 216516940
Adipose	4.4	Renal ca. TK-10	40.1
Melanoma* Hs688(A).T	0.9	Bladder	5.0
Melanoma* Hs688(B).T	1.8	Gastric ca. (liver met.) NCI-N87	4.5
Melanoma* M14	2.7	Gastric ca. KATO III	20.0
Melanoma*	0.3	Colon ca. SW-948	0.0

LOXIMVI			
Melanoma* SK-MEL-5	0.9	Colon ca. SW480	100.0
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	33.0
Testis Pool	2.1	Colon ca. HT29	5.0
Prostate ca.* (bone met) PC-3	2.4	Colon ca. HCT-116	0.1
Prostate Pool	0.5	Colon ca. CaCo-2	37.1
Placenta	5.7	Colon cancer tissue	2.3
Uterus Pool	0.3	Colon ca. SW1116	16.2
Ovarian ca. OVCAR-3	52.9	Colon ca. Colo-205	0.2
Ovarian ca. SK-OV-3	0.6	Colon ca. SW-48	0.2
Ovarian ca. OVCAR-4	17.9	Colon Pool	2.2
Ovarian ca. OVCAR-5	4.5	Small Intestine Pool	1.0
Ovarian ca. IGROV-1	0.9	Stomach Pool	0.9
Ovarian ca. OVCAR-8	15.4	Bone Marrow Pool	1.8
Ovary	4.2	Fetal Heart	10.9
Breast ca. MCF-7	0.7	Heart Pool	2.8
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	4.4
Breast ca. BT 549	42.0	Fetal Skeletal Muscle	1.1
Breast ca. T47D	13.0	Skeletal Muscle Pool	46.7
Breast ca. MDA-N	0.1	Spleen Pool	0.0
Breast Pool	2.4	Thymus Pool	2.3
Trachea	2.4	CNS cancer (glio/astro) U87-MG	0.9
Lung	0.2	CNS cancer (glio/astro) U-118-MG	0.3
Fetal Lung	0.9	CNS cancer (neuro;met) SK-N-AS	69.7
Lung ca. NCI-N417	17.1	CNS cancer (astro) SF-539	2.2
Lung ca. LX-1	1.1	CNS cancer (astro) SNB-75	15.9
Lung ca. NCI-H146	14.5	CNS cancer (glio) SNB-19	0.6
Lung ca. SHP-77	37.6	CNS cancer (glio) SF-295	6.0

Lung ca. A549	0.4	Brain (Amygdala) Pool	28.5
Lung ca. NCI-H526	23.5	Brain (cerebellum)	29.1
Lung ca. NCI-H23	8.2	Brain (fetal)	21.3
Lung ca. NCI-H460	14.3	Brain (Hippocampus) Pool	27.7
Lung ca. HOP-62	1.7	Cerebral Cortex Pool	36.1
Lung ca. NCI-H522	86.5	Brain (Substantia nigra) Pool	40.1
Liver	1.6	Brain (Thalamus) Pool	37.6
Fetal Liver	0.7	Brain (whole)	59.5
Liver ca. HepG2	6.2	Spinal Cord Pool	12.3
Kidney Pool	3.8	Adrenal Gland	4.7
Fetal Kidney	7.4	Pituitary gland Pool	3.7
Renal ca. 786-0	0.2	Salivary Gland	48.0
Renal ca. A498	20.9	Thyroid (female)	1.1
Renal ca. ACHN	8.5	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	3.0	Pancreas Pool	4.0

Table PD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3333, Run 165084139	Tissue Name	Rel. Exp.(%) Ag3333, Run 165084139
Secondary Th1 act	0.8	HUVEC IL-1beta	0.0
Secondary Th2 act	3.0	HUVEC IFN gamma	0.5
Secondary Tr1 act	0.6	HUVEC TNF alpha + IFN gamma	0.8
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.5	HUVEC IL-11	0.3
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.6
Primary Th1 act	5.7	Lung Microvascular EC TNFalpha + IL-1beta	0.4
Primary Th2 act	9.8	Microvascular Dermal EC none	0.0
Primary Tr1 act	3.8	Microvascular Dermal EC TNFalpha + IL-1beta	0.4
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	1.1
Primary Th2 rest	0.4	Small airway epithelium none	1.9
Primary Tr1 rest	0.6	Small airway epithelium	1.4

		TNFalpha + IL-1beta	
CD45RA CD4 lymphocyte act	4.1	Coronary artery SMC rest	1.7
CD45RO CD4 lymphocyte act	1.7	Coronary artery SMC TNFalpha + IL-1beta	1.2
CD8 lymphocyte act	1.4	Astrocytes rest	100.0
Secondary CD8 lymphocyte rest	7.4	Astrocytes TNFalpha + IL-1beta	59.9
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	2.0
CD4 lymphocyte none	0.8	KU-812 (Basophil) PMA/ionomycin	4.1
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.5	CCD1106 (Keratinocytes) none	12.5
LAK cells rest	0.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.2
LAK cells IL-2	0.3	Liver cirrhosis	0.9
LAK cells IL-2+IL-12	0.5	Lupus kidney	3.9
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	29.3
LAK cells IL-2+ IL-18	0.6	NCI-H292 IL-4	39.5
LAK cells PMA/ionomycin	0.3	NCI-H292 IL-9	23.3
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	21.9
Two Way MLR 3 day	0.8	NCI-H292 IFN gamma	14.5
Two Way MLR 5 day	0.9	HPAEC none	0.5
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	4.5
PBMC PWM	8.1	Lung fibroblast TNF alpha + IL-1 beta	2.2
PBMC PHA-L	11.6	Lung fibroblast IL-4	12.9
Ramos (B cell) none	0.0	Lung fibroblast IL-9	9.2
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	8.5
B lymphocytes PWM	15.4	Lung fibroblast IFN gamma	8.4
B lymphocytes CD40L and IL-4	2.1	Dermal fibroblast CCD1070 rest	40.6
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	20.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	19.3
Dendritic cells none	0.0	Dermal fibroblast IFN	1.8

		gamma	
Dendritic cells LPS	0.5	Dermal fibroblast IL-4	3.8
Dendritic cells anti-CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	2.5
Monocytes LPS	0.0	Colon	4.2
Macrophages rest	0.0	Lung	9.1
Macrophages LPS	0.0	Thymus	11.3
HUVEC none	0.4	Kidney	2.6
HUVEC starved	0.6		

CNS_neurodegeneration_v1.0 Summary: This panel confirms the expression of this gene in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3333 This gene is expressed at moderate to low levels in many of the samples on this panel, with the highest expression in colon cancer cell line SW480 (CT=27.8). Expression is significantly lower in SW680, a cell line derived from a metastasis of the primary tumor represented by SW480. Thus, expression of this gene could be used to differentiate between these two cell lines and potentially between primary colon cancer and its metastases.

Based on expression in this panel, this gene may be involved in gastric, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this

gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3333 The CG57789-01 gene is expressed at moderate to low levels in several samples on this panel, with the highest expression in resting astrocytes (CT=28.4). Moderate expression of this gene is seen in treated and untreated dermal and lung fibroblasts and the airway epithelial tumor line NCI-H292 cells. Thus, the transcript or the protein it encodes may be involved in pathological and inflammatory skin and lung conditions, including psoriasis, asthma, allergy, emphysema, and COPD.

10 **Q. CG57758-01 and CG57758-02: SODIUM/LITHIUM-DEPENDENT DICARBOXYLATE TRANSPORTER**

Expression of gene CG57758-01, a splice variant of CG57758-02, and CG57758-02 was assessed using the primer-probe sets Ag3326 and Ag3692, described in Tables QA and QB. Results of the RTQ-PCR runs are shown in Tables QC, QD, QE and QF.

Table QA. Probe Name Ag3326

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	149	432
Probe	TET-5'-atccctctggctgtcacctctctcat-3'-TAMRA	26	172	433
Reverse	5'-ggagtccagaatctggaagagt-3'	22	216	434

15 Table QB. Probe Name Ag3692

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	149	435
Probe	TET-5'-atccctctggctgtcacctctctcat-3'-TAMRA	26	172	436
Reverse	5'-ggagtccagaatctggaagagt-3'	22	216	437

Table QC. CNS_neurodegeneration_v1.0

SECRET

Tissue Name	Rel. Exp.(%) Ag3326, Run 210144197	Rel. Exp.(%) Ag3692, Run 211145262	Rel. Exp.(%) Ag3692, Run 224337942	Tissue Name	Rel. Exp.(%) Ag3326, Run 210144197	Rel. Exp.(%) Ag3692, Run 211145262	Rel. Exp.(%) Ag3692, Run 224337942
AD 1 Hippo	2.1	4.3	1.0	Control (Path) 3 Temporal Ctx	8.5	15.3	12.0
AD 2 Hippo	20.9	28.3	25.0	Control (Path) 4 Temporal Ctx	31.2	36.6	52.1
AD 3 Hippo	0.0	0.9	0.6	AD 1 Occipital Ctx	2.7	3.0	0.0
AD 4 Hippo	2.1	7.1	2.6	AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 5 hippo	72.7	97.9	85.3	AD 3 Occipital Ctx	1.5	7.2	1.3
AD 6 Hippo	13.7	18.3	5.5	AD 4 Occipital Ctx	71.7	35.6	30.6
Control 2 Hippo	14.5	20.2	15.2	AD 5 Occipital Ctx	25.3	31.9	12.4
Control 4 Hippo	11.7	7.4	5.1	AD 6 Occipital Ctx	17.2	19.1	11.2
Control (Path) 3 Hippo	6.7	4.4	4.5	Control 1 Occipital Ctx	7.0	9.0	8.1
AD 1 Temporal Ctx	4.0	1.7	2.8	Control 2 Occipital Ctx	33.2	44.8	26.1
AD 2 Temporal Ctx	80.7	50.7	37.4	Control 3 Occipital Ctx	30.1	37.6	21.9
AD 3 Temporal Ctx	3.6	0.0	1.1	Control 4 Occipital	16.3	12.6	8.2

				Ctx			
AD 4 Temporal Ctx	19.5	30.6	15.2	Control (Path) 1 Occipital Ctx	42.0	55.9	52.9
AD 5 Inf Temporal Ctx	100.0	100.0	99.3	Control (Path) 2 Occipital Ctx	6.7	13.0	7.7
AD 5 Sup Temporal Ctx	32.8	29.1	33.2	Control (Path) 3 Occipital Ctx	8.7	6.6	5.4
AD 6 Inf Temporal Ctx	27.7	21.3	26.6	Control (Path) 4 Occipital Ctx	8.1	9.0	7.4
AD 6 Sup Temporal Ctx	41.8	53.6	17.0	Control 1 Parietal Ctx	21.2	23.0	15.3
Control 1 Temporal Ctx	12.0	33.9	18.3	Control 2 Parietal Ctx	48.6	38.2	22.1
Control 2 Temporal Ctx	30.1	49.3	44.4	Control 3 Parietal Ctx	28.3	34.4	32.8
Control 3 Temporal Ctx	38.7	39.5	33.4	Control (Path) 1 Parietal Ctx	78.5	97.3	100.0
Control 4 Temporal Ctx	17.6	25.2	24.1	Control (Path) 2 Parietal Ctx	50.7	50.7	37.9
Control (Path) 1 Temporal Ctx	69.7	70.7	49.7	Control (Path) 3 Parietal Ctx	10.7	10.1	9.6
Control (Path) 2 Temporal Ctx	35.4	50.7	33.4	Control (Path) 4 Parietal Ctx	30.6	24.5	40.9

Table QD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3326, Run 215678613	Rel. Exp.(%) Ag3692, Run 217131191	Tissue Name	Rel. Exp.(%) Ag3326, Run 215678613	Rel. Exp.(%) Ag3692, Run 217131191
Adipose	0.0	0.0	Renal ca. TK-10	11.4	12.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.0	0.1
Melanoma* Hs688(B).T	0.1	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW- 948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.9	0.7	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.1	0.2	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT- 116	0.0	0.0
Prostate Pool	0.0	0.0	Colon ca. CaCo- 2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.1	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo- 205	0.0	0.0
Ovarian ca. SK-OV-3	0.0	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.1	0.0	Colon Pool	0.6	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.1	0.0
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.0	0.0
Ovarian ca. OVCAR-8	2.8	2.2	Bone Marrow Pool	0.0	0.1
Ovary	0.7	0.6	Fetal Heart	0.0	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.0	0.0
Breast ca. MDA-MB- 231	0.0	0.0	Lymph Node Pool	0.1	0.0

Breast ca. BT 549	0.6	0.8	Fetal Skeletal Muscle	0.0	0.0
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	0.0	0.0
Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.4	0.2
Breast Pool	0.0	0.1	Thymus Pool	0.0	0.0
Trachea	0.2	0.1	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	0.0
Fetal Lung	0.2	0.1	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	0.0	0.0	CNS cancer (glio) SF-295	0.1	0.1
Lung ca. A549	0.0	0.1	Brain (Amygdala) Pool	0.4	0.4
Lung ca. NCI-H526	2.0	0.0	Brain (cerebellum)	1.4	1.0
Lung ca. NCI-H23	0.7	0.6	Brain (fetal)	0.7	0.4
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.5	0.7
Lung ca. HOP-62	0.1	0.2	Cerebral Cortex Pool	1.4	1.5
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	1.4	1.4
Liver	28.7	24.1	Brain (Thalamus) Pool	1.1	0.9
Fetal Liver	100.0	100.0	Brain (whole)	4.1	3.7
Liver ca. HepG2	29.5	26.2	Spinal Cord Pool	0.1	0.2
Kidney Pool	0.0	0.0	Adrenal Gland	2.6	1.9
Fetal Kidney	0.1	0.1	Pituitary gland Pool	0.0	0.2
Renal ca.	0.0	0.0	Salivary Gland	40.9	35.1

786-0					
Renal ca. A498	0.0	0.0	Thyroid (female)	0.0	0.0
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.5	0.8
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	0.0

Table QE. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3692, Run 169987356	Tissue Name	Rel. Exp.(%) Ag3692, Run 169987356
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	11.3
Primary Tr1 act	4.2	Microvasular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	28.5
Primary Th2 rest	0.0	Small airway epithelium none	5.7
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	3.9	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	3.6
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	4.3

2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	10.7
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	94.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	3.2	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	2.4
HUVEC none	0.0	Kidney	100.0
HUVEC starved	0.0		

Table QF. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365	Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365
97457_Patient-02go_adipose	0.0	94709_Donor 2 AM - A_adipose	0.2
97476_Patient-07sk_skeletal muscle	0.0	94710_Donor 2 AM - B_adipose	0.0
97477_Patient-07ut_uterus	0.0	94711_Donor 2 AM - C_adipose	0.0
97478_Patient-07pl_placenta	0.0	94712_Donor 2 AD - A_adipose	0.0
99167_Bayer Patient 1	0.3	94713_Donor 2 AD - B_adipose	0.0
97482_Patient-08ut_uterus	0.0	94714_Donor 2 AD - C_adipose	0.0
97483_Patient-08pl_placenta	0.0	94742_Donor 3 U - A_Mesenchymal Stem Cells	0.0
97486_Patient-09sk_skeletal muscle	0.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	0.0
97487_Patient-09ut_uterus	0.0	94730_Donor 3 AM - A_adipose	0.0
97488_Patient-09pl_placenta	0.0	94731_Donor 3 AM - B_adipose	0.0
97492_Patient-10ut_uterus	0.0	94732_Donor 3 AM - C_adipose	0.0
97493_Patient-10pl_placenta	0.0	94733_Donor 3 AD - A_adipose	0.0
97495_Patient-11go_adipose	0.0	94734_Donor 3 AD - B_adipose	0.0
97496_Patient-11sk_skeletal muscle	0.0	94735_Donor 3 AD - C_adipose	0.0
97497_Patient-11ut_uterus	0.0	77138_Liver_HepG2untreated	100.0
97498_Patient-11pl_placenta	0.0	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	0.1	81735_Small Intestine	39.5
97501_Patient-12sk_skeletal muscle	0.3	72409_Kidney_Proximal Convoluted Tubule	0.0
97502_Patient-12ut_uterus	0.0	82685_Small intestine_Duodenum	0.0
97503_Patient-12pl_placenta	0.0	90650_Adrenal_Adrenocortical adenoma	0.0
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3326/Ag3692 - Three experiments done with two primer pairs (same sequence) are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3326/Ag3692 Two experiments with the same probe and primer set produce results that are in excellent agreement. This gene is highly expressed in fetal liver (CT=26.5-27.0) and moderately expressed in adult liver (CT=28.5-28.8) and liver cancer cell line HepG2 (CT=28.4-28.8). This result agrees with the results seen in Panel 5 (expression in HepG2 (CT=29.2). These results are in agreement with published data that show a novel sodium dicarboxylate transporter in brain, choroid plexus kidney, intestine and liver. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for liver derived tissue.

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and cerebral cortex. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Low but significant levels of expression are also seen in the adrenal gland. Thus, this gene product may also be involved in metabolic disorders of this gland, including adrenoleukodystrophy and congenital adrenal hyperplasia.

References:

1. Pajor AM, Gangula R, Yao X. Cloning and functional characterization of a high-affinity Na(+)/dicarboxylate cotransporter from mouse brain. Am J Physiol Cell Physiol 2001 May;280(5):C1215-23.

2. Chen XZ, Shayakul C, Berger UV, Tian W, Hediger MA. Characterization of a rat Na⁺-dicarboxylate cotransporter. J Biol Chem 1998 Aug 14;273(33):20972-81.

Panel 4.1D Summary: Ag3692 Significant expression of this gene is seen only in kidney and a liver cirrhosis sample (CTs=34.0). These results confirm that this gene is expressed in liver derived samples. The presence in the kidney is also in agreement with published results. Please see Panel 1.4. This gene product may be involved in maintaining or restoring normal function to the kidney during inflammation.

Panel 4D Summary: Ag3326 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 5 Islet Summary: Ag3326 - The highest expression of this gene is in liver cancer cell line HepG2 (CT=29.2). There is also moderate expression in the small intestine (CT=30.5). These results compare well with previously published reports of sodium dicarboxylate transporter expression in mouse and rat (see discussion Panel 1.4).

R. CG57758-04 and CG57758-05: Sodium:sulfate symporter

Expression of gene CG57758-04 and CG57758-05, both splice variants of CG577584-01, was assessed using the primer-probe sets Ag3326, Ag3692 and Ag5818, described in Tables RA, RB and RC. Results of the RTQ-PCR runs are shown in Tables RD, RE, RF, RG and RH.

Table RA. Probe Name Ag3326

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - ccatttactggtgcacagaagt - 3'	22	138	438
Probe	TET-5' - atccctctggtgtcacctctctcat - 3' - TAMRA	26	161	439
Reverse	5' - ggagtcacagaatctggaagagt - 3'	22	205	440

Table RB. Probe Name Ag3692

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	138	441
Probe	TET-5'-atccctctggtgtcacctctctcat-3'-TAMRA	26	161	442
Reverse	5'-ggagtccagaatctggaagagt-3'	22	205	443

Table RC. Probe Name Ag5818

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatcaccttgatcttgtcc-3'	20	1341	444
Probe	TET-5'-ttatgactcctgttttcacatggaggca-3'-TAMRA	29	1429	445
Reverse	5'-cagaagactccaattatgttca-3'	22	1458	446

Table RD. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3326, Run 210144197	Rel. Exp.(%) Ag3692, Run 211145262	Rel. Exp.(%) Ag3692, Run 224337942	Tissue Name	Rel. Exp.(%) Ag3326, Run 210144197	Rel. Exp.(%) Ag3692, Run 211145262	Rel. Exp.(%) Ag3692, Run 224337942
AD 1 Hippo	2.1	4.3	1.0	Control (Path) 3 Temporal Ctx	8.5	15.3	12.0
AD 2 Hippo	20.9	28.3	25.0	Control (Path) 4 Temporal Ctx	31.2	36.6	52.1
AD 3 Hippo	0.0	0.9	0.6	AD 1 Occipital Ctx	2.7	3.0	0.0
AD 4 Hippo	2.1	7.1	2.6	AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 5 hippo	72.7	97.9	85.3	AD 3 Occipital Ctx	1.5	7.2	1.3
AD 6 Hippo	13.7	18.3	5.5	AD 4 Occipital Ctx	71.7	35.6	30.6
Control 2 Hippo	14.5	20.2	15.2	AD 5 Occipital	25.3	31.9	12.4

				Ctx			
Control 4 Hippo	11.7	7.4	5.1	AD 6 Occipital Ctx	17.2	19.1	11.2
Control (Path) 3 Hippo	6.7	4.4	4.5	Control 1 Occipital Ctx	7.0	9.0	8.1
AD 1 Temporal Ctx	4.0	1.7	2.8	Control 2 Occipital Ctx	33.2	44.8	26.1
AD 2 Temporal Ctx	80.7	50.7	37.4	Control 3 Occipital Ctx	30.1	37.6	21.9
AD 3 Temporal Ctx	3.6	0.0	1.1	Control 4 Occipital Ctx	16.3	12.6	8.2
AD 4 Temporal Ctx	19.5	30.6	15.2	Control (Path) 1 Occipital Ctx	42.0	55.9	52.9
AD 5 Inf Temporal Ctx	100.0	100.0	99.3	Control (Path) 2 Occipital Ctx	6.7	13.0	7.7
AD 5 SupTemp oral Ctx	32.8	29.1	33.2	Control (Path) 3 Occipital Ctx	8.7	6.6	5.4
AD 6 Inf Temporal Ctx	27.7	21.3	26.6	Control (Path) 4 Occipital Ctx	8.1	9.0	7.4
AD 6 Sup Temporal Ctx	41.8	53.6	17.0	Control 1 Parietal Ctx	21.2	23.0	15.3
Control 1 Temporal Ctx	12.0	33.9	18.3	Control 2 Parietal Ctx	48.6	38.2	22.1
Control 2 Temporal Ctx	30.1	49.3	44.4	Control 3 Parietal Ctx	28.3	34.4	32.8

Control 3 Temporal Ctx	38.7	39.5	33.4	Control (Path) 1 Parietal Ctx	78.5	97.3	100.0
Control 4 Temporal Ctx	17.6	25.2	24.1	Control (Path) 2 Parietal Ctx	50.7	50.7	37.9
Control (Path) 1 Temporal Ctx	69.7	70.7	49.7	Control (Path) 3 Parietal Ctx	10.7	10.1	9.6
Control (Path) 2 Temporal Ctx	35.4	50.7	33.4	Control (Path) 4 Parietal Ctx	30.6	24.5	40.9

Table RE. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3326, Run 215678613	Rel. Exp.(%) Ag3692, Run 217131191	Tissue Name	Rel. Exp.(%) Ag3326, Run 215678613	Rel. Exp.(%) Ag3692, Run 217131191
Adipose	0.0	0.0	Renal ca. TK-10	11.4	12.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.0	0.1
Melanoma* Hs688(B).T	0.1	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW- 948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.9	0.7	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.1	0.2	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT- 116	0.0	0.0
Prostate Pool	0.0	0.0	Colon ca. CaCo- 2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.1	0.0
Uterus Pool	0.0	0.0	Colon ca.	0.0	0.0

			SW1116		
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	0.0	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.1	0.0	Colon Pool	0.6	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.1	0.0
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.0	0.0
Ovarian ca. OVCAR-8	2.8	2.2	Bone Marrow Pool	0.0	0.1
Ovary	0.7	0.6	Fetal Heart	0.0	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.0	0.0
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	0.1	0.0
Breast ca. BT 549	0.6	0.8	Fetal Skeletal Muscle	0.0	0.0
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	0.0	0.0
Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.4	0.2
Breast Pool	0.0	0.1	Thymus Pool	0.0	0.0
Trachea	0.2	0.1	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	0.0
Fetal Lung	0.2	0.1	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	0.0	0.0	CNS cancer (glio) SF-295	0.1	0.1
Lung ca. A549	0.0	0.1	Brain (Amygdala) Pool	0.4	0.4
Lung ca.	2.0	0.0	Brain	1.4	1.0

NCI-H526			(cerebellum)		
Lung ca. NCI-H23	0.7	0.6	Brain (fetal)	0.7	0.4
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.5	0.7
Lung ca. HOP-62	0.1	0.2	Cerebral Cortex Pool	1.4	1.5
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	1.4	1.4
Liver	28.7	24.1	Brain (Thalamus) Pool	1.1	0.9
Fetal Liver	100.0	100.0	Brain (whole)	4.1	3.7
Liver ca. HepG2	29.5	26.2	Spinal Cord Pool	0.1	0.2
Kidney Pool	0.0	0.0	Adrenal Gland	2.6	1.9
Fetal Kidney	0.1	0.1	Pituitary gland Pool	0.0	0.2
Renal ca. 786-0	0.0	0.0	Salivary Gland	40.9	35.1
Renal ca. A498	0.0	0.0	Thyroid (female)	0.0	0.0
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.5	0.8
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	0.0

Table RE. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5818, Run 245382899	Tissue Name	Rel. Exp.(%) Ag5818, Run 245382899
Adipose	0.0	Renal ca. TK-10	13.4
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	1.4	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.5	Colon ca. HT29	0.0

Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.4
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	1.9	Bone Marrow Pool	0.0
Ovary	0.3	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.7
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.2	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.2	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	0.7
Lung ca. NCI-H526	0.0	Brain (cerebellum)	1.1
Lung ca. NCI-H23	1.5	Brain (fetal)	0.8
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.6

Lung ca. HOP-62	0.0	Cerebral Cortex Pool	1.7
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.2
Liver	40.3	Brain (Thalamus) Pool	1.3
Fetal Liver	100.0	Brain (whole)	5.6
Liver ca. HepG2	33.2	Spinal Cord Pool	0.3
Kidney Pool	0.0	Adrenal Gland	6.0
Fetal Kidney	0.0	Pituitary gland Pool	0.2
Renal ca. 786-0	0.0	Salivary Gland	67.4
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.7
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table RG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3692, Run 169987356	Rel. Exp.(%) Ag5818, Run 246920287	Tissue Name	Rel. Exp.(%) Ag3692, Run 169987356	Rel. Exp.(%) Ag5818, Run 246920287
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0
Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	0.0	0.0	HUVEC IL-11	0.0	0.0
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0
Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	11.3	0.0
Primary Tr1 act	4.2	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium	28.5	0.0

			TNFalpha + IL1beta		
Primary Th2 rest	0.0	0.0	Small airway epithelium none	5.7	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	3.9	0.0	Coronary artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	0.0	Astrocytes rest	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	3.6	24.3
CD4 lymphocyte none	0.0	0.0	KU-812 (Basophil) PMA/ionomycin	4.3	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	CCD1106 (Keratinocytes) none	10.7	0.0
LAK cells rest	0.0	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	0.0	0.0	Liver cirrhosis	94.0	27.5
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+IL-18	0.0	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.0	0.0	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	NCI-H292 IFN gamma	0.0	0.0
Two Way MLR 3 day	0.0	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	3.2	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0
Two Way MLR 7	0.0	0.0	Lung fibroblast	0.0	0.0

day			none		
PBMC rest	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	0.0	0.0
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.0	0.0
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	0.0
EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	Dermal fibroblast IFN gamma	0.0	0.0
Dendritic cells none	0.0	0.0	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	0.0	0.0	Dermal Fibroblasts rest	0.0	0.0
Dendritic cells anti-CD40	0.0	0.0	Neutrophils TNFa+LPS	0.0	0.0
Monocytes rest	0.0	0.0	Neutrophils rest	0.0	0.0
Monocytes LPS	0.0	0.0	Colon	0.0	0.0
Macrophages rest	0.0	0.0	Lung	0.0	0.0
Macrophages LPS	0.0	0.0	Thymus	2.4	0.0
HUVEC none	0.0	0.0	Kidney	100.0	100.0
HUVEC starved	0.0	0.0			

Table RH. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365	Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365
97457_Patient- 02go_adipose	0.0	94709_Donor 2 AM - A_adipose	0.2
97476_Patient- 07sk_skeletal muscle	0.0	94710_Donor 2 AM - B_adipose	0.0
97477_Patient-	0.0	94711_Donor 2 AM - C_adipose	0.0

07ut_uterus			
97478_Patient-07pl_placenta	0.0	94712_Donor 2 AD - A_adipose	0.0
99167_Bayer Patient 1	0.3	94713_Donor 2 AD - B_adipose	0.0
97482_Patient-08ut_uterus	0.0	94714_Donor 2 AD - C_adipose	0.0
97483_Patient-08pl_placenta	0.0	94742_Donor 3 U - A_Mesenchymal Stem Cells	0.0
97486_Patient-09sk_skeletal muscle	0.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	0.0
97487_Patient-09ut_uterus	0.0	94730_Donor 3 AM - A_adipose	0.0
97488_Patient-09pl_placenta	0.0	94731_Donor 3 AM - B_adipose	0.0
97492_Patient-10ut_uterus	0.0	94732_Donor 3 AM - C_adipose	0.0
97493_Patient-10pl_placenta	0.0	94733_Donor 3 AD - A_adipose	0.0
97495_Patient-11go_adipose	0.0	94734_Donor 3 AD - B_adipose	0.0
97496_Patient-11sk_skeletal muscle	0.0	94735_Donor 3 AD - C_adipose	0.0
97497_Patient-11ut_uterus	0.0	77138_Liver_HepG2untreated	100.0
97498_Patient-11pl_placenta	0.0	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	0.1	81735_Small Intestine	39.5
97501_Patient-12sk_skeletal muscle	0.3	72409_Kidney_Proximal Convoluted Tubule	0.0
97502_Patient-12ut_uterus	0.0	82685_Small intestine_Duodenum	0.0
97503_Patient-12pl_placenta	0.0	90650_Adrenal_Adrenocortical adenoma	0.0
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	0.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.0	72411_Kidney_HRE	0.0
94723_Donor 2 U - C_Mesenchymal Stem Cells	0.0	73139_Uterus_Uterine smooth muscle cells	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3326/Ag3692 - Three experiments done with two primer pairs (same sequence) are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's
 5 diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders. Ag5818 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag3326/Ag3692 Two experiments with the
 10 same probe and primer set produce results that are in excellent agreement. This gene is highly expressed in fetal liver (CT=26.5-27.0) and moderately expressed in adult liver (CT=28.5-28.8) and liver cancer cell line HepG2 (CT=28.4-28.8). This result agrees with the results seen in Panel 5 (expression in HepG2 (CT=29.2). These results are in agreement with published data that show a novel sodium dicarboxylate transporter in brain, choroid
 15 plexus kidney, intestine and liver. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for liver derived tissue.

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and cerebral cortex. Therefore, this gene may play a
 20 role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Low but significant levels of expression are also seen in the adrenal gland. Thus, this gene product may also be involved in metabolic disorders of this gland, including adrenoleukodystrophy and congenital adrenal hyperplasia.

25 **References:**

1. Pajor AM, Gangula R, Yao X. Cloning and functional characterization of a high-affinity Na(+)/dicarboxylate cotransporter from mouse brain. *Am J Physiol Cell Physiol* 2001 May;280(5):C1215-23.

2. Chen XZ, Shayakul C, Berger UV, Tian W, Hediger MA. Characterization of a
 30 rat Na⁺-dicarboxylate cotransporter. *J Biol Chem* 1998 Aug 14;273(33):20972-81.

General_screening_panel_v1.5 Summary: Ag5818 Results using this primer pair are in excellent agreement with the results seen in panel 1.4. See Panel 1.4 for discussion.

Panel 4.1D Summary: Ag3692 Significant expression of this gene is seen only in kidney and a liver cirrhosis sample (CTs=34.0). These results confirm that this gene is expressed in liver derived samples. The presence in the kidney is also in agreement with published results. Please see Panel 1.4. This gene product may be involved in maintaining or restoring normal function to the kidney during inflammation.

Panel 4D Summary: Ag3326 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 5 Islet Summary: Ag3326 The highest expression of this gene is in liver cancer cell line HepG2 (CT=29.2). There is also moderate expression in the small intestine (CT=30.5). These results compare well with previously published reports of sodium dicarboxylate transporter expression in mouse and rat (see discussion Panel 1.4).

15 **S. CG57732-01 and CG57732-02 and CG57732-03: CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE**

Expression of gene CG57732-01 and full length clones CG57732-02 and CG57732-03, was assessed using the primer-probe set Ag3317, described in Table SA. Results of the RTQ-PCR runs are shown in Tables SB, SC and SD. Please note CG57732-03 represents a splice variant of CG57732-01.

20 **Table SA.** Probe Name Ag3317

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggcctacaacgaaagtgaaga-3'	21	451	447
Probe	TET-5'-cagacactatgcaatgaaagtcctttcca-3'-TAMRA	29	472	448
Reverse	5'-ggaaagccatactgcttcagta-3'	22	510	449

Table SB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3317, Run 210144081	Tissue Name	Rel. Exp.(%) Ag3317, Run 210144081
AD 1 Hippo	10.7	Control (Path) 3	4.1

		Temporal Ctx	
AD 2 Hippo	23.7	Control (Path) 4 Temporal Ctx	42.6
AD 3 Hippo	4.5	AD 1 Occipital Ctx	12.5
AD 4 Hippo	7.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	97.9	AD 3 Occipital Ctx	5.4
AD 6 Hippo	25.7	AD 4 Occipital Ctx	18.4
Control 2 Hippo	24.8	AD 5 Occipital Ctx	21.8
Control 4 Hippo	4.3	AD 6 Occipital Ctx	58.6
Control (Path) 3 Hippo	2.8	Control 1 Occipital Ctx	1.5
AD 1 Temporal Ctx	10.4	Control 2 Occipital Ctx	94.0
AD 2 Temporal Ctx	35.8	Control 3 Occipital Ctx	21.5
AD 3 Temporal Ctx	5.8	Control 4 Occipital Ctx	2.6
AD 4 Temporal Ctx	23.2	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	88.9	Control (Path) 2 Occipital Ctx	13.8
AD 5 SupTemporal Ctx	26.6	Control (Path) 3 Occipital Ctx	0.9
AD 6 Inf Temporal Ctx	39.5	Control (Path) 4 Occipital Ctx	19.6
AD 6 Sup Temporal Ctx	47.3	Control 1 Parietal Ctx	4.9
Control 1 Temporal Ctx	4.4	Control 2 Parietal Ctx	33.0
Control 2 Temporal Ctx	63.3	Control 3 Parietal Ctx	27.4
Control 3 Temporal Ctx	20.4	Control (Path) 1 Parietal Ctx	95.9
Control 4 Temporal Ctx	8.7	Control (Path) 2 Parietal Ctx	24.5
Control (Path) 1 Temporal Ctx	77.4	Control (Path) 3 Parietal Ctx	2.0
Control (Path) 2 Temporal Ctx	38.7	Control (Path) 4 Parietal Ctx	51.8

Table SC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3317, Run	Tissue Name	Rel. Exp.(%) Ag3317, Run
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	215678602		215678602
Adipose	2.4	Renal ca. TK-10	14.2
Melanoma* Hs688(A).T	6.2	Bladder	10.5
Melanoma* Hs688(B).T	7.9	Gastric ca. (liver met.) NCI-N87	22.2
Melanoma* M14	18.2	Gastric ca. KATO III	23.0
Melanoma* LOXIMVI	9.4	Colon ca. SW-948	11.1
Melanoma* SK- MEL-5	9.8	Colon ca. SW480	20.9
Squamous cell carcinoma SCC-4	1.6	Colon ca.* (SW480 met) SW620	21.6
Testis Pool	13.1	Colon ca. HT29	11.3
Prostate ca.* (bone met) PC-3	6.4	Colon ca. HCT-116	27.0
Prostate Pool	3.1	Colon ca. CaCo-2	1.6
Placenta	1.8	Colon cancer tissue	11.3
Uterus Pool	3.9	Colon ca. SW1116	9.7
Ovarian ca. OVCAR-3	11.6	Colon ca. Colo-205	1.7
Ovarian ca. SK- OV-3	18.7	Colon ca. SW-48	8.8
Ovarian ca. OVCAR-4	3.4	Colon Pool	17.1
Ovarian ca. OVCAR-5	17.2	Small Intestine Pool	21.2
Ovarian ca. IGROV-1	6.2	Stomach Pool	5.3
Ovarian ca. OVCAR-8	4.7	Bone Marrow Pool	5.1
Ovary	2.9	Fetal Heart	6.8
Breast ca. MCF-7	6.1	Heart Pool	5.4
Breast ca. MDA- MB-231	20.3	Lymph Node Pool	13.4
Breast ca. BT 549	7.4	Fetal Skeletal Muscle	2.6
Breast ca. T47D	37.9	Skeletal Muscle Pool	2.3
Breast ca. MDA-N	9.0	Spleen Pool	2.8
Breast Pool	12.0	Thymus Pool	9.0
Trachea	17.2	CNS cancer (glio/astro) U87-MG	66.4
Lung	0.7	CNS cancer (glio/astro) U-118-MG	53.2
Fetal Lung	6.0	CNS cancer	4.6

		(neuro;met) SK-N-AS	
Lung ca. NCI-N417	16.5	CNS cancer (astro) SF-539	17.2
Lung ca. LX-1	20.9	CNS cancer (astro) SNB-75	21.5
Lung ca. NCI-H146	7.0	CNS cancer (glio) SNB-19	5.1
Lung ca. SHP-77	23.0	CNS cancer (glio) SF-295	12.2
Lung ca. A549	23.7	Brain (Amygdala) Pool	46.3
Lung ca. NCI-H526	4.4	Brain (cerebellum)	92.7
Lung ca. NCI-H23	5.8	Brain (fetal)	25.7
Lung ca. NCI-H460	10.3	Brain (Hippocampus) Pool	42.9
Lung ca. HOP-62	7.0	Cerebral Cortex Pool	100.0
Lung ca. NCI-H522	2.9	Brain (Substantia nigra) Pool	76.3
Liver	0.1	Brain (Thalamus) Pool	63.7
Fetal Liver	1.3	Brain (whole)	56.6
Liver ca. HepG2	1.4	Spinal Cord Pool	9.3
Kidney Pool	26.2	Adrenal Gland	16.2
Fetal Kidney	3.5	Pituitary gland Pool	16.4
Renal ca. 786-0	26.4	Salivary Gland	13.4
Renal ca. A498	14.2	Thyroid (female)	6.3
Renal ca. ACHN	33.2	Pancreatic ca. CAPAN2	2.6
Renal ca. UO-31	4.3	Pancreas Pool	19.6

Tissue Name	Rel. Exp.(%) Ag3317, Run 164683049	Tissue Name	Rel. Exp.(%) Ag3317, Run 164683049
Secondary Th1 act	21.6	HUVEC IL-1beta	3.8
Secondary Th2 act	23.2	HUVEC IFN gamma	12.5
Secondary Tr1 act	22.8	HUVEC TNF alpha + IFN gamma	2.9
Secondary Th1 rest	12.7	HUVEC TNF alpha + IL4	9.0
Secondary Th2 rest	9.3	HUVEC IL-11	4.0
Secondary Tr1 rest	33.7	Lung Microvascular EC none	24.3
Primary Th1 act	44.1	Lung Microvascular EC TNFalpha + IL-1beta	11.3

Primary Th2 act	49.3	Microvascular Dermal EC none	41.5
Primary Tr1 act	74.2	Microvascular Dermal EC TNFalpha + IL-1beta	17.2
Primary Th1 rest	38.2	Bronchial epithelium TNFalpha + IL1beta	31.2
Primary Th2 rest	44.4	Small airway epithelium none	8.0
Primary Tr1 rest	50.0	Small airway epithelium TNFalpha + IL-1beta	11.1
CD45RA CD4 lymphocyte act	41.2	Coronary artery SMC rest	20.6
CD45RO CD4 lymphocyte act	25.0	Coronary artery SMC TNFalpha + IL-1beta	19.6
CD8 lymphocyte act	17.8	Astrocytes rest	14.7
Secondary CD8 lymphocyte rest	21.8	Astrocytes TNFalpha + IL-1beta	11.0
Secondary CD8 lymphocyte act	7.4	KU-812 (Basophil) rest	2.1
CD4 lymphocyte none	21.8	KU-812 (Basophil) PMA/ionomycin	12.9
2ry Th1/Th2/Tr1_anti- CD95 CH11	5.8	CCD1106 (Keratinocytes) none	30.6
LAK cells rest	51.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	23.7
LAK cells IL-2	7.0	Liver cirrhosis	0.8
LAK cells IL-2+IL-12	25.5	Lupus kidney	2.2
LAK cells IL-2+IFN gamma	35.4	NCI-H292 none	33.7
LAK cells IL-2+ IL-18	28.7	NCI-H292 IL-4	43.5
LAK cells PMA/ionomycin	20.6	NCI-H292 IL-9	36.3
NK Cells IL-2 rest	13.5	NCI-H292 IL-13	35.6
Two Way MLR 3 day	33.0	NCI-H292 IFN gamma	24.3
Two Way MLR 5 day	9.6	HPAEC none	22.8
Two Way MLR 7 day	10.0	HPAEC TNF alpha + IL- 1 beta	8.3
PBMC rest	12.0	Lung fibroblast none	11.8
PBMC PWM	24.7	Lung fibroblast TNF alpha + IL-1 beta	1.2
PBMC PHA-L	32.5	Lung fibroblast IL-4	19.2
Ramos (B cell) none	1.5	Lung fibroblast IL-9	12.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	14.8

CNS_neurodegeneration_v1.0 Summary: Ag3317 - This panel does not show differential expression of this gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

- 5 **General_screening_panel_v1.4 Summary:** Ag3317 - There is low to moderate expression this gene across all samples on this panel. This gene is expressed at moderate levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and cerebral cortex. Highest expression is observed in the cerebral cortex (CT=29.0). This gene encodes a calmodulin-dependent protein kinase IV homolog, which is known to play
- 10 a role in Ca²⁺ signaling in the CNS that controls neuronal growth, differentiation, and plasticity. Mice deficient in calmodulin-dependent protein kinase IV were found to have cerebellar defects. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

15 This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis,

and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Based on expression in this panel, this gene may be also be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

References:

1. Okuno S, Kitani T, Fujisawa H. Evidence for the existence of Ca²⁺/calmodulin-dependent protein kinase IV kinase isoforms in rat brain. J Biochem (Tokyo) 1996 Jun;119(6):1176-81.

2. Ribar TJ, Rodriguiz RM, Khiroug L, Wetsel WC, Augustine GJ, Means AR. Cerebellar defects in Ca²⁺/calmodulin kinase IV-deficient mice. J Neurosci 2000 Nov 15;20(22):RC107.

Panel 4D Summary: Ag3317 - This gene was found to have low expression across almost all the samples on this panel, with the highest level of expression seen in kidney and resting dermal fibroblasts (CTs=32). Expression of Ca²⁺/calmodulin-dependent kinase type IV in thymocytes has been found in mice, where it plays a role in Ca²⁺-dependent gene transcription.

Reference

1. Raman V, Blaeser F, Ho N, Engle DL, Williams CB, Chatila TA. Requirement for Ca²⁺/calmodulin-dependent kinase type IV/Gr in setting the thymocyte selection threshold. J Immunol 2001 Dec 1;167(11):6270-8.

T. CG57709-01: Novel mitochondrial protein

Expression of gene CG57709-01 was assessed using the primer-probe set Ag3323, described in Table TA. Results of the RTQ-PCR runs are shown in Tables TB, TC and TD.

Table TA. Probe Name Ag3323

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atgtgcagaggatacgcatg-3'	20	589	450
Probe	TET-5'-tgcaaaacaggaagacaaaggaaggg-3'-TAMRA	26	626	451
Reverse	5'-tggttctggcattctagacg-3'	20	665	452

Table TB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3323, Run 210144152	Tissue Name	Rel. Exp.(%) Ag3323, Run 210144152
AD 1 Hippo	22.5	Control (Path) 3 Temporal Ctx	5.2
AD 2 Hippo	29.5	Control (Path) 4 Temporal Ctx	32.5
AD 3 Hippo	6.9	AD 1 Occipital Ctx	18.6
AD 4 Hippo	7.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	82.4	AD 3 Occipital Ctx	7.6
AD 6 Hippo	66.4	AD 4 Occipital Ctx	17.8
Control 2 Hippo	27.5	AD 5 Occipital Ctx	30.8
Control 4 Hippo	11.9	AD 6 Occipital Ctx	48.6
Control (Path) 3 Hippo	8.4	Control 1 Occipital Ctx	4.0
AD 1 Temporal Ctx	18.6	Control 2 Occipital Ctx	58.2
AD 2 Temporal Ctx	30.6	Control 3 Occipital Ctx	14.2
AD 3 Temporal Ctx	7.6	Control 4 Occipital Ctx	6.6
AD 4 Temporal Ctx	21.5	Control (Path) 1 Occipital Ctx	70.7
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	12.6
AD 5 Sup Temporal Ctx	42.6	Control (Path) 3 Occipital Ctx	2.4
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	14.6
AD 6 Sup Temporal Ctx	42.0	Control 1 Parietal Ctx	6.5

Control 1 Temporal Ctx	6.3	Control 2 Parietal Ctx	48.0
Control 2 Temporal Ctx	39.0	Control 3 Parietal Ctx	19.6
Control 3 Temporal Ctx	13.1	Control (Path) 1 Parietal Ctx	61.1
Control 4 Temporal Ctx	8.9	Control (Path) 2 Parietal Ctx	19.3
Control (Path) 1 Temporal Ctx	53.6	Control (Path) 3 Parietal Ctx	3.8
Control (Path) 2 Temporal Ctx	34.2	Control (Path) 4 Parietal Ctx	42.6

Table TC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3323, Run 165678151	Tissue Name	Rel. Exp.(%) Ag3323, Run 165678151
Liver adenocarcinoma	25.0	Kidney (fetal)	6.5
Pancreas	12.8	Renal ca. 786-0	14.3
Pancreatic ca. CAPAN 2	24.5	Renal ca. A498	34.2
Adrenal gland	12.2	Renal ca. RXF 393	14.2
Thyroid	6.9	Renal ca. ACHN	12.9
Salivary gland	14.0	Renal ca. UO-31	48.6
Pituitary gland	10.1	Renal ca. TK-10	7.2
Brain (fetal)	13.7	Liver	20.2
Brain (whole)	29.7	Liver (fetal)	22.1
Brain (amygdala)	21.3	Liver ca. (hepatoblast) HepG2	21.3
Brain (cerebellum)	24.7	Lung	6.7
Brain (hippocampus)	25.7	Lung (fetal)	14.8
Brain (substantia nigra)	20.0	Lung ca. (small cell) LX-1	39.8
Brain (thalamus)	27.2	Lung ca. (small cell) NCI-H69	25.0
Cerebral Cortex	33.0	Lung ca. (s.cell var.) SHP-77	42.3
Spinal cord	16.5	Lung ca. (large cell) NCI-H460	25.7
glio/astro U87-MG	8.9	Lung ca. (non-sm. cell) A549	12.0
glio/astro U-118-MG	100.0	Lung ca. (non-s.cell) NCI-H23	9.1

astrocytoma SW1783	14.6	Lung ca. (non-s.cell) HOP-62	9.5
neuro*; met SK-N-AS	43.2	Lung ca. (non-s.cl) NCI-H522	10.7
astrocytoma SF-539	13.9	Lung ca. (squam.) SW 900	12.4
astrocytoma SNB-75	29.7	Lung ca. (squam.) NCI-H596	59.0
glioma SNB-19	13.5	Mammary gland	10.6
glioma U251	43.8	Breast ca.* (pl.ef) MCF-7	46.3
glioma SF-295	17.7	Breast ca.* (pl.ef) MDA-MB-231	31.6
Heart (fetal)	22.7	Breast ca.* (pl.ef) T47D	15.1
Heart	14.5	Breast ca. BT-549	54.0
Skeletal muscle (fetal)	6.8	Breast ca. MDA-N	11.5
Skeletal muscle	55.5	Ovary	8.7
Bone marrow	10.7	Ovarian ca. OVCAR-3	26.2
Thymus	5.5	Ovarian ca. OVCAR-4	21.6
Spleen	13.3	Ovarian ca. OVCAR-5	20.9
Lymph node	24.8	Ovarian ca. OVCAR-8	12.6
Colorectal	8.8	Ovarian ca. IGROV-1	4.4
Stomach	15.1	Ovarian ca.* (ascites) SK-OV-3	23.5
Small intestine	28.3	Uterus	14.3
Colon ca. SW480	27.5	Placenta	6.9
Colon ca.* SW620(SW480 met)	17.6	Prostate	9.5
Colon ca. HT29	14.6	Prostate ca.* (bone met)PC-3	17.7
Colon ca. HCT-116	43.2	Testis	10.1
Colon ca. CaCo-2	12.7	Melanoma Hs688(A).T	7.6
Colon ca. tissue(ODO3866)	22.5	Melanoma* (met) Hs688(B).T	6.6
Colon ca. HCC-2998	25.2	Melanoma UACC-62	19.6
Gastric ca.* (liver met) NCI-N87	29.5	Melanoma M14	39.2

Bladder	6.1	Melanoma LOX IMVI	13.4
Trachea	13.2	Melanoma* (met) SK-MEL-5	21.2
Kidney	15.6	Adipose	6.5

Tissue Name	Rel. Exp.(%) Ag3323, Run 165296416	Tissue Name	Rel. Exp.(%) Ag3323, Run 165296416
Secondary Th1 act	32.3	HUVEC IL-1beta	3.8
Secondary Th2 act	22.8	HUVEC IFN gamma	12.0
Secondary Tr1 act	29.9	HUVEC TNF alpha + IFN gamma	8.1
Secondary Th1 rest	3.8	HUVEC TNF alpha + IL4	11.1
Secondary Th2 rest	4.3	HUVEC IL-11	8.4
Secondary Tr1 rest	6.0	Lung Microvascular EC none	7.6
Primary Th1 act	33.0	Lung Microvascular EC TNFalpha + IL-1beta	6.9
Primary Th2 act	25.0	Microvascular Dermal EC none	14.7
Primary Tr1 act	40.1	Microsvascular Dermal EC TNFalpha + IL-1beta	7.6
Primary Th1 rest	17.8	Bronchial epithelium TNFalpha + IL1beta	17.3
Primary Th2 rest	11.6	Small airway epithelium none	6.6
Primary Tr1 rest	15.0	Small airway epithelium TNFalpha + IL-1beta	18.4
CD45RA CD4 lymphocyte act	15.0	Coronary artery SMC rest	9.9
CD45RO CD4 lymphocyte act	24.7	Coronary artery SMC TNFalpha + IL-1beta	6.5
CD8 lymphocyte act	19.3	Astrocytes rest	5.1
Secondary CD8 lymphocyte rest	22.7	Astrocytes TNFalpha + IL-1beta	3.9
Secondary CD8 lymphocyte act	12.9	KU-812 (Basophil) rest	14.0
CD4 lymphocyte none	2.9	KU-812 (Basophil) PMA/ionomycin	22.1
2ry Th1/Th2/Tr1_anti- CD95 CH11	5.4	CCD1106 (Keratinocytes) none	16.0

LAK cells rest	7.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	8.1
LAK cells IL-2	17.2	Liver cirrhosis	1.7
LAK cells IL-2+IL-12	15.1	Lupus kidney	1.0
LAK cells IL-2+IFN gamma	27.9	NCI-H292 none	30.1
LAK cells IL-2+ IL-18	17.7	NCI-H292 IL-4	49.0
LAK cells PMA/ionomycin	1.9	NCI-H292 IL-9	33.2
NK Cells IL-2 rest	8.4	NCI-H292 IL-13	26.2
Two Way MLR 3 day	9.9	NCI-H292 IFN gamma	26.6
Two Way MLR 5 day	18.4	HPAEC none	11.7
Two Way MLR 7 day	8.9	HPAEC TNF alpha + IL- 1 beta	7.5
PBMC rest	3.8	Lung fibroblast none	8.0
PBMC PWM	50.3	Lung fibroblast TNF alpha + IL-1 beta	5.5
PBMC PHA-L	29.3	Lung fibroblast IL-4	19.1
Ramos (B cell) none	33.9	Lung fibroblast IL-9	15.3
Ramos (B cell) ionomycin	83.5	Lung fibroblast IL-13	11.4
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	16.5
B lymphocytes CD40L and IL-4	22.4	Dermal fibroblast CCD1070 rest	28.9
EOL-1 dbcAMP	10.5	Dermal fibroblast CCD1070 TNF alpha	31.2
EOL-1 dbcAMP PMA/ionomycin	3.7	Dermal fibroblast CCD1070 IL-1 beta	11.3
Dendritic cells none	9.9	Dermal fibroblast IFN gamma	5.2
Dendritic cells LPS	6.3	Dermal fibroblast IL-4	12.3
Dendritic cells anti- CD40	7.3	IBD Colitis 2	0.7
Monocytes rest	7.0	IBD Crohn's	1.0
Monocytes LPS	1.4	Colon	8.8
Macrophages rest	13.5	Lung	5.8
Macrophages LPS	3.5	Thymus	17.3
HUVEC none	11.9	Kidney	12.3
HUVEC starved	24.8		

CNS_neurodegeneration_v1.0 Summary: Ag3323 This panel does not show differential expression of the CG57709-01 gene in Alzheimer's disease. However, this expression

profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

Panel 1.3D Summary: Ag3323 - This gene is expressed at moderate levels in all samples on this panel, with highest expression in a brain cancer cell line. Expression is also seen in all the cancer cell lines on this panel. Thus, expression of this gene could be used to differentiate between this brain cancer cell line sample and other samples on this panel and as a marker for brain cancer.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This molecule is also expressed at moderate to low levels in the CNS and may be a small molecule target for the treatment of neurologic diseases such as Alzheimer's disease, Parkinson's disease, epilepsy, schizophrenia, stroke and multiple sclerosis.

Panel 4D Summary: Ag3323 - This gene is expressed at high to moderate levels in all samples on this panel, with highest expression in B lymphocytes stimulated with pokeweed mitogen (CT=24.5). In addition, this gene is expressed at higher levels in ionomycin-activated Ramos B lymphocytes. The high levels of expression in activated B lymphocytes suggests that therapies that antagonize the function of this gene product may reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

U. CG57700-01: HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II)

Expression of gene CG57700-01 was assessed using the primer-probe set Ag3311, described in Table UA. Results of the RTQ-PCR runs are shown in Table UB.

Table UA. Probe Name Ag3311

CD95 CH11		(Keratinocytes) none	
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.7
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	4.5	NCI-H292 IFN gamma	1.9
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL- 1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	3.7	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	14.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	4.3
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	1.6	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	2.1	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	3.0
Dendritic cells anti- CD40	2.5	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	100.0
Macrophages rest	0.0	Lung	29.3
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	2.4
HUVEC starved	0.0		

AI_comprehensive_panel_v1.0 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CNS_neurodegeneration_v1.0 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

- 5 **General_screening_panel_v1.4 Summary:** Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

- 10 **Panel 4D Summary:** Ag3311 - Significant expression of this gene is seen only in colon (CT=33.9). Therefore, expression of this gene can be used to distinguish between this sample and the others on the panel and between healthy and inflamed bowel. Since expression is not detectable in samples derived from Crohn's and colitis patients, therapeutic modulation of the expression or function of this gene may be useful in the treatment of inflammatory bowel disease.

V. CG58553-01: vasopressin receptor

- 15 Expression of gene CG58553-01 was assessed using the primer-probe set Ag3372, described in Table VA. Results of the RTQ-PCR runs are shown in Tables VB and VC.

Table VA. Probe Name Ag3372

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - cggatctggtcatcacaca - 3'	19	1983	457
Probe	TET-5' - ccacccacaacctcccaaggaact - 3' - TAMRA	24	2017	458
Reverse	5' - agcctcagaaggctcgagatg - 3'	20	2041	459

Table VB. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3372, Run 165524269	Tissue Name	Rel. Exp.(%) Ag3372, Run 165524269
Liver adenocarcinoma	0.7	Kidney (fetal)	0.0
Pancreas	0.2	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.1
Adrenal gland	0.0	Renal ca. RXF 393	0.0
Thyroid	0.1	Renal ca. ACHN	0.0

Salivary gland	0.1	Renal ca. UO-31	0.0
Pituitary gland	0.2	Renal ca. TK-10	0.0
Brain (fetal)	0.0	Liver	2.1
Brain (whole)	0.3	Liver (fetal)	0.0
Brain (amygdala)	0.0	Liver ca. (hepatoblast) HepG2	0.2
Brain (cerebellum)	0.1	Lung	2.4
Brain (hippocampus)	0.5	Lung (fetal)	0.2
Brain (substantia nigra)	0.2	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	0.0	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.0	Lung ca. (s.cell var.) SHP-77	0.1
Spinal cord	1.0	Lung ca. (large cell)NCI-H460	0.0
glio/astro U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.1
glio/astro U-118-MG	0.0	Lung ca. (non-s.cell) NCI-H23	0.6
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.1
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.0
astrocytoma SNB-75	0.1	Lung ca. (squam.) NCI-H596	0.0
glioma SNB-19	0.4	Mammary gland	0.7
glioma U251	0.2	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.0
Heart (fetal)	0.0	Breast ca.* (pl.ef) T47D	0.1
Heart	0.0	Breast ca. BT-549	0.0
Skeletal muscle (fetal)	0.0	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	1.6	Ovarian ca. OVCAR-3	0.2
Thymus	1.7	Ovarian ca. OVCAR-4	0.0
Spleen	2.8	Ovarian ca. OVCAR-5	0.2
Lymph node	5.5	Ovarian ca.	0.2

		OVCAR-8	
Colorectal	0.2	Ovarian ca. IGROV-1	0.0
Stomach	1.2	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	100.0	Uterus	0.0
Colon ca. SW480	0.0	Placenta	0.8
Colon ca.* SW620(SW480 met)	0.0	Prostate	0.1
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	1.4
Colon ca. CaCo-2	0.3	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	0.7	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	3.8	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	1.0	Melanoma M14	0.2
Bladder	0.0	Melanoma LOX IMVI	0.2
Trachea	0.1	Melanoma* (met) SK-MEL-5	0.4
Kidney	0.6	Adipose	1.3

Table VC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3372, Run 165296616	Tissue Name	Rel. Exp.(%) Ag3372, Run 165296616
Secondary Th1 act	1.4	HUVEC IL-1beta	0.0
Secondary Th2 act	1.4	HUVEC IFN gamma	0.0
Secondary Tr1 act	2.9	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	5.4	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	6.4	HUVEC IL-11	0.0
Secondary Tr1 rest	12.0	Lung Microvascular EC none	0.0
Primary Th1 act	11.4	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	18.9	Microvascular Dermal EC none	0.0
Primary Tr1 act	27.0	Microvascular Dermal	0.0

		EC TNFalpha + IL-1beta	
Primary Th1 rest	27.5	Bronchial epithelium TNFalpha + IL1beta	0.1
Primary Th2 rest	13.6	Small airway epithelium none	0.0
Primary Tr1 rest	32.8	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	3.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	8.5	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	5.8	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	3.1	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	2.9	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	4.7	KU-812 (Basophil) PMA/ionomycin	0.1
2ry Th1/Th2/Tr1_anti- CD95 CH11	7.5	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	1.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	5.8	Liver cirrhosis	1.5
LAK cells IL-2+IL-12	2.3	Lupus kidney	0.6
LAK cells IL-2+IFN gamma	5.5	NCI-H292 none	2.5
LAK cells IL-2+ IL-18	5.5	NCI-H292 IL-4	1.8
LAK cells PMA/ionomycin	2.7	NCI-H292 IL-9	5.9
NK Cells IL-2 rest	6.0	NCI-H292 IL-13	2.3
Two Way MLR 3 day	2.1	NCI-H292 IFN gamma	3.0
Two Way MLR 5 day	0.9	HPAEC none	0.0
Two Way MLR 7 day	1.8	HPAEC TNF alpha + IL- 1 beta	0.0
PBMC rest	1.5	Lung fibroblast none	0.0
PBMC PWM	5.6	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.9	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.2	Lung fibroblast IL-13	0.0
B lymphocytes PWM	2.2	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L	3.7	Dermal fibroblast	0.0

and IL-4		CCD1070 rest	
EOL-1 dbcAMP	1.0	Dermal fibroblast CCD1070 TNF alpha	5.2
EOL-1 dbcAMP PMA/ionomycin	0.4	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.2	Dermal fibroblast IFN gamma	0.1
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.0	IBD Colitis 2	0.4
Monocytes rest	0.3	IBD Crohn's	8.4
Monocytes LPS	0.2	Colon	100.0
Macrophages rest	0.7	Lung	0.9
Macrophages LPS	0.0	Thymus	8.1
HUVEC none	0.0	Kidney	6.8
HUVEC starved	0.0		

Panel 1.3D Summary: Ag3372 Highest expression of the CG58553-01 gene is seen in the small intestine sample (CT=26.8). This gene encodes a novel vasopressin gene that plays a role in regulating electrolyte transport in the colon. Therefore, regulation of the transcript or the protein it encodes could be important in maintaining normal cellular homeostasis and in the treatment of Crohn's disease and ulcerative colitis.

Among tissues with metabolic function, this gene is expressed in liver and adipose. Thus, this gene product may be involved in disorders that affect these tissues, such as obesity and type II diabetes.

Low, but significant expression is also seen in the hippocampus. The hippocampus is critical for learning and memory. Thus, this gene product may have utility treating CNS disorders involving memory deficits, including Alzheimer's disease and aging.

References:

1. Sato Y, Hanai H, Nogaki A, Hirasawa K, Kaneko E, Hayashi H, Suzuki Y. Role of the vasopressin V(1) receptor in regulating the epithelial functions of the guinea pig distal colon. Am J Physiol 1999 Oct;277(4 Pt 1):G819-28.

Panel 4D Summary: Ag3372 In agreement with the results seen in panel 1.4, the highest level of expression of this gene is in the colon sample (CT=27.5). Interestingly, the

expression is significantly lower in the IBD colitis 2 (CT>35) and IBD Crohn's (CT=30.9)samples. Therefore, alterations in the expression of this gene may be used in the treatment of Crohn's disease and ulcerative colitis.

In addition, the expression of the CG58553-01 gene in several preparations of T lymphocytes suggests that small molecule antagonists, therapeutic antibodies specific for this molecule, or the extracellular domain of this protein, may be useful to reduce or eliminate the symptoms of Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

10 W. CG58626-01: Phospholipase

Expression of gene CG58626-01 was assessed using the primer-probe set Ag3386, described in Table WA. Results of the RTQ-PCR runs are shown in Tables WB, WC and WD.

Table WA. Probe Name Ag3386

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-agtggcgggtcaaaacttactct-3'	22	1386	460
Probe	TET-5'-tggagacactgttgattccattactcctg-3'-TAMRA	29	1411	461
Reverse	5'-ctgctgttcagcatatccctta-3'	22	1455	462

15 Table WB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3386, Run 210154893	Tissue Name	Rel. Exp.(%) Ag3386, Run 210154893
AD 1 Hippo	6.4	Control (Path) 3 Temporal Ctx	4.2
AD 2 Hippo	21.5	Control (Path) 4 Temporal Ctx	25.0
AD 3 Hippo	5.0	AD 1 Occipital Ctx	14.4
AD 4 Hippo	5.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	95.3	AD 3 Occipital Ctx	3.3
AD 6 Hippo	51.1	AD 4 Occipital	18.7

		Ctx	
Control 2 Hippo	26.4	AD 5 Occipital Ctx	28.7
Control 4 Hippo	4.5	AD 6 Occipital Ctx	52.5
Control (Path) 3 Hippo	4.0	Control 1 Occipital Ctx	2.4
AD 1 Temporal Ctx	13.5	Control 2 Occipital Ctx	56.3
AD 2 Temporal Ctx	24.5	Control 3 Occipital Ctx	11.0
AD 3 Temporal Ctx	3.8	Control 4 Occipital Ctx	4.3
AD 4 Temporal Ctx	18.9	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	95.9	Control (Path) 2 Occipital Ctx	8.8
AD 5 Sup Temporal Ctx	37.6	Control (Path) 3 Occipital Ctx	1.7
AD 6 Inf Temporal Ctx	52.5	Control (Path) 4 Occipital Ctx	12.3
AD 6 Sup Temporal Ctx	63.7	Control 1 Parietal Ctx	5.4
Control 1 Temporal Ctx	4.9	Control 2 Parietal Ctx	39.5
Control 2 Temporal Ctx	38.4	Control 3 Parietal Ctx	11.3
Control 3 Temporal Ctx	12.2	Control (Path) 1 Parietal Ctx	77.4
Control 4 Temporal Ctx	5.0	Control (Path) 2 Parietal Ctx	20.7
Control (Path) 1 Temporal Ctx	76.8	Control (Path) 3 Parietal Ctx	2.7
Control (Path) 2 Temporal Ctx	37.6	Control (Path) 4 Parietal Ctx	45.4

Table WC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3386, Run 217043839	Tissue Name	Rel. Exp.(%) Ag3386, Run 217043839
Adipose	12.2	Renal ca. TK-10	10.7
Melanoma* Hs688(A).T	26.4	Bladder	18.4
Melanoma*	30.4	Gastric ca. (liver met.)	26.6

Hs688(B).T		NCI-N87	
Melanoma* M14	13.1	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	22.8	Colon ca. SW-948	10.8
Melanoma* SK-MEL-5	22.7	Colon ca. SW480	40.9
Squamous cell carcinoma SCC-4	11.2	Colon ca.* (SW480 met) SW620	20.4
Testis Pool	47.0	Colon ca. HT29	5.2
Prostate ca.* (bone met) PC-3	80.1	Colon ca. HCT-116	100.0
Prostate Pool	7.1	Colon ca. CaCo-2	13.8
Placenta	3.2	Colon cancer tissue	13.6
Uterus Pool	6.4	Colon ca. SW1116	10.2
Ovarian ca. OVCAR-3	22.8	Colon ca. Colo-205	1.8
Ovarian ca. SK-OV-3	94.0	Colon ca. SW-48	2.4
Ovarian ca. OVCAR-4	4.7	Colon Pool	27.7
Ovarian ca. OVCAR-5	29.3	Small Intestine Pool	14.6
Ovarian ca. IGROV-1	12.7	Stomach Pool	12.2
Ovarian ca. OVCAR-8	11.1	Bone Marrow Pool	6.9
Ovary	11.6	Fetal Heart	8.1
Breast ca. MCF-7	36.9	Heart Pool	6.3
Breast ca. MDA-MB-231	39.5	Lymph Node Pool	13.9
Breast ca. BT 549	28.5	Fetal Skeletal Muscle	3.6
Breast ca. T47D	52.9	Skeletal Muscle Pool	6.7
Breast ca. MDA-N	11.3	Spleen Pool	17.1
Breast Pool	28.1	Thymus Pool	26.1
Trachea	11.0	CNS cancer (glio/astro) U87-MG	33.2
Lung	6.0	CNS cancer (glio/astro) U-118-MG	44.1
Fetal Lung	39.2	CNS cancer (neuro;met) SK-N-AS	44.4
Lung ca. NCI-N417	6.3	CNS cancer (astro) SF-539	10.4
Lung ca. LX-1	33.9	CNS cancer (astro) SNB-75	27.7

Lung ca. NCI-H146	14.3	CNS cancer (glio) SNB-19	10.2
Lung ca. SHP-77	73.2	CNS cancer (glio) SF-295	28.7
Lung ca. A549	25.3	Brain (Amygdala) Pool	23.2
Lung ca. NCI-H526	5.8	Brain (cerebellum)	19.8
Lung ca. NCI-H23	30.1	Brain (fetal)	35.6
Lung ca. NCI-H460	20.2	Brain (Hippocampus) Pool	25.2
Lung ca. HOP-62	11.9	Cerebral Cortex Pool	39.2
Lung ca. NCI-H522	20.7	Brain (Substantia nigra) Pool	23.0
Liver	0.7	Brain (Thalamus) Pool	45.7
Fetal Liver	29.5	Brain (whole)	24.0
Liver ca. HepG2	10.1	Spinal Cord Pool	22.5
Kidney Pool	21.3	Adrenal Gland	8.5
Fetal Kidney	19.5	Pituitary gland Pool	7.0
Renal ca. 786-0	15.9	Salivary Gland	1.9
Renal ca. A498	3.5	Thyroid (female)	3.2
Renal ca. ACHN	8.0	Pancreatic ca. CAPAN2	3.7
Renal ca. UO-31	12.2	Pancreas Pool	18.2

Table WD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3386, Run 165296474	Tissue Name	Rel. Exp.(%) Ag3386, Run 165296474
Secondary Th1 act	30.4	HUVEC IL-1beta	2.0
Secondary Th2 act	35.6	HUVEC IFN gamma	3.3
Secondary Tr1 act	27.9	HUVEC TNF alpha + IFN gamma	3.8
Secondary Th1 rest	8.9	HUVEC TNF alpha + IL4	3.3
Secondary Th2 rest	8.0	HUVEC IL-11	1.5
Secondary Tr1 rest	11.3	Lung Microvascular EC none	5.5
Primary Th1 act	57.4	Lung Microvascular EC TNFalpha + IL-1beta	4.8
Primary Th2 act	36.9	Microvascular Dermal EC none	3.7
Primary Tr1 act	51.1	Microvascular Dermal EC TNFalpha + IL-1beta	3.3
Primary Th1 rest	54.0	Bronchial epithelium	5.5

		TNFalpha + IL1beta	
Primary Th2 rest	18.8	Small airway epithelium none	2.1
Primary Tr1 rest	24.7	Small airway epithelium TNFalpha + IL-1beta	6.1
CD45RA CD4 lymphocyte act	12.4	Coronary artery SMC rest	4.6
CD45RO CD4 lymphocyte act	33.9	Coronary artery SMC TNFalpha + IL-1beta	2.4
CD8 lymphocyte act	29.3	Astrocytes rest	3.0
Secondary CD8 lymphocyte rest	26.1	Astrocytes TNFalpha + IL-1beta	3.0
Secondary CD8 lymphocyte act	20.7	KU-812 (Basophil) rest	12.1
CD4 lymphocyte none	1.1	KU-812 (Basophil) PMA/ionomycin	27.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	12.8	CCD1106 (Keratinocytes) none	2.7
LAK cells rest	12.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.8
LAK cells IL-2	24.3	Liver cirrhosis	0.3
LAK cells IL-2+IL-12	28.7	Lupus kidney	0.7
LAK cells IL-2+IFN gamma	42.0	NCI-H292 none	8.1
LAK cells IL-2+ IL-18	45.1	NCI-H292 IL-4	9.5
LAK cells PMA/ionomycin	8.8	NCI-H292 IL-9	8.5
NK Cells IL-2 rest	21.8	NCI-H292 IL-13	4.5
Two Way MLR 3 day	18.7	NCI-H292 IFN gamma	3.6
Two Way MLR 5 day	11.0	HPAEC none	2.5
Two Way MLR 7 day	10.9	HPAEC TNF alpha + IL-1 beta	3.0
PBMC rest	4.5	Lung fibroblast none	4.6
PBMC PWM	66.0	Lung fibroblast TNF alpha + IL-1 beta	3.3
PBMC PHA-L	17.9	Lung fibroblast IL-4	12.1
Ramos (B cell) none	26.1	Lung fibroblast IL-9	12.3
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	6.7
B lymphocytes PWM	88.9	Lung fibroblast IFN gamma	16.6
B lymphocytes CD40L and IL-4	49.3	Dermal fibroblast CCD1070 rest	8.2
EOL-1 dbcAMP	13.0	Dermal fibroblast	37.1

		CCD1070 TNF alpha	
EOL-1 dbcAMP PMA/ionomycin	9.5	Dermal fibroblast CCD1070 IL-1 beta	4.4
Dendritic cells none	8.9	Dermal fibroblast IFN gamma	6.0
Dendritic cells LPS	5.4	Dermal fibroblast IL-4	12.1
Dendritic cells anti- CD40	4.3	IBD Colitis 2	0.7
Monocytes rest	4.7	IBD Crohn's	0.5
Monocytes LPS	2.6	Colon	3.4
Macrophages rest	8.8	Lung	4.9
Macrophages LPS	2.8	Thymus	4.1
HUVEC none	2.8	Kidney	13.0
HUVEC starved	6.4		

CNS_neurodegeneration_v1.0 Summary: Ag3386 This panel confirms the expression of this gene at moderate to low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3386 This gene is moderately expressed in most of the samples on this panel. Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3386 The CG58626-01 transcript is expressed ubiquitously in this panel. Highest expression of this transcript is seen in activated Ramos cells and activated B cells (CTs=27). The expression of this transcript in activated lymphoid cells when compared to non activated cells suggests that the CG58626-01 gene may be important for the diagnosis or pathogenesis of immune mediated diseases. Therefore, modulation of the expression and/or activity of this gene product might important for the treatment of autoimmune diseases, allergy, and delayed type hypersensitivity.

X. CG57597-01: Hypothetical protein

Expression of gene CG57597-01 was assessed using the primer-probe set Ag3293, described in Table XA.

Table XA. Probe Name Ag3293

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - cagaaacctgtgaactctgcat - 3'	22	40	463
Probe	TET-5' - atgcaccaccactcctggctaatttt - 3' - TAMRA	26	69	464
Reverse	5' - ataaaagggtttgagccggatt - 3'	21	115	465

CNS_neurodegeneration_v1.0 Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Y. CG57804-01: talin

Expression of gene CG57804-01 was assessed using the primer-probe set Ag3337, described in Table YA. Results of the RTQ-PCR runs are shown in Tables YB, YC and YD.

Table YA. Probe Name Ag3337

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggatttcaagcccagatacaat-3'	22	781	466
Probe	TET-5'-tggaacctcatgtggaacataaacaca-3'-TAMRA	26	804	467
Reverse	5'-ggcaggaattccttcagatc-3'	20	844	468

Table YB. CNS neurodegeneration v1.0

Tissue Name	Rel. Exp.(%) Ag3337, Run 210138775	Tissue Name	Rel. Exp.(%) Ag3337, Run 210138775
AD 1 Hippo	6.8	Control (Path) 3 Temporal Ctx	3.6
AD 2 Hippo	25.3	Control (Path) 4 Temporal Ctx	22.4
AD 3 Hippo	3.6	AD 1 Occipital Ctx	5.6
AD 4 Hippo	5.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	78.5	AD 3 Occipital Ctx	2.2
AD 6 Hippo	27.5	AD 4 Occipital Ctx	14.7
Control 2 Hippo	27.4	AD 5 Occipital Ctx	44.1
Control 4 Hippo	8.1	AD 6 Occipital Ctx	16.6
Control (Path) 3 Hippo	4.3	Control 1 Occipital Ctx	1.6
AD 1 Temporal Ctx	7.6	Control 2 Occipital Ctx	67.8
AD 2 Temporal Ctx	24.5	Control 3 Occipital Ctx	11.9
AD 3 Temporal Ctx	3.3	Control 4 Occipital Ctx	3.0
AD 4 Temporal Ctx	15.3	Control (Path) 1 Occipital Ctx	89.5
AD 5 Inf Temporal Ctx	89.5	Control (Path) 2 Occipital Ctx	8.2
AD 5 Sup Temporal Ctx	35.8	Control (Path) 3 Occipital Ctx	0.6
AD 6 Inf Temporal Ctx	27.4	Control (Path) 4 Occipital Ctx	10.3
AD 6 Sup Temporal Ctx	32.8	Control 1 Parietal Ctx	3.6
Control 1 Temporal Ctx	3.4	Control 2 Parietal Ctx	23.7
Control 2 Temporal Ctx	47.6	Control 3 Parietal Ctx	14.1
Control 3	12.4	Control (Path) 1	100.0

Temporal Ctx		Parietal Ctx	
Control 3 Temporal Ctx	5.8	Control (Path) 2 Parietal Ctx	21.9
Control (Path) 1 Temporal Ctx	64.2	Control (Path) 3 Parietal Ctx	2.0
Control (Path) 2 Temporal Ctx	42.0	Control (Path) 4 Parietal Ctx	39.2

Table YC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3337, Run 215773748	Tissue Name	Rel. Exp.(%) Ag3337, Run 215773748
Adipose	20.2	Renal ca. TK-10	22.1
Melanoma* Hs688(A).T	58.6	Bladder	14.2
Melanoma* Hs688(B).T	22.8	Gastric ca. (liver met.) NCI-N87	16.2
Melanoma* M14	5.7	Gastric ca. KATO III	100.0
Melanoma* LOXIMVI	5.5	Colon ca. SW-948	16.3
Melanoma* SK- MEL-5	3.4	Colon ca. SW480	4.2
Squamous cell carcinoma SCC-4	4.4	Colon ca.* (SW480 met) SW620	2.6
Testis Pool	5.1	Colon ca. HT29	0.7
Prostate ca.* (bone met) PC-3	6.4	Colon ca. HCT-116	7.6
Prostate Pool	3.4	Colon ca. CaCo-2	81.8
Placenta	1.6	Colon cancer tissue	1.7
Uterus Pool	2.1	Colon ca. SW1116	1.6
Ovarian ca. OVCAR-3	8.9	Colon ca. Colo-205	0.1
Ovarian ca. SK- OV-3	32.1	Colon ca. SW-48	3.2
Ovarian ca. OVCAR-4	7.2	Colon Pool	8.0
Ovarian ca. OVCAR-5	21.0	Small Intestine Pool	7.9
Ovarian ca. IGROV-1	23.5	Stomach Pool	5.7
Ovarian ca. OVCAR-8	5.4	Bone Marrow Pool	3.8
Ovary	11.7	Fetal Heart	24.8
Breast ca. MCF-7	5.1	Heart Pool	10.2

Breast ca. MDA-MB-231	19.5	Lymph Node Pool	10.6
Breast ca. BT 549	11.7	Fetal Skeletal Muscle	30.1
Breast ca. T47D	30.8	Skeletal Muscle Pool	24.8
Breast ca. MDA-N	5.0	Spleen Pool	2.9
Breast Pool	6.9	Thymus Pool	0.0
Trachea	10.3	CNS cancer (glio/astro) U87-MG	10.7
Lung	2.2	CNS cancer (glio/astro) U-118-MG	68.3
Fetal Lung	10.8	CNS cancer (neuro;met) SK-N-AS	23.5
Lung ca. NCI-N417	0.8	CNS cancer (astro) SF-539	21.5
Lung ca. LX-1	1.7	CNS cancer (astro) SNB-75	40.3
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	27.7
Lung ca. SHP-77	11.9	CNS cancer (glio) SF-295	38.2
Lung ca. A549	13.6	Brain (Amygdala) Pool	28.7
Lung ca. NCI-H526	7.6	Brain (cerebellum)	38.7
Lung ca. NCI-H23	10.2	Brain (fetal)	58.6
Lung ca. NCI-H460	5.1	Brain (Hippocampus) Pool	25.7
Lung ca. HOP-62	3.8	Cerebral Cortex Pool	59.0
Lung ca. NCI-H522	10.1	Brain (Substantia nigra) Pool	39.2
Liver	0.3	Brain (Thalamus) Pool	51.4
Fetal Liver	15.3	Brain (whole)	58.2
Liver ca. HepG2	53.2	Spinal Cord Pool	18.6
Kidney Pool	18.4	Adrenal Gland	11.1
Fetal Kidney	11.4	Pituitary gland Pool	4.7
Renal ca. 786-0	31.0	Salivary Gland	14.0
Renal ca. A498	0.7	Thyroid (female)	4.9
Renal ca. ACHN	20.3	Pancreatic ca. CAPAN2	7.5
Renal ca. UO-31	8.1	Pancreas Pool	9.4

Table YD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3337, Run 165725932	Tissue Name	Rel. Exp.(%) Ag3337, Run 165725932
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Secondary Th1 act	0.0	HUVEC IL-1beta	0.7
Secondary Th2 act	0.0	HUVEC IFN gamma	3.9
Secondary Tr1 act	0.4	HUVEC TNF alpha + IFN gamma	0.3
Secondary Th1 rest	0.4	HUVEC TNF alpha + IL4	0.6
Secondary Th2 rest	0.0	HUVEC IL-11	0.3
Secondary Tr1 rest	0.3	Lung Microvascular EC none	2.1
Primary Th1 act	0.3	Lung Microvascular EC TNFalpha + IL-1beta	5.1
Primary Th2 act	1.3	Microvascular Dermal EC none	16.4
Primary Tr1 act	0.6	Microvascular Dermal EC TNFalpha + IL-1beta	9.8
Primary Th1 rest	1.3	Bronchial epithelium TNFalpha + IL1beta	1.2
Primary Th2 rest	0.6	Small airway epithelium none	1.3
Primary Tr1 rest	0.3	Small airway epithelium TNFalpha + IL-1beta	2.1
CD45RA CD4 lymphocyte act	18.7	Coronary artery SMC rest	9.9
CD45RO CD4 lymphocyte act	0.6	Coronary artery SMC TNFalpha + IL-1beta	3.5
CD8 lymphocyte act	1.2	Astrocytes rest	100.0
Secondary CD8 lymphocyte rest	0.9	Astrocytes TNFalpha + IL-1beta	65.5
Secondary CD8 lymphocyte act	0.2	KU-812 (Basophil) rest	11.7
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	8.5
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	CCD1106 (Keratinocytes) none	2.0
LAK cells rest	4.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.0
LAK cells IL-2	1.2	Liver cirrhosis	3.6
LAK cells IL-2+IL-12	0.4	Lupus kidney	13.6
LAK cells IL-2+IFN gamma	2.1	NCI-H292 none	11.0
LAK cells IL-2+ IL-18	1.2	NCI-H292 IL-4	25.0
LAK cells PMA/ionomycin	2.0	NCI-H292 IL-9	15.6
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	12.5

Two Way MLR 3 day	5.2	NCI-H292 IFN gamma	4.6
Two Way MLR 5 day	2.7	HPAEC none	1.5
Two Way MLR 7 day	1.8	HPAEC TNF alpha + IL-1 beta	2.5
PBMC rest	0.2	Lung fibroblast none	80.1
PBMC PWM	1.9	Lung fibroblast TNF alpha + IL-1 beta	22.7
PBMC PHA-L	0.3	Lung fibroblast IL-4	97.3
Ramos (B cell) none	2.4	Lung fibroblast IL-9	47.6
Ramos (B cell) ionomycin	2.1	Lung fibroblast IL-13	81.8
B lymphocytes PWM	0.7	Lung fibroblast IFN gamma	50.7
B lymphocytes CD40L and IL-4	0.6	Dermal fibroblast CCD1070 rest	94.6
EOL-1 dbcAMP	4.9	Dermal fibroblast CCD1070 TNF alpha	43.2
EOL-1 dbcAMP PMA/ionomycin	1.2	Dermal fibroblast CCD1070 IL-1 beta	31.2
Dendritic cells none	12.8	Dermal fibroblast IFN gamma	14.2
Dendritic cells LPS	1.3	Dermal fibroblast IL-4	95.9
Dendritic cells anti-CD40	11.4	IBD Colitis 2	1.2
Monocytes rest	0.5	IBD Crohn's	9.1
Monocytes LPS	1.3	Colon	60.7
Macrophages rest	13.6	Lung	8.0
Macrophages LPS	2.8	Thymus	39.2
HUVEC none	1.0	Kidney	10.4
HUVEC starved	1.6		

CNS_neurodegeneration_v1.0 Summary: Ag3337 - This panel confirms the expression of this gene at low to moderate levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders

General_screening_panel_v1.4 Summary: Ag3337 - This gene is expressed in almost all samples on this panel. This gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, this gene is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and

5 Types 1 and 2 diabetes.

Panel 4D Summary: Ag3337 This gene is most highly expressed in resting astrocytes (CT=28.9). In addition, this gene is highly expressed in a cluster of treated and untreated samples derived from lung and dermal fibroblasts. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pathological and inflammatory lung and skin diseases, such as psoriasis, asthma, emphysema, and allergies.

Z. CG57551-01: NAC-1 Like Gene

Expression of gene CG57551-01 was assessed using the primer-probe set Ag3282, described in Table ZA. Results of the RTQ-PCR runs are shown in Tables ZB, ZC and ZD.

Table ZA. Probe Name Ag3282

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cagatcctcagcttctgctaca-3'	22	269	469
Probe	TET-5'-accagttcctgctcatgtacacggct-3'- TAMRA	26	318	470
Reverse	5'-atctcctggatctgcaggaa-3'	20	347	471

15 Table ZB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3282, Run 210060482	Tissue Name	Rel. Exp.(%) Ag3282, Run 210060482
AD 1 Hippo	22.8	Control (Path) 3 Temporal Ctx	9.7
AD 2 Hippo	49.0	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	11.5	AD 1 Occipital Ctx	16.5
AD 4 Hippo	12.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	66.9	AD 3 Occipital Ctx	10.2
AD 6 Hippo	59.9	AD 4 Occipital	18.2

		Ctx	
Control 2 Hippo	49.3	AD 5 Occipital Ctx	9.5
Control 4 Hippo	18.7	AD 6 Occipital Ctx	41.5
Control (Path) 3 Hippo	6.3	Control 1 Occipital Ctx	6.8
AD 1 Temporal Ctx	19.2	Control 2 Occipital Ctx	91.4
AD 2 Temporal Ctx	40.3	Control 3 Occipital Ctx	16.3
AD 3 Temporal Ctx	14.3	Control 4 Occipital Ctx	12.2
AD 4 Temporal Ctx	18.3	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	66.0	Control (Path) 2 Occipital Ctx	9.2
AD 5 Sup Temporal Ctx	37.4	Control (Path) 3 Occipital Ctx	5.3
AD 6 Inf Temporal Ctx	36.1	Control (Path) 4 Occipital Ctx	15.8
AD 6 Sup Temporal Ctx	34.4	Control 1 Parietal Ctx	11.7
Control 1 Temporal Ctx	10.0	Control 2 Parietal Ctx	34.2
Control 2 Temporal Ctx	74.7	Control 3 Parietal Ctx	23.3
Control 3 Temporal Ctx	15.0	Control (Path) 1 Parietal Ctx	72.7
Control 4 Temporal Ctx	15.5	Control (Path) 2 Parietal Ctx	21.6
Control (Path) 1 Temporal Ctx	74.2	Control (Path) 3 Parietal Ctx	5.5
Control (Path) 2 Temporal Ctx	31.2	Control (Path) 4 Parietal Ctx	35.8

Table ZC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3282, Run 216512995	Tissue Name	Rel. Exp.(%) Ag3282, Run 216512995
Adipose	1.8	Renal ca. TK-10	22.7
Melanoma* Hs688(A).T	16.3	Bladder	6.3
Melanoma*	25.0	Gastric ca. (liver met.)	47.0

Hs688(B).T		NCI-N87	
Melanoma* M14	25.3	Gastric ca. KATO III	45.7
Melanoma* LOXIMVI	21.6	Colon ca. SW-948	19.3
Melanoma* SK-MEL-5	17.0	Colon ca. SW480	50.3
Squamous cell carcinoma SCC-4	24.7	Colon ca.* (SW480 met) SW620	25.9
Testis Pool	6.1	Colon ca. HT29	17.7
Prostate ca.* (bone met) PC-3	67.8	Colon ca. HCT-116	100.0
Prostate Pool	3.5	Colon ca. CaCo-2	29.1
Placenta	9.6	Colon cancer tissue	14.0
Uterus Pool	0.6	Colon ca. SW1116	12.7
Ovarian ca. OVCAR-3	41.2	Colon ca. Colo-205	7.6
Ovarian ca. SK-OV-3	65.5	Colon ca. SW-48	5.8
Ovarian ca. OVCAR-4	35.8	Colon Pool	4.9
Ovarian ca. OVCAR-5	37.6	Small Intestine Pool	2.4
Ovarian ca. IGROV-1	28.9	Stomach Pool	3.3
Ovarian ca. OVCAR-8	14.2	Bone Marrow Pool	1.5
Ovary	3.9	Fetal Heart	3.0
Breast ca. MCF-7	42.3	Heart Pool	2.2
Breast ca. MDA-MB-231	69.7	Lymph Node Pool	5.6
Breast ca. BT 549	51.4	Fetal Skeletal Muscle	1.5
Breast ca. T47D	86.5	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	26.4	Spleen Pool	2.8
Breast Pool	4.6	Thymus Pool	3.8
Trachea	8.7	CNS cancer (glio/astro) U87-MG	60.3
Lung	0.2	CNS cancer (glio/astro) U-118-MG	100.0
Fetal Lung	6.3	CNS cancer (neuro;met) SK-N-AS	47.3
Lung ca. NCI-N417	8.4	CNS cancer (astro) SF-539	22.8
Lung ca. LX-1	17.3	CNS cancer (astro) SNB-75	47.3

Tissue Name	Rel. Exp.(%) Ag3282, Run 164634321	Tissue Name	Rel. Exp.(%) Ag3282, Run 164634321
Secondary Th1 act	52.9	HUVEC IL-1beta	13.6
Secondary Th2 act	67.8	HUVEC IFN gamma	42.9
Secondary Tr1 act	75.3	HUVEC TNF alpha + IFN gamma	37.1
Secondary Th1 rest	8.4	HUVEC TNF alpha + IL4	42.6
Secondary Th2 rest	11.4	HUVEC IL-11	25.9
Secondary Tr1 rest	12.2	Lung Microvascular EC none	41.2
Primary Th1 act	53.6	Lung Microvascular EC TNFalpha + IL-1beta	36.3
Primary Th2 act	44.4	Microvascular Dermal EC none	50.3
Primary Tr1 act	60.7	Microsvascular Dermal EC TNFalpha + IL-1beta	33.0
Primary Th1 rest	37.6	Bronchial epithelium	51.4

		TNFalpha + IL1beta	
Primary Th2 rest	15.8	Small airway epithelium none	23.3
Primary Tr1 rest	18.3	Small airway epithelium TNFalpha + IL-1beta	71.7
CD45RA CD4 lymphocyte act	33.0	Coronary artery SMC rest	43.5
CD45RO CD4 lymphocyte act	54.7	Coronary artery SMC TNFalpha + IL-1beta	31.0
CD8 lymphocyte act	42.9	Astrocytes rest	38.4
Secondary CD8 lymphocyte rest	50.3	Astrocytes TNFalpha + IL-1beta	37.1
Secondary CD8 lymphocyte act	32.5	KU-812 (Basophil) rest	36.1
CD4 lymphocyte none	2.4	KU-812 (Basophil) PMA/ionomycin	90.8
2ry Th1/Th2/Tr1_anti-CD95 CH11	11.7	CCD1106 (Keratinocytes) none	64.2
LAK cells rest	18.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	34.4
LAK cells IL-2	41.2	Liver cirrhosis	2.9
LAK cells IL-2+IL-12	29.5	Lupus kidney	2.2
LAK cells IL-2+IFN gamma	36.3	NCI-H292 none	38.4
LAK cells IL-2+ IL-18	34.2	NCI-H292 IL-4	66.9
LAK cells PMA/ionomycin	11.8	NCI-H292 IL-9	62.4
NK Cells IL-2 rest	29.3	NCI-H292 IL-13	65.1
Two Way MLR 3 day	21.9	NCI-H292 IFN gamma	48.3
Two Way MLR 5 day	27.7	HPAEC none	31.2
Two Way MLR 7 day	27.0	HPAEC TNF alpha + IL-1 beta	37.6
PBMC rest	6.5	Lung fibroblast none	35.6
PBMC PWM	89.5	Lung fibroblast TNF alpha + IL-1 beta	20.7
PBMC PHA-L	53.6	Lung fibroblast IL-4	63.3
Ramos (B cell) none	40.6	Lung fibroblast IL-9	55.5
Ramos (B cell) ionomycin	56.3	Lung fibroblast IL-13	44.8
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	71.2
B lymphocytes CD40L and IL-4	41.2	Dermal fibroblast CCD1070 rest	78.5
EOL-1 dbcAMP	50.0	Dermal fibroblast	88.9

		CCD1070 TNF alpha	
EOL-1 dbcAMP PMA/ionomycin	46.3	Dermal fibroblast CCD1070 IL-1 beta	49.7
Dendritic cells none	33.2	Dermal fibroblast IFN gamma	21.5
Dendritic cells LPS	26.1	Dermal fibroblast IL-4	43.8
Dendritic cells anti- CD40	29.9	IBD Colitis 2	1.2
Monocytes rest	17.1	IBD Crohn's	1.8
Monocytes LPS	14.0	Colon	15.4
Macrophages rest	59.0	Lung	16.6
Macrophages LPS	29.1	Thymus	15.6
HUVEC none	35.1	Kidney	18.9
HUVEC starved	62.0		

- CNS_neurodegeneration_v1.0 Summary:** Ag3282 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

- General_screening_panel_v1.4 Summary:** Ag3282 Highest expression of this gene is seen in a brain cancer cell line (CT=24.3). This gene appears to be expressed more highly in the cancer cell lines than in the normal tissue samples on this panel and may be involved in cellular growth and proliferation. Based on this expression profile, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

- This gene is also expressed at high levels in all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

- In addition, this gene product is expressed in adipose, pancreas, adrenal, thyroid, pituitary, fetal skeletal muscle, heart, and liver. This widespread expression in tissues with

metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Furthermore, this gene is more highly expressed in fetal skeletal muscle (CT=30.4) and liver (CT=27) when compared to expression in the adult skeletal muscle (CT>35) and liver (CT=30) may be useful for the differentiation of the fetal and adult sources of this tissue.

Panel 4D Summary: Ag3282 This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. Highest expression is seen in polkweed mitogen stimulated B lymphocytes (CT=25.7). In addition, expression is seen in members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in Panel 1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AA. CG57411-01: KELCH-LIKE PROTEIN KLHL3C

Expression of gene CG57411-01 was assessed using the primer-probe set Ag3229, described in Table AAA. Results of the RTQ-PCR runs are shown in Tables AAB, AAC, AAD and AAE.

Table AAA. Probe Name Ag3229

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -gcagcgagctctaccacat-3'	19	287	472

Probe	TET-5'-aaggccttcgcgctgcagatcctt-3'-TAMRA	23	310	473
Reverse	5'-aagtcgtcctctggagatgct-3'	20	364	474

Tissue Name	Rel. Exp.(%) Ag3229, Run 209862301	Tissue Name	Rel. Exp.(%) Ag3229, Run 209862301
AD 1 Hippo	16.3	Control (Path) 3 Temporal Ctx	8.0
AD 2 Hippo	34.6	Control (Path) 4 Temporal Ctx	35.8
AD 3 Hippo	15.9	AD 1 Occipital Ctx	18.6
AD 4 Hippo	6.9	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	100.0	AD 3 Occipital Ctx	11.7
AD 6 Hippo	35.4	AD 4 Occipital Ctx	17.7
Control 2 Hippo	31.2	AD 5 Occipital Ctx	49.7
Control 4 Hippo	12.1	AD 6 Occipital Ctx	14.2
Control (Path) 3 Hippo	6.2	Control 1 Occipital Ctx	3.3
AD 1 Temporal Ctx	21.6	Control 2 Occipital Ctx	69.3
AD 2 Temporal Ctx	33.0	Control 3 Occipital Ctx	26.6
AD 3 Temporal Ctx	14.1	Control 4 Occipital Ctx	7.5
AD 4 Temporal Ctx	16.8	Control (Path) 1 Occipital Ctx	72.2
AD 5 Inf Temporal Ctx	71.7	Control (Path) 2 Occipital Ctx	13.7
AD 5 Sup Temporal Ctx	32.3	Control (Path) 3 Occipital Ctx	6.3
AD 6 Inf Temporal Ctx	30.6	Control (Path) 4 Occipital Ctx	16.8
AD 6 Sup Temporal Ctx	33.9	Control 1 Parietal Ctx	8.6
Control 1 Temporal Ctx	4.4	Control 2 Parietal Ctx	39.8
Control 2 Temporal Ctx	56.6	Control 3 Parietal Ctx	21.5
Control 3 Temporal Ctx	19.6	Control (Path) 1 Parietal Ctx	66.4
Control 3 Temporal Ctx	14.2	Control (Path) 2 Parietal Ctx	26.8

Tissue Name	Rel. Exp.(%) Ag3229, Run 174442765	Tissue Name	Rel. Exp.(%) Ag3229, Run 174442765
Normal Colon	15.5	Kidney Margin (OD04348)	100.0
Colon cancer	31.9	Kidney malignant	10.7

(OD06064)		cancer (OD06204B)	
Colon Margin (OD06064)	20.6	Kidney normal adjacent tissue (OD06204E)	11.6
Colon cancer (OD06159)	6.0	Kidney Cancer (OD04450-01)	38.4
Colon Margin (OD06159)	12.7	Kidney Margin (OD04450-03)	17.4
Colon cancer (OD06297-04)	3.7	Kidney Cancer 8120613	0.0
Colon Margin (OD06297-05)	22.4	Kidney Margin 8120614	6.0
CC Gr.2 ascend colon (ODO3921)	6.5	Kidney Cancer 9010320	12.0
CC Margin (ODO3921)	10.5	Kidney Margin 9010321	9.9
Colon cancer metastasis (OD06104)	8.6	Kidney Cancer 8120607	47.3
Lung Margin (OD06104)	6.2	Kidney Margin 8120608	5.6
Colon mets to lung (OD04451-01)	31.0	Normal Uterus	48.3
Lung Margin (OD04451-02)	39.5	Uterine Cancer 064011	14.9
Normal Prostate	41.2	Normal Thyroid	2.6
Prostate Cancer (OD04410)	8.1	Thyroid Cancer 064010	4.3
Prostate Margin (OD04410)	10.6	Thyroid Cancer A302152	15.3
Normal Ovary	23.2	Thyroid Margin A302153	2.7
Ovarian cancer (OD06283-03)	7.2	Normal Breast	46.0
Ovarian Margin (OD06283-07)	17.8	Breast Cancer (OD04566)	5.9
Ovarian Cancer 064008	22.2	Breast Cancer 1024	27.4
Ovarian cancer (OD06145)	9.0	Breast Cancer (OD04590-01)	19.5
Ovarian Margin (OD06145)	13.4	Breast Cancer Mets (OD04590-03)	13.5
Ovarian cancer (OD06455-03)	6.3	Breast Cancer Metastasis (OD04655-05)	12.2
Ovarian Margin (OD06455-07)	12.9	Breast Cancer 064006	8.1

Normal Lung	14.5	Breast Cancer 9100266	3.0
Invasive poor diff. lung adeno (ODO4945-01)	5.0	Breast Margin 9100265	3.4
Lung Margin (ODO4945-03)	37.4	Breast Cancer A209073	11.2
Lung Malignant Cancer (OD03126)	9.6	Breast Margin A2090734	61.1
Lung Margin (OD03126)	14.2	Breast cancer (OD06083)	4.7
Lung Cancer (OD05014A)	4.9	Breast cancer node metastasis (OD06083)	12.7
Lung Margin (OD05014B)	39.0	Normal Liver	2.8
Lung cancer (OD06081)	17.4	Liver Cancer 1026	13.6
Lung Margin (OD06081)	32.3	Liver Cancer 1025	12.9
Lung Cancer (OD04237-01)	4.2	Liver Cancer 6004-T	13.2
Lung Margin (OD04237-02)	24.7	Liver Tissue 6004-N	1.3
Ocular Melanoma Metastasis	12.9	Liver Cancer 6005-T	43.2
Ocular Melanoma Margin (Liver)	10.7	Liver Tissue 6005-N	4.8
Melanoma Metastasis	52.9	Liver Cancer 064003	39.5
Melanoma Margin (Lung)	21.0	Normal Bladder	9.3
Normal Kidney	4.7	Bladder Cancer 1023	5.8
Kidney Ca, Nuclear grade 2 (OD04338)	40.3	Bladder Cancer A302173	4.2
Kidney Margin (OD04338)	7.5	Normal Stomach	31.4
Kidney Ca Nuclear grade 1/2 (OD04339)	82.4	Gastric Cancer 9060397	1.2
Kidney Margin (OD04339)	13.2	Stomach Margin 9060396	7.1
Kidney Ca, Clear cell type (OD04340)	8.3	Gastric Cancer 9060395	7.4
Kidney Margin (OD04340)	24.7	Stomach Margin 9060394	10.9
Kidney Ca, Nuclear grade 3 (OD04348)	13.1	Gastric Cancer 064005	10.4

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Tissue Name	Rel. Exp.(%) Ag3229, Run 164389704	Tissue Name	Rel. Exp.(%) Ag3229, Run 164389704
Secondary Th1 act	3.4	HUVEC IL-1beta	20.0
Secondary Th2 act	4.8	HUVEC IFN gamma	32.5
Secondary Tr1 act	2.1	HUVEC TNF alpha + IFN gamma	26.6
Secondary Th1 rest	1.2	HUVEC TNF alpha + IL4	35.1
Secondary Th2 rest	2.0	HUVEC IL-11	17.6
Secondary Tr1 rest	4.5	Lung Microvascular EC none	34.2
Primary Th1 act	17.7	Lung Microvascular EC TNFalpha + IL-1beta	49.0
Primary Th2 act	5.3	Microvascular Dermal EC none	30.6
Primary Tr1 act	25.9	Microvascular Dermal EC TNFalpha + IL-1beta	38.7
Primary Th1 rest	14.0	Bronchial epithelium TNFalpha + IL1beta	46.7
Primary Th2 rest	6.5	Small airway epithelium none	22.1
Primary Tr1 rest	22.1	Small airway epithelium TNFalpha + IL-1beta	97.9
CD45RA CD4 lymphocyte act	12.7	Coronary artery SMC rest	31.2
CD45RO CD4 lymphocyte act	6.6	Coronary artery SMC TNFalpha + IL-1beta	10.5
CD8 lymphocyte act	2.4	Astrocytes rest	7.5
Secondary CD8 lymphocyte rest	4.2	Astrocytes TNFalpha + IL-1beta	8.6
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.8
CD4 lymphocyte none	5.6	KU-812 (Basophil) PMA/ionomycin	2.9
2ry Th1/Th2/Tr1_anti- CD95 CH11	3.7	CCD1106 (Keratinocytes) none	6.2
LAK cells rest	5.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.0
LAK cells IL-2	3.0	Liver cirrhosis	15.5
LAK cells IL-2+IL-12	6.2	Lupus kidney	12.2
LAK cells IL-2+IFN gamma	10.7	NCI-H292 none	30.8
LAK cells IL-2+ IL-18	5.0	NCI-H292 IL-4	49.7

LAK cells PMA/ionomycin	4.0	NCI-H292 IL-9	43.5
NK Cells IL-2 rest	1.9	NCI-H292 IL-13	31.6
Two Way MLR 3 day	9.0	NCI-H292 IFN gamma	17.7
Two Way MLR 5 day	3.3	HPAEC none	18.0
Two Way MLR 7 day	1.2	HPAEC TNF alpha + IL-1 beta	58.2
PBMC rest	0.8	Lung fibroblast none	40.6
PBMC PWM	10.7	Lung fibroblast TNF alpha + IL-1 beta	11.0
PBMC PHA-L	10.2	Lung fibroblast IL-4	100.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	55.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	78.5
B lymphocytes PWM	23.3	Lung fibroblast IFN gamma	82.4
B lymphocytes CD40L and IL-4	18.6	Dermal fibroblast CCD1070 rest	45.4
EOL-1 dbcAMP	1.8	Dermal fibroblast CCD1070 TNF alpha	36.3
EOL-1 dbcAMP PMA/ionomycin	2.0	Dermal fibroblast CCD1070 IL-1 beta	23.8
Dendritic cells none	5.9	Dermal fibroblast IFN gamma	4.6
Dendritic cells LPS	8.0	Dermal fibroblast IL-4	16.6
Dendritic cells anti-CD40	3.3	IBD Colitis 2	6.2
Monocytes rest	4.2	IBD Crohn's	3.6
Monocytes LPS	0.9	Colon	30.1
Macrophages rest	3.1	Lung	19.9
Macrophages LPS	1.4	Thymus	20.6
HUVEC none	35.1	Kidney	20.9
HUVEC starved	58.2		

- CNS_neurodegeneration_v1.0 Summary:** Ag3229 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a
- 5 discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3229 - Highest levels of expression of this gene are seen in breast cancer cell line T47D (CT=28.5). Based on expression in this panel, this gene may be involved in gastric, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, and heart. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at low to moderate levels in all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 2.2 Summary: Ag3229 Highest expression of the CG57411-01 gene is seen in the kidney (CT=32.2). In addition, significant levels of expression are seen in samples derived from normal lung and breast. Expression in these normal tissues is also higher than in the corresponding malignant tissue. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of lung, breast and kidney cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung, breast and kidney cancer.

Panel 4D Summary: Ag3229 Highest expression of the CG57411-01 gene is seen in IL-4 treated lung fibroblasts (CT=31.3). Significant levels of expression are seen in activated-NCI-H292 mucoepidermoid cells as well as untreated NCI-H292 cells. Moderate expression is also detected in IL-9, IL-13 and IFN gamma activated lung fibroblasts, human pulmonary aortic endothelial cells (treated and untreated), small airway epithelium (treated and untreated), treated bronchial epithelium and lung microvascular endothelial cells (treated and untreated). The expression of this gene in cells derived from or within the lung suggests that this gene may be involved in normal conditions as well as pathological

and inflammatory lung disorders that include chronic obstructive pulmonary disease, asthma, allergy and emphysema. Moderate/low expression of this gene is also detected in treated and untreated HUVECs (endothelial cells) and coronary artery smooth muscle cells (treated and untreated) and normal tissues that include lung, colon, thymus and kidney.

- 5 Expression in the various immune cell types and tissue samples suggests that therapeutic modulation of this gene product may ameliorate symptoms associated with infectious conditions as well as inflammatory and autoimmune disorders that include psoriasis, allergy, asthma, inflammatory bowel disease, rheumatoid arthritis and osteoarthritis.

10 **AB. CG57399-01 and CG57399-03: PHOSPHOLIPASE ADRAB-B PRECURSOR**

Expression of gene CG57399-01 and variant CG57399-03 was assessed using the primer-probe sets Ag3952 and Ag3226, described in Tables ABA and ABB. Results of the RTQ-PCR runs are shown in Tables ABC and ABD.

15 Table ABA. Probe Name Ag3952

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -ctgtgtccctgtgtcctgaa-3'	20	1633	475
Probe	TET-5' -tcaacagaacttgctaccctcatcga-3' -TAMRA	26	1666	476
Reverse	5' -gtgggtcttctcctgaaacttc-3'	22	1701	477

Table ABB. Probe Name Ag3226

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -gatgatcctcaggtcactgtgt-3'	22	1617	478
Probe	TET-5' -ccctgtgtcctgaagtttgatgataactca-3' -TAMRA	30	1639	479
Reverse	5' -tcgatgagggttagcaagttct-3'	21	1671	480

Table ABC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126	Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126
Adipose	9.0	Renal ca. TK-10	15.0
Melanoma* Hs688(A).T	3.0	Bladder	22.7
Melanoma* Hs688(B).T	3.4	Gastric ca. (liver met.) NCI-N87	13.0

Melanoma* M14	0.9	Gastric ca. KATO III	75.3
Melanoma* LOXIMVI	11.7	Colon ca. SW-948	4.3
Melanoma* SK-MEL-5	1.5	Colon ca. SW480	97.3
Squamous cell carcinoma SCC-4	8.7	Colon ca.* (SW480 met) SW620	4.4
Testis Pool	12.8	Colon ca. HT29	0.4
Prostate ca.* (bone met) PC-3	10.5	Colon ca. HCT-116	1.2
Prostate Pool	12.9	Colon ca. CaCo-2	60.7
Placenta	5.1	Colon cancer tissue	28.7
Uterus Pool	6.5	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	7.3	Colon ca. Colo-205	0.9
Ovarian ca. SK-OV-3	26.4	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	1.9	Colon Pool	18.8
Ovarian ca. OVCAR-5	6.7	Small Intestine Pool	5.3
Ovarian ca. IGROV-1	9.2	Stomach Pool	7.9
Ovarian ca. OVCAR-8	4.2	Bone Marrow Pool	8.4
Ovary	10.0	Fetal Heart	1.2
Breast ca. MCF-7	0.4	Heart Pool	5.7
Breast ca. MDA-MB-231	92.0	Lymph Node Pool	32.1
Breast ca. BT 549	5.5	Fetal Skeletal Muscle	1.2
Breast ca. T47D	2.5	Skeletal Muscle Pool	4.7
Breast ca. MDA-N	1.6	Spleen Pool	18.2
Breast Pool	19.6	Thymus Pool	19.3
Trachea	10.3	CNS cancer (glio/astro) U87-MG	38.2
Lung	1.2	CNS cancer (glio/astro) U-118-MG	12.2
Fetal Lung	8.3	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.9	CNS cancer (astro) SF-539	7.6
Lung ca. LX-1	27.2	CNS cancer (astro) SNB-75	17.1
Lung ca. NCI-H146	10.7	CNS cancer (glio) SNB-19	6.8

Lung ca. SHP-77	47.3	CNS cancer (glio) SF-295	5.7
Lung ca. A549	5.1	Brain (Amygdala) Pool	7.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	3.2
Lung ca. NCI-H23	4.1	Brain (fetal)	19.3
Lung ca. NCI-H460	0.5	Brain (Hippocampus) Pool	13.1
Lung ca. HOP-62	2.7	Cerebral Cortex Pool	14.8
Lung ca. NCI-H522	1.3	Brain (Substantia nigra) Pool	6.3
Liver	0.0	Brain (Thalamus) Pool	15.2
Fetal Liver	1.7	Brain (whole)	10.4
Liver ca. HepG2	0.5	Spinal Cord Pool	5.3
Kidney Pool	21.2	Adrenal Gland	100.0
Fetal Kidney	1.6	Pituitary gland Pool	4.3
Renal ca. 786-0	1.7	Salivary Gland	3.4
Renal ca. A498	1.3	Thyroid (female)	14.5
Renal ca. ACHN	4.3	Pancreatic ca. CAPAN2	1.7
Renal ca. UO-31	17.4	Pancreas Pool	24.5

Table ABD. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3226, Run 167994701	Tissue Name	Rel. Exp.(%) Ag3226, Run 167994701
Liver adenocarcinoma	2.5	Kidney (fetal)	16.3
Pancreas	0.0	Renal ca. 786-0	0.9
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	1.4
Adrenal gland	19.6	Renal ca. RXF 393	3.4
Thyroid	16.3	Renal ca. ACHN	1.4
Salivary gland	0.0	Renal ca. UO-31	2.8
Pituitary gland	1.9	Renal ca. TK-10	4.4
Brain (fetal)	25.5	Liver	0.0
Brain (whole)	4.6	Liver (fetal)	1.1
Brain (amygdala)	6.7	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	1.6	Lung	8.8
Brain (hippocampus)	22.2	Lung (fetal)	1.7
Brain (substantia nigra)	3.1	Lung ca. (small cell) LX-1	18.6
Brain (thalamus)	3.2	Lung ca. (small cell) NCI-H69	4.2

Cerebral Cortex	26.2	Lung ca. (s.cell var.) SHP-77	100.0
Spinal cord	3.1	Lung ca. (large cell)NCI-H460	0.0
glio/astro U87-MG	7.5	Lung ca. (non-sm. cell) A549	6.7
glio/astro U-118-MG	4.2	Lung ca. (non-s.cell) NCI-H23	5.7
astrocytoma SW1783	1.2	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.9
astrocytoma SNB-75	4.3	Lung ca. (squam.) NCI-H596	3.7
glioma SNB-19	6.0	Mammary gland	6.3
glioma U251	14.1	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	45.4
Heart (fetal)	1.4	Breast ca.* (pl.ef) T47D	4.3
Heart	1.0	Breast ca. BT-549	7.1
Skeletal muscle (fetal)	0.7	Breast ca. MDA-N	0.0
Skeletal muscle	3.2	Ovary	10.9
Bone marrow	3.1	Ovarian ca. OVCAR-3	0.0
Thymus	5.7	Ovarian ca. OVCAR-4	2.4
Spleen	7.2	Ovarian ca. OVCAR-5	5.2
Lymph node	0.0	Ovarian ca. OVCAR-8	0.0
Colorectal	4.8	Ovarian ca. IGROV- 1	0.0
Stomach	5.1	Ovarian ca.* (ascites) SK-OV-3	3.0
Small intestine	1.5	Uterus	5.8
Colon ca. SW480	33.2	Placenta	0.0
Colon ca.* SW620(SW480 met)	8.8	Prostate	1.6
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	2.6
Colon ca. HCT-116	0.0	Testis	7.4

Colon ca. CaCo-2	35.4	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	24.5	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	15.7	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	6.4	Melanoma M14	0.0
Bladder	14.6	Melanoma LOX IMVI	0.0
Trachea	4.4	Melanoma* (met) SK-MEL-5	0.0
Kidney	2.4	Adipose	17.3

General_screening_panel_v1.4 Summary: Ag3952 Highest expression of this gene is seen in the adrenal gland (CT=29). Thus, this gene product may be a treatment for Addison's disease and other adrenalopathies. This gene also has low levels of expression in
5 adipose, heart, skeletal muscle, pituitary, thyroid, and pancreas. Therapeutic modulation of this gene product may be important for the diagnosis or treatment of endocrine or metabolic disease, including Types 1 and 2 diabetes, obesity and pancreatitis.

Expression of this gene is also seen in sample derived from colon, gastric, lung and breast cancers. Thus, expression of this gene could be used to differentiate between these
10 samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Low but significant levels of expression are also seen for all regions of the CNS examined. Thus, this gene product may be useful for treatment of CNS disorders such as
15 Alzheimer's disease, Parkinson's disease, stroke, epilepsy, schizophrenia and multiple sclerosis.

Panel 1.3D Summary: Ag3952 Highest expression of the CG57399-01 gene is seen in a lung cancer cell line (CT=32.5). Low but significant expression is also seen in cell lines
20 derived from breast and colon cancers. Overall, expression is consistent with expression seen in Panel 1.4. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Among metabolic tissues, significant levels of expression are seen in adipose and the adrenal gland. Thus, this gene product may be useful for treatment of obesity, Addison's disease and other adrenalopathies.

In addition, this gene is expressed in the hippocampus, and cerebral cortex. Both these regions of the brain undergo degeneration in Alzheimer's disease. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of this disease or any other neurodegenerative disorders.

AC. CG57399-02: PHOSPHOLIPASE ADRAB-B PRECURSOR

Expression of gene CG57399-02 was assessed using the primer-probe set Ag3952, described in Table ACA. Results of the RTQ-PCR runs are shown in Table ACB. Please note that this gene represents a variant of CG57399-01. This sequence however, only corresponds to probe and primer set Ag3952.

Table ACA. Probe Name Ag3952

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctgtgtccctgtgtcctgaa-3'	20	578	481
Probe	TET-5'-tcaacagaacttgctaccctcatcga-3'-TAMRA	26	611	482
Reverse	5'-gtgggtcttctcctgaaacttc-3'	22	646	483

Table ACB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126	Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126
Adipose	9.0	Renal ca. TK-10	15.0
Melanoma* Hs688(A).T	3.0	Bladder	22.7
Melanoma* Hs688(B).T	3.4	Gastric ca. (liver met.) NCI-N87	13.0
Melanoma* M14	0.9	Gastric ca. KATO III	75.3
Melanoma* LOXIMVI	11.7	Colon ca. SW-948	4.3
Melanoma* SK- MEL-5	1.5	Colon ca. SW480	97.3
Squamous cell carcinoma SCC-4	8.7	Colon ca.* (SW480 met) SW620	4.4

Testis Pool	12.8	Colon ca. HT29	0.4
Prostate ca.* (bone met) PC-3	10.5	Colon ca. HCT-116	1.2
Prostate Pool	12.9	Colon ca. CaCo-2	60.7
Placenta	5.1	Colon cancer tissue	28.7
Uterus Pool	6.5	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	7.3	Colon ca. Colo-205	0.9
Ovarian ca. SK-OV-3	26.4	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	1.9	Colon Pool	18.8
Ovarian ca. OVCAR-5	6.7	Small Intestine Pool	5.3
Ovarian ca. IGROV-1	9.2	Stomach Pool	7.9
Ovarian ca. OVCAR-8	4.2	Bone Marrow Pool	8.4
Ovary	10.0	Fetal Heart	1.2
Breast ca. MCF-7	0.4	Heart Pool	5.7
Breast ca. MDA-MB-231	92.0	Lymph Node Pool	32.1
Breast ca. BT 549	5.5	Fetal Skeletal Muscle	1.2
Breast ca. T47D	2.5	Skeletal Muscle Pool	4.7
Breast ca. MDA-N	1.6	Spleen Pool	18.2
Breast Pool	19.6	Thymus Pool	19.3
Trachea	10.3	CNS cancer (glio/astro) U87-MG	38.2
Lung	1.2	CNS cancer (glio/astro) U-118-MG	12.2
Fetal Lung	8.3	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.9	CNS cancer (astro) SF-539	7.6
Lung ca. LX-1	27.2	CNS cancer (astro) SNB-75	17.1
Lung ca. NCI-H146	10.7	CNS cancer (glio) SNB-19	6.8
Lung ca. SHP-77	47.3	CNS cancer (glio) SF-295	5.7
Lung ca. A549	5.1	Brain (Amygdala) Pool	7.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	3.2
Lung ca. NCI-H23	4.1	Brain (fetal)	19.3
Lung ca. NCI-H460	0.5	Brain (Hippocampus)	13.1

		Pool	
Lung ca. HOP-62	2.7	Cerebral Cortex Pool	14.8
Lung ca. NCI-H522	1.3	Brain (Substantia nigra) Pool	6.3
Liver	0.0	Brain (Thalamus) Pool	15.2
Fetal Liver	1.7	Brain (whole)	10.4
Liver ca. HepG2	0.5	Spinal Cord Pool	5.3
Kidney Pool	21.2	Adrenal Gland	100.0
Fetal Kidney	1.6	Pituitary gland Pool	4.3
Renal ca. 786-0	1.7	Salivary Gland	3.4
Renal ca. A498	1.3	Thyroid (female)	14.5
Renal ca. ACHN	4.3	Pancreatic ca. CAPAN2	1.7
Renal ca. UO-31	17.4	Pancreas Pool	24.5

General_screening_panel_v1.4 Summary: Ag3952 Highest expression of this gene is seen in the adrenal gland (CT=29). Thus, this gene product may be a treatment for Addison's disease and other adrenalopathies. This gene also has low levels of expression in adipose, heart, skeletal muscle, pituitary, thyroid, and pancreas. Therapeutic modulation of this gene product may be important for the diagnosis or treatment of endocrine or metabolic disease, including Types 1 and 2 diabetes, obesity and pancreatitis.

Expression of this gene is also seen in cell line samples derived from colon, gastric, lung and breast cancers. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Low but significant levels of expression are also seen for all regions of the CNS examined. Thus, this gene product may be useful for treatment of CNS disorders such as Alzheimer's disease, Parkinson's disease, stroke, epilepsy, schizophrenia and multiple sclerosis.

AD. CG59311-01: ACYL-COENZYME A THIOESTER HYDROLASE bp.

Expression of gene CG59311-01, splice variant CG59311-02, and full length clone CG59311-03, was assessed using the primer-probe set Ag3541, described in Table ADA. Results of the RTQ-PCR runs are shown in Tables ADB and ADC.

Table ADA. Probe Name Ag3541

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctcactcaaaggcacaggtaga-3'	22	1199	484
Probe	TET-5'-tggcagcaaattcaaactttcttcca-3'-TAMRA	26	1225	485
Reverse	5'-tttgctgtgcttgacagatttt-3'	22	1269	486

Table ADB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3541, Run 217049294	Tissue Name	Rel. Exp.(%) Ag3541, Run 217049294
Adipose	0.0	Renal ca. TK-10	6.0
Melanoma* Hs688(A).T	0.7	Bladder	3.7
Melanoma* Hs688(B).T	1.6	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	2.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	5.4
Testis Pool	3.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	1.4	Colon ca. HCT-116	0.6
Prostate Pool	2.3	Colon ca. CaCo-2	0.6
Placenta	0.5	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	2.9	Colon ca. Colo-205	0.0
Ovarian ca. SK- OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.9	Colon Pool	4.6
Ovarian ca. OVCAR-5	27.0	Small Intestine Pool	6.6
Ovarian ca. IGROV-1	0.0	Stomach Pool	3.1
Ovarian ca. OVCAR-8	1.8	Bone Marrow Pool	1.4
Ovary	2.5	Fetal Heart	9.2

Breast ca. MCF-7	2.4	Heart Pool	3.4
Breast ca. MDA-MB-231	8.0	Lymph Node Pool	3.9
Breast ca. BT 549	4.9	Fetal Skeletal Muscle	4.9
Breast ca. T47D	52.9	Skeletal Muscle Pool	13.5
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	6.7	Thymus Pool	4.7
Trachea	0.9	CNS cancer (glio/astro) U87-MG	0.9
Lung	1.7	CNS cancer (glio/astro) U-118-MG	12.1
Fetal Lung	2.2	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	4.2	CNS cancer (astro) SNB-75	5.2
Lung ca. NCI-H146	2.1	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	6.7	CNS cancer (glio) SF-295	0.7
Lung ca. A549	0.0	Brain (Amygdala) Pool	4.2
Lung ca. NCI-H526	0.0	Brain (cerebellum)	100.0
Lung ca. NCI-H23	10.2	Brain (fetal)	14.7
Lung ca. NCI-H460	3.4	Brain (Hippocampus) Pool	9.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	9.7
Lung ca. NCI-H522	8.5	Brain (Substantia nigra) Pool	3.5
Liver	0.5	Brain (Thalamus) Pool	10.5
Fetal Liver	1.5	Brain (whole)	12.9
Liver ca. HepG2	0.5	Spinal Cord Pool	7.6
Kidney Pool	9.8	Adrenal Gland	10.2
Fetal Kidney	7.9	Pituitary gland Pool	3.1
Renal ca. 786-0	0.0	Salivary Gland	1.7
Renal ca. A498	0.0	Thyroid (female)	0.9
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	2.8
Renal ca. UO-31	3.3	Pancreas Pool	6.6

Table ADC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3541, Run	Tissue Name	Rel. Exp.(%) Ag3541, Run
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	166447041		166447041
Secondary Th1 act	2.7	HUVEC IL-1beta	0.0
Secondary Th2 act	4.1	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	2.1
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	2.7	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	2.3
CD45RO CD4 lymphocyte act	1.7	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	1.8
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	4.2
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	1.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	2.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.8
LAK cells IL-2	0.0	Liver cirrhosis	22.2
LAK cells IL-2+IL-12	0.0	Lupus kidney	18.4
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	10.4
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	7.2
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	15.2

NK Cells IL-2 rest	1.7	NCI-H292 IL-13	3.1
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	7.3
Two Way MLR 5 day	5.3	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	1.7
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	5.7
PBMC PHA-L	2.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	2.2	Lung fibroblast IL-13	3.2
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	2.9
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	2.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	3.5	Dermal fibroblast IL-4	1.5
Dendritic cells anti-CD40	0.0	IBD Colitis 2	5.4
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	14.1
Macrophages rest	4.5	Lung	0.0
Macrophages LPS	2.1	Thymus	100.0
HUVEC none	0.0	Kidney	2.3
HUVEC starved	2.5		

CNS_neurodegeneration_v1.0 Summary: Ag3541 - Expression of this gene is low/undetectable (CTs > 34.5) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3541 Significant expression of this gene is seen only in cerebellum, fetal brain, the breast cancer cell line T47D, and ovarian cancer cell line OVCAR-5 (CTs=32-35). Therefore, expression of this gene can be used to differentiate between these samples and others on this panel.

Panel 4D Summary: Ag3541 - There is significant expression of this gene only in thymus (CT=33.8). Therefore, expression of this gene may be used to identify thymic tissue.

Furthermore, drugs that inhibit the function of this protein may regulate T cell development in the thymus and reduce or eliminate the symptoms of T cell mediated autoimmune or inflammatory diseases, including asthma, allergies, inflammatory bowel disease, lupus erythematosus, or rheumatoid arthritis. Additionally, therapeutics designed against this putative protein may disrupt T cell development in the thymus and function as an immunosuppressant for tissue transplant.

AE. CG59309-01: ACYL-COENZYME A THIOESTER HYDROLASE

Expression of gene CG59309-01 was assessed using the primer-probe set Ag3540, described in Table AEA. Results of the RTQ-PCR runs are shown in Tables AEB, AEC, AED and AEE.

Table AEA. Probe Name Ag3540

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccacgttggctctagcttatta-3'	22	649	487
Probe	TET-5'-tgaagatctccccaataacatggaca-3'- TAMRA	26	677	488
Reverse	5'-ttcgaagtactccagggatatg-3'	22	704	489

Table AEB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3540, Run 210638385	Tissue Name	Rel. Exp.(%) Ag3540, Run 210638385
AD 1 Hippo	13.7	Control (Path) 3 Temporal Ctx	8.2
AD 2 Hippo	26.2	Control (Path) 4 Temporal Ctx	34.2
AD 3 Hippo	13.1	AD 1 Occipital Ctx	23.2
AD 4 Hippo	3.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	30.4	AD 3 Occipital Ctx	7.8
AD 6 Hippo	55.9	AD 4 Occipital Ctx	15.0
Control 2 Hippo	24.0	AD 5 Occipital Ctx	8.1
Control 4 Hippo	4.5	AD 6 Occipital Ctx	76.3

Control (Path) 3 Hippo	6.2	Control 1 Occipital Ctx	3.6
AD 1 Temporal Ctx	11.0	Control 2 Occipital Ctx	96.6
AD 2 Temporal Ctx	19.5	Control 3 Occipital Ctx	36.3
AD 3 Temporal Ctx	4.8	Control 4 Occipital Ctx	3.9
AD 4 Temporal Ctx	15.6	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	36.9	Control (Path) 2 Occipital Ctx	7.6
AD 5 Sup Temporal Ctx	27.4	Control (Path) 3 Occipital Ctx	1.6
AD 6 Inf Temporal Ctx	47.3	Control (Path) 4 Occipital Ctx	16.6
AD 6 Sup Temporal Ctx	64.2	Control 1 Parietal Ctx	8.7
Control 1 Temporal Ctx	7.0	Control 2 Parietal Ctx	20.7
Control 2 Temporal Ctx	53.2	Control 3 Parietal Ctx	27.2
Control 3 Temporal Ctx	19.9	Control (Path) 1 Parietal Ctx	88.9
Control 4 Temporal Ctx	10.5	Control (Path) 2 Parietal Ctx	10.8
Control (Path) 1 Temporal Ctx	68.3	Control (Path) 3 Parietal Ctx	10.1
Control (Path) 2 Temporal Ctx	25.3	Control (Path) 4 Parietal Ctx	47.6

Table AEC. General screening panel v1.4

Tissue Name	Rel. Exp.(%) Ag3540, Run 217049291	Tissue Name	Rel. Exp.(%) Ag3540, Run 217049291
Adipose	1.3	Renal ca. TK-10	0.1
Melanoma* Hs688(A).T	0.7	Bladder	1.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	5.6
Melanoma* M14	0.2	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-	0.0	Colon ca. SW480	10.3

MEL-5			
Squamous cell carcinoma SCC-4	0.3	Colon ca.* (SW480 met) SW620	2.8
Testis Pool	0.3	Colon ca. HT29	0.8
Prostate ca.* (bone met) PC-3	0.8	Colon ca. HCT-116	0.0
Prostate Pool	0.3	Colon ca. CaCo-2	3.5
Placenta	1.4	Colon cancer tissue	1.4
Uterus Pool	0.1	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	1.6	Colon ca. Colo-205	3.3
Ovarian ca. SK-OV-3	3.6	Colon ca. SW-48	1.7
Ovarian ca. OVCAR-4	0.4	Colon Pool	0.2
Ovarian ca. OVCAR-5	23.7	Small Intestine Pool	0.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.1
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.2
Ovary	0.1	Fetal Heart	0.4
Breast ca. MCF-7	0.0	Heart Pool	0.2
Breast ca. MDA-MB-231	2.5	Lymph Node Pool	0.3
Breast ca. BT 549	3.0	Fetal Skeletal Muscle	0.1
Breast ca. T47D	100.0	Skeletal Muscle Pool	0.4
Breast ca. MDA-N	0.0	Spleen Pool	0.2
Breast Pool	0.3	Thymus Pool	0.3
Trachea	0.4	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.3
Fetal Lung	0.2	CNS cancer (neuro;met) SK-N-AS	1.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.6
Lung ca. LX-1	3.5	CNS cancer (astro) SNB-75	3.1
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	0.2
Lung ca. A549	1.4	Brain (Amygdala) Pool	0.7

Lung ca. NCI-H526	0.7	Brain (cerebellum)	2.1
Lung ca. NCI-H23	1.3	Brain (fetal)	0.5
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	1.0
Lung ca. HOP-62	1.2	Cerebral Cortex Pool	0.9
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.3
Liver	2.6	Brain (Thalamus) Pool	1.1
Fetal Liver	0.8	Brain (whole)	1.4
Liver ca. HepG2	0.1	Spinal Cord Pool	0.5
Kidney Pool	0.7	Adrenal Gland	0.8
Fetal Kidney	0.6	Pituitary gland Pool	0.1
Renal ca. 786-0	0.0	Salivary Gland	0.2
Renal ca. A498	0.0	Thyroid (female)	0.7
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	9.4
Renal ca. UO-31	1.1	Pancreas Pool	0.9

Table AED. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3540, Run 166447040	Tissue Name	Rel. Exp.(%) Ag3540, Run 166447040
Secondary Th1 act	4.8	HUVEC IL-1beta	1.7
Secondary Th2 act	10.2	HUVEC IFN gamma	0.9
Secondary Tr1 act	12.9	HUVEC TNF alpha + IFN gamma	1.5
Secondary Th1 rest	2.1	HUVEC TNF alpha + IL4	0.8
Secondary Th2 rest	1.4	HUVEC IL-11	1.5
Secondary Tr1 rest	1.6	Lung Microvascular EC none	0.6
Primary Th1 act	4.7	Lung Microvascular EC TNFalpha + IL-1beta	0.8
Primary Th2 act	6.8	Microvascular Dermal EC none	1.5
Primary Tr1 act	7.3	Microsvascular Dermal EC TNFalpha + IL-1beta	0.8
Primary Th1 rest	6.6	Bronchial epithelium TNFalpha + IL1beta	1.3
Primary Th2 rest	2.6	Small airway epithelium none	0.6
Primary Tr1 rest	4.2	Small airway epithelium TNFalpha + IL-1beta	0.0

CD45RA CD4 lymphocyte act	4.1	Coronary artery SMC rest	0.9
CD45RO CD4 lymphocyte act	10.9	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	6.6	Astrocytes rest	2.6
Secondary CD8 lymphocyte rest	17.0	Astrocytes TNFalpha + IL-1beta	2.1
Secondary CD8 lymphocyte act	6.0	KU-812 (Basophil) rest	2.2
CD4 lymphocyte none	2.0	KU-812 (Basophil) PMA/ionomycin	10.2
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.4	CCD1106 (Keratinocytes) none	6.8
LAK cells rest	2.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	25.7
LAK cells IL-2	16.2	Liver cirrhosis	12.0
LAK cells IL-2+IL-12	12.8	Lupus kidney	5.1
LAK cells IL-2+IFN gamma	15.6	NCI-H292 none	44.8
LAK cells IL-2+ IL-18	7.4	NCI-H292 IL-4	37.6
LAK cells PMA/ionomycin	3.4	NCI-H292 IL-9	41.2
NK Cells IL-2 rest	9.0	NCI-H292 IL-13	19.8
Two Way MLR 3 day	10.5	NCI-H292 IFN gamma	30.1
Two Way MLR 5 day	7.2	HPAEC none	1.2
Two Way MLR 7 day	8.9	HPAEC TNF alpha + IL-1 beta	3.3
PBMC rest	0.5	Lung fibroblast none	0.9
PBMC PWM	3.8	Lung fibroblast TNF alpha + IL-1 beta	0.7
PBMC PHA-L	1.0	Lung fibroblast IL-4	0.5
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.9
B lymphocytes PWM	10.3	Lung fibroblast IFN gamma	1.2
B lymphocytes CD40L and IL-4	3.8	Dermal fibroblast CCD1070 rest	1.1
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	18.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	1.9
Dendritic cells none	14.9	Dermal fibroblast IFN gamma	0.0

Dendritic cells LPS	8.9	Dermal fibroblast IL-4	1.5
Dendritic cells anti-CD40	7.9	IBD Colitis 2	2.9
Monocytes rest	0.0	IBD Crohn's	1.9
Monocytes LPS	0.6	Colon	82.9
Macrophages rest	40.3	Lung	9.7
Macrophages LPS	6.1	Thymus	100.0
HUVEC none	1.1	Kidney	1.8
HUVEC starved	1.4		

Table AEE. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3540, Run 242386396	Tissue Name	Rel. Exp.(%) Ag3540, Run 242386396
97457_Patient-02go_adipose	3.3	94709_Donor 2 AM - A_adipose	9.1
97476_Patient-07sk_skeletal muscle	0.8	94710_Donor 2 AM - B_adipose	1.6
97477_Patient-07ut_uterus	0.0	94711_Donor 2 AM - C_adipose	1.4
97478_Patient-07pl_placenta	12.9	94712_Donor 2 AD - A_adipose	2.8
99167_Bayer Patient 1	15.5	94713_Donor 2 AD - B_adipose	5.8
97482_Patient-08ut_uterus	3.4	94714_Donor 2 AD - C_adipose	4.2
97483_Patient-08pl_placenta	3.4	94742_Donor 3 U - A_Mesenchymal Stem Cells	3.0
97486_Patient-09sk_skeletal muscle	100.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	1.1
97487_Patient-09ut_uterus	1.6	94730_Donor 3 AM - A_adipose	4.3
97488_Patient-09pl_placenta	2.6	94731_Donor 3 AM - B_adipose	2.0
97492_Patient-10ut_uterus	3.1	94732_Donor 3 AM - C_adipose	2.0
97493_Patient-10pl_placenta	23.2	94733_Donor 3 AD - A_adipose	10.7
97495_Patient-11go_adipose	0.8	94734_Donor 3 AD - B_adipose	3.0
97496_Patient-11sk_skeletal muscle	0.0	94735_Donor 3 AD - C_adipose	4.0
97497_Patient-11ut_uterus	2.5	77138_Liver_HepG2untreated	0.7

97498_Patient-11pl_placenta	6.7	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	6.5	81735_Small Intestine	4.8
97501_Patient-12sk_skeletal muscle	4.5	72409_Kidney_Proximal Convoluted Tubule	0.7
97502_Patient-12ut_uterus	6.7	82685_Small intestine_Duodenum	3.6
97503_Patient-12pl_placenta	2.4	90650_Adrenal_Adrenocortical adenoma	0.6
94721_Donor 2 U - A_Mesenchymal Stem Cells	2.2	72410_Kidney_HRCE	8.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.6	72411_Kidney_HRE	8.5
94723_Donor 2 U - C_Mesenchymal Stem Cells	3.1	73139_Uterus_Uterine smooth muscle cells	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3540 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment.

- 5 **General_screening_panel_v1.4 Summary:** Ag3540 This gene is most highly expressed in a breast cancer cell line (CT=27.1). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of breast cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of breast cancer.

- 10 Among metabolic tissues, this gene, an acyl coA thioesterase homolog, has a low level of expression in adipose, adult and fetal liver, adrenal, thyroid and pancreas. Acyl CoA thioesterases have multiple roles in lipid homeostasis. Therefore, therapeutic modulation of this gene product may be a treatment for endocrine and metabolic disease, including Types 1 and 2 diabetes and obesity.

- 15 In addition, this gene is expressed in all CNS regions examined. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of

neurologic disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, stroke, schizophrenia and multiple sclerosis.

References:

1. Hunt MC, Alexson SE. The role Acyl-CoA thioesterases play in mediating
5 intracellular lipid metabolism. *Prog Lipid Res.* 2002 Mar;41(2):99-130.

2. Hunt MC, Nousiainen SE, Huttunen MK, Orit KE, Svensson LT, Alexson SE. Peroxisome proliferator-induced long chain acyl-CoA thioesterases comprise a highly conserved novel multi-gene family involved in lipid metabolism. *J Biol Chem.* 1999 Nov
10 26;274(48):34317-26.

Panel 4D Summary: Ag3540 Highest expression of the CG59309-01 gene is seen in the thymus and colon (CTs=31.5). Significant levels of expression are also seen in a cluster of treated and untreated samples derived from the NCI-H292 mucocarcinoid cell line. Thus, expression of this gene could be used as a marker for thymus and colon. Furthermore,
15 therapeutic modulation of the expression or function of this gene may regulate T cell development in the thymus and reduce or eliminate the symptoms of T cell mediated autoimmune or inflammatory diseases, including asthma, allergies, inflammatory bowel disease, lupus erythematosus, or rheumatoid arthritis. Additionally, small molecule or antibody therapeutics designed against this putative protein may disrupt T cell development
20 in the thymus and function as an immunosuppressant for tissue transplant.

Panel 5 Islet Summary: Ag3540 This gene has moderate expression in skeletal muscle, (highest expression CT=30.5). Acyl CoA thioesterases function in peroxisomal fatty acid oxidation. Therefore, therapeutic modulation of this homolog may increase fatty acid oxidation in muscle and be a treatment for Type 2 diabetes and obesity.

25 References:

1. Hunt MC, Solaas K, Kase BF, Alexson SE. Characterization of an acyl-coA thioesterase that functions as a major regulator of peroxisomal lipid metabolism. *J Biol Chem.* 2002 Jan 11;277(2):1128-38.

REPORT OF THE

5 Table AFA. Probe Name Ag3218

Table AFB. Probe Name Ag3378

Table AFC. CNS_neurodegeneration_v1.0

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			Occipital Ctx		
AD 6 Hippo	62.9	55.9	AD 4 Occipital Ctx	80.1	24.3
Control 2 Hippo	55.1	52.9	AD 5 Occipital Ctx	17.9	25.2
Control 4 Hippo	35.4	39.5	AD 6 Occipital Ctx	66.9	55.5
Control (Path) 3 Hippo	22.8	26.8	Control 1 Occipital Ctx	27.9	17.4
AD 1 Temporal Ctx	40.3	28.3	Control 2 Occipital Ctx	94.0	64.6
AD 2 Temporal Ctx	83.5	94.6	Control 3 Occipital Ctx	43.5	40.6
AD 3 Temporal Ctx	30.8	24.5	Control 4 Occipital Ctx	20.3	22.5
AD 4 Temporal Ctx	61.1	26.8	Control (Path) 1 Occipital Ctx	79.6	51.4
AD 5 Inf Temporal Ctx	84.7	100.0	Control (Path) 2 Occipital Ctx	34.4	24.7
AD 5 Sup Temporal Ctx	55.9	39.8	Control (Path) 3 Occipital Ctx	25.2	16.2
AD 6 Inf Temporal Ctx	47.0	46.0	Control (Path) 4 Occipital Ctx	76.3	45.1
AD 6 Sup Temporal Ctx	63.7	41.2	Control 1 Parietal Ctx	31.0	21.9
Control 1 Temporal Ctx	32.8	18.0	Control 2 Parietal Ctx	67.4	45.1
Control 2 Temporal Ctx	52.1	39.2	Control 3 Parietal Ctx	31.4	29.3
Control 3 Temporal Ctx	34.9	28.1	Control (Path) 1	48.6	58.6

			Parietal Ctx		
Control 4 Temporal Ctx	62.9	36.3	Control (Path) 2 Parietal Ctx	46.3	27.0
Control (Path) 1 Temporal Ctx	75.8	50.0	Control (Path) 3 Parietal Ctx	26.1	23.8
Control (Path) 2 Temporal Ctx	56.6	41.8	Control (Path) 4 Parietal Ctx	48.0	54.3

Table AFD. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3218, Run 168013878	Rel. Exp.(%) Ag3378, Run 165674263	Tissue Name	Rel. Exp.(%) Ag3218, Run 168013878	Rel. Exp.(%) Ag3378, Run 165674263
Liver adenocarcinoma	10.7	20.2	Kidney (fetal)	48.3	13.9
Pancreas	10.8	13.1	Renal ca. 786- 0	15.6	10.4
Pancreatic ca. CAPAN 2	9.6	5.4	Renal ca. A498	19.2	14.9
Adrenal gland	5.1	18.4	Renal ca. RXF 393	39.0	33.2
Thyroid	12.3	33.2	Renal ca. ACHN	12.1	11.3
Salivary gland	5.1	5.5	Renal ca. UO- 31	18.9	17.8
Pituitary gland	21.5	74.7	Renal ca. TK- 10	20.0	10.1
Brain (fetal)	19.5	36.1	Liver	18.0	8.7
Brain (whole)	22.1	29.9	Liver (fetal)	5.5	25.3
Brain (amygdala)	57.4	46.7	Liver ca. (hepatoblast) HepG2	14.2	14.1
Brain (cerebellum)	25.2	23.5	Lung	14.1	18.7
Brain (hippocampus)	28.1	85.9	Lung (fetal)	17.2	4.0
Brain (substantia nigra)	11.5	16.7	Lung ca. (small cell) LX-1	6.5	14.8
Brain (thalamus)	57.0	67.4	Lung ca. (small cell) NCI-H69	20.6	4.8

Colorectal	18.2	11.8	Ovarian ca. IGROV-1	11.3	15.1
Stomach	14.8	33.7	Ovarian ca.* (ascites) SK- OV-3	43.5	17.0
Small intestine	18.3	66.0	Uterus	10.5	21.8
Colon ca. SW480	12.9	14.2	Placenta	2.6	15.0
Colon ca.* SW620(SW480 met)	17.0	14.2	Prostate	11.7	30.6
Colon ca. HT29	17.2	18.8	Prostate ca.* (bone met)PC- 3	35.4	40.3
Colon ca. HCT- 116	16.5	18.2	Testis	23.3	100.0
Colon ca. CaCo-2	20.9	7.4	Melanoma Hs688(A).T	5.0	1.4
Colon ca. tissue(ODO3866)	14.7	21.9	Melanoma* (met) Hs688(B).T	6.0	3.5
Colon ca. HCC- 2998	22.1	13.1	Melanoma UACC-62	14.3	12.2
Gastric ca.* (liver met) NCI-N87	48.6	82.4	Melanoma M14	3.1	8.2
Bladder	6.2	4.7	Melanoma LOX IMVI	30.1	8.4
Trachea	12.8	49.3	Melanoma* (met) SK- MEL-5	21.8	13.1
Kidney	43.5	35.4	Adipose	9.2	3.0

Table AFE. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag3218, Run 174416494	Tissue Name	Rel. Exp.(%) Ag3218, Run 174416494
Normal Colon	5.9	Kidney Margin (OD04348)	70.2
Colon cancer (OD06064)	5.6	Kidney malignant cancer (OD06204B)	3.9
Colon Margin (OD06064)	3.6	Kidney normal adjacent tissue (OD06204E)	6.7
Colon cancer (OD06159)	6.3	Kidney Cancer (OD04450-01)	15.1
Colon Margin	7.0	Kidney Margin	3.1

(OD06159)		(OD04450-03)	
Colon cancer (OD06297-04)	2.6	Kidney Cancer 8120613	2.5
Colon Margin (OD06297-05)	5.6	Kidney Margin 8120614	18.2
CC Gr.2 ascend colon (ODO3921)	20.0	Kidney Cancer 9010320	2.4
CC Margin (ODO3921)	13.7	Kidney Margin 9010321	4.4
Colon cancer metastasis (OD06104)	0.0	Kidney Cancer 8120607	23.0
Lung Margin (OD06104)	11.0	Kidney Margin 8120608	15.1
Colon mets to lung (OD04451-01)	29.9	Normal Uterus	2.3
Lung Margin (OD04451-02)	0.3	Uterine Cancer 064011	6.1
Normal Prostate	5.6	Normal Thyroid	6.6
Prostate Cancer (OD04410)	3.9	Thyroid Cancer 064010	6.8
Prostate Margin (OD04410)	6.1	Thyroid Cancer A302152	11.9
Normal Ovary	7.0	Thyroid Margin A302153	7.7
Ovarian cancer (OD06283-03)	1.3	Normal Breast	3.4
Ovarian Margin (OD06283-07)	0.0	Breast Cancer (OD04566)	9.9
Ovarian Cancer 064008	31.2	Breast Cancer 1024	16.8
Ovarian cancer (OD06145)	3.5	Breast Cancer (OD04590-01)	100.0
Ovarian Margin (OD06145)	8.4	Breast Cancer Mets (OD04590-03)	26.2
Ovarian cancer (OD06455-03)	13.7	Breast Cancer Metastasis (OD04655-05)	36.3
Ovarian Margin (OD06455-07)	1.1	Breast Cancer 064006	5.4
Normal Lung	5.4	Breast Cancer 9100266	12.8
Invasive poor diff. lung adeno (ODO4945-01)	14.5	Breast Margin 9100265	1.0
Lung Margin (ODO4945-03)	2.7	Breast Cancer A209073	3.3
Lung Malignant Cancer (OD03126)	1.8	Breast Margin A2090734	11.7

Lung Margin (OD03126)	5.1	Breast cancer (OD06083)	6.9
Lung Cancer (OD05014A)	12.8	Breast cancer node metastasis (OD06083)	10.7
Lung Margin (OD05014B)	3.3	Normal Liver	9.4
Lung cancer (OD06081)	6.3	Liver Cancer 1026	2.6
Lung Margin (OD06081)	2.7	Liver Cancer 1025	9.7
Lung Cancer (OD04237-01)	12.9	Liver Cancer 6004-T	10.4
Lung Margin (OD04237-02)	6.4	Liver Tissue 6004-N	5.3
Ocular Melanoma Metastasis	4.6	Liver Cancer 6005-T	4.2
Ocular Melanoma Margin (Liver)	0.1	Liver Tissue 6005-N	11.5
Melanoma Metastasis	1.6	Liver Cancer 064003	22.5
Melanoma Margin (Lung)	4.6	Normal Bladder	6.1
Normal Kidney	10.4	Bladder Cancer 1023	10.8
Kidney Ca, Nuclear grade 2 (OD04338)	14.6	Bladder Cancer A302173	15.1
Kidney Margin (OD04338)	10.5	Normal Stomach	15.0
Kidney Ca Nuclear grade 1/2 (OD04339)	44.8	Gastric Cancer 9060397	7.1
Kidney Margin (OD04339)	17.7	Stomach Margin 9060396	10.4
Kidney Ca, Clear cell type (OD04340)	5.3	Gastric Cancer 9060395	8.4
Kidney Margin (OD04340)	25.3	Stomach Margin 9060394	10.4
Kidney Ca, Nuclear grade 3 (OD04348)	7.5	Gastric Cancer 064005	7.7

Table AFF. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3218, Run 164682519	Rel. Exp.(%) Ag3378, Run 165296553	Tissue Name	Rel. Exp.(%) Ag3218, Run 164682519	Rel. Exp.(%) Ag3378, Run 165296553
Secondary Th1 act	18.2	25.7	HUVEC IL-1beta	14.5	12.9

Secondary Th2 act	39.0	26.6	HUVEC IFN gamma	47.0	25.3
Secondary Tr1 act	33.2	19.1	HUVEC TNF alpha + IFN gamma	43.5	45.1
Secondary Th1 rest	9.5	12.2	HUVEC TNF alpha + IL4	37.1	48.0
Secondary Th2 rest	11.2	5.1	HUVEC IL-11	43.5	18.0
Secondary Tr1 rest	22.7	8.0	Lung Microvascular EC none	16.8	61.6
Primary Th1 act	43.2	27.9	Lung Microvascular EC TNFalpha + IL-1beta	18.6	14.7
Primary Th2 act	30.1	12.0	Microvascular Dermal EC none	31.2	23.8
Primary Tr1 act	24.7	14.4	Microvascular Dermal EC TNFalpha + IL-1beta	66.4	22.1
Primary Th1 rest	25.2	17.4	Bronchial epithelium TNFalpha + IL1beta	30.6	29.3
Primary Th2 rest	15.5	7.5	Small airway epithelium none	36.1	24.3
Primary Tr1 rest	21.3	6.7	Small airway epithelium TNFalpha + IL-1beta	76.3	62.9
CD45RA CD4 lymphocyte act	35.4	16.6	Coronary artery SMC rest	49.7	28.1
CD45RO CD4 lymphocyte act	27.9	25.9	Coronary artery SMC TNFalpha + IL-1beta	25.3	23.7
CD8 lymphocyte act	21.0	14.8	Astrocytes rest	22.2	31.2
Secondary CD8 lymphocyte rest	39.2	17.8	Astrocytes TNFalpha + IL-1beta	26.1	25.0
Secondary CD8 lymphocyte act	20.9	7.4	KU-812 (Basophil) rest	90.8	85.3
CD4 lymphocyte none	4.5	11.8	KU-812 (Basophil) PMA/ionomycin	87.1	72.2
2ry	2.6	10.0	CCD1106	36.6	36.9

Th1/Th2/Tr1_anti-CD95 CH11			(Keratinocytes) none		
LAK cells rest	11.7	12.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	33.4	20.4
LAK cells IL-2	6.8	27.5	Liver cirrhosis	25.5	19.9
LAK cells IL-2+IL-12	37.1	11.6	Lupus kidney	44.4	15.7
LAK cells IL-2+IFN gamma	20.7	19.1	NCI-H292 none	79.6	64.6
LAK cells IL-2+IL-18	21.9	14.7	NCI-H292 IL-4	85.3	96.6
LAK cells PMA/ionomycin	4.7	3.3	NCI-H292 IL-9	100.0	98.6
NK Cells IL-2 rest	11.9	11.3	NCI-H292 IL-13	68.8	50.7
Two Way MLR 3 day	23.7	11.0	NCI-H292 IFN gamma	80.1	56.6
Two Way MLR 5 day	12.5	6.1	HPAEC none	38.4	27.2
Two Way MLR 7 day	12.3	8.7	HPAEC TNF alpha + IL-1 beta	42.6	43.2
PBMC rest	6.0	5.7	Lung fibroblast none	31.2	21.3
PBMC PWM	40.3	27.7	Lung fibroblast TNF alpha + IL-1 beta	14.7	24.5
PBMC PHA-L	37.9	17.7	Lung fibroblast IL-4	47.0	42.6
Ramos (B cell) none	11.7	14.9	Lung fibroblast IL-9	49.3	30.6
Ramos (B cell) ionomycin	33.9	26.8	Lung fibroblast IL-13	36.6	42.6
B lymphocytes PWM	33.7	40.9	Lung fibroblast IFN gamma	44.8	22.5
B lymphocytes CD40L and IL-4	34.4	18.3	Dermal fibroblast CCD1070 rest	33.7	47.3
EOL-1 dbcAMP	50.0	28.1	Dermal fibroblast CCD1070 TNF alpha	47.3	33.2
EOL-1 dbcAMP PMA/ionomycin	44.1	32.1	Dermal fibroblast CCD1070 IL-1 beta	50.0	34.6
Dendritic cells none	33.9	19.6	Dermal fibroblast IFN gamma	24.0	34.4
Dendritic cells LPS	21.9	10.2	Dermal fibroblast	24.3	32.8

			IL-4		
Dendritic cells anti-CD40	49.7	33.9	IBD Colitis 2	6.0	11.7
Monocytes rest	10.7	10.3	IBD Crohn's	25.3	26.1
Monocytes LPS	30.6	9.3	Colon	70.7	100.0
Macrophages rest	41.2	33.7	Lung	64.6	17.7
Macrophages LPS	20.0	7.5	Thymus	80.7	56.3
HUVEC none	26.8	29.5	Kidney	26.4	41.5
HUVEC starved	26.2	37.6			

CNS_neurodegeneration_v1.0 Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in very good agreement. This panel confirms the expression of this gene at low levels to moderate levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.3D for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

Panel 1.3D Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in good agreement. Highest expression is seen in testis and a lung cancer cell line (CTs=30-31). This panel confirms the expression of this gene at low levels in the brain. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene product is also expressed in adipose, pancreas, thyroid, pituitary, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

Panel 2.2 Summary: Ag3218 - This gene is expressed at low to moderate levels in many samples on this panel, with the highest levels of expression in breast cancer sample OD04590-01 (CT=30.3). This gene is expressed in a cluster of breast cancer samples with no expression in normal breast (CT>35). Similarly, this gene is expressed in ovarian cancer samples at higher levels than the matched margin samples.

Interestingly, this gene is expressed at higher levels in kidney cancer margin samples than in the matched cancer samples.

This gene is homologous to a mouse myosin phosphatase targeting subunit (MYPT) which have been found to play a role in cell division. MYPT undergoes mitosis-specific phosphorylation which is reversed during cytokinesis.

References:

1. Totsukawa G, Yamakita Y, Yamashiro S, Hosoya H, Hartshorne DJ, Matsumura F. Activation of myosin phosphatase targeting subunit by mitosis-specific phosphorylation. J Cell Biol 1999 Feb 22;144(4):735-44.

Panel 4D Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in very good agreement. Highest expression is seen in the colon and a mucoepidermoid cell line (CTs=30-32). This gene is expressed at low to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AG. CG59241-01: Amiloride-sensitive sodium channel

Expression of gene CG59241-01 was assessed using the primer-probe set Ag3407, described in Table AGA. Results of the RTQ-PCR runs are shown in Tables AGB, AGC and AGD.

Table AGA. Probe Name Ag3407

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcaccctctgcaacactaatg-3'	22	268	496
Probe	TET-5'-ctgtcccagctcagctaccctgactt-3'- TAMRA	26	298	497
Reverse	5'-tttcatccagtcaccagcat-3'	19	340	498

5 Table AGB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3407, Run 210349883	Tissue Name	Rel. Exp.(%) Ag3407, Run 210349883
AD 1 Hippo	18.4	Control (Path) 3 Temporal Ctx	4.1
AD 2 Hippo	29.7	Control (Path) 4 Temporal Ctx	40.3
AD 3 Hippo	18.3	AD 1 Occipital Ctx	36.9
AD 4 Hippo	5.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	91.4	AD 3 Occipital Ctx	19.1
AD 6 Hippo	80.7	AD 4 Occipital Ctx	18.8
Control 2 Hippo	9.3	AD 5 Occipital Ctx	18.3
Control 4 Hippo	19.9	AD 6 Occipital Ctx	28.9
Control (Path) 3 Hippo	8.8	Control 1 Occipital Ctx	4.3
AD 1 Temporal Ctx	28.5	Control 2 Occipital Ctx	80.1
AD 2 Temporal Ctx	41.8	Control 3 Occipital Ctx	20.2
AD 3 Temporal Ctx	32.5	Control 4 Occipital Ctx	6.0
AD 4 Temporal Ctx	36.3	Control (Path) 1 Occipital Ctx	92.7
AD 5 Inf Temporal	100.0	Control (Path) 2	25.3

Ctx		Occipital Ctx	
AD 5 SupTemporal Ctx	56.6	Control (Path) 3 Occipital Ctx	3.0
AD 6 Inf Temporal Ctx	82.4	Control (Path) 4 Occipital Ctx	41.2
AD 6 Sup Temporal Ctx	44.1	Control 1 Parietal Ctx	21.9
Control 1 Temporal Ctx	15.3	Control 2 Parietal Ctx	79.0
Control 2 Temporal Ctx	24.1	Control 3 Parietal Ctx	22.2
Control 3 Temporal Ctx	34.6	Control (Path) 1 Parietal Ctx	77.9
Control 4 Temporal Ctx	12.0	Control (Path) 2 Parietal Ctx	47.6
Control (Path) 1 Temporal Ctx	53.6	Control (Path) 3 Parietal Ctx	6.2
Control (Path) 2 Temporal Ctx	56.6	Control (Path) 4 Parietal Ctx	67.4

Table AGC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3407, Run 216821458	Tissue Name	Rel. Exp.(%) Ag3407, Run 216821458
Adipose	0.2	Renal ca. TK-10	16.6
Melanoma* Hs688(A).T	2.3	Bladder	0.3
Melanoma* Hs688(B).T	0.4	Gastric ca. (liver met.) NCI-N87	8.8
Melanoma* M14	2.0	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	2.5	Colon ca. SW-948	3.7
Melanoma* SK- MEL-5	8.7	Colon ca. SW480	14.1
Squamous cell carcinoma SCC-4	1.2	Colon ca.* (SW480 met) SW620	21.2
Testis Pool	0.4	Colon ca. HT29	10.7
Prostate ca.* (bone met) PC-3	4.4	Colon ca. HCT-116	64.2
Prostate Pool	2.3	Colon ca. CaCo-2	32.3
Placenta	0.5	Colon cancer tissue	13.2
Uterus Pool	0.0	Colon ca. SW1116	12.5
Ovarian ca. OVCAR-3	8.4	Colon ca. Colo-205	0.3

Ovarian ca. SK-OV-3	9.7	Colon ca. SW-48	0.6
Ovarian ca. OVCAR-4	1.6	Colon Pool	2.8
Ovarian ca. OVCAR-5	18.9	Small Intestine Pool	4.5
Ovarian ca. IGROV-1	4.9	Stomach Pool	1.4
Ovarian ca. OVCAR-8	5.9	Bone Marrow Pool	1.8
Ovary	2.0	Fetal Heart	2.4
Breast ca. MCF-7	16.7	Heart Pool	0.3
Breast ca. MDA-MB-231	12.1	Lymph Node Pool	3.5
Breast ca. BT 549	22.7	Fetal Skeletal Muscle	1.9
Breast ca. T47D	27.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	4.5	Spleen Pool	0.0
Breast Pool	2.9	Thymus Pool	2.1
Trachea	9.0	CNS cancer (glio/astro) U87-MG	0.9
Lung	0.0	CNS cancer (glio/astro) U-118-MG	11.7
Fetal Lung	10.8	CNS cancer (neuro;met) SK-N-AS	58.6
Lung ca. NCI-N417	1.3	CNS cancer (astro) SF-539	28.1
Lung ca. LX-1	21.8	CNS cancer (astro) SNB-75	24.7
Lung ca. NCI-H146	5.4	CNS cancer (glio) SNB-19	7.3
Lung ca. SHP-77	11.7	CNS cancer (glio) SF-295	4.8
Lung ca. A549	8.0	Brain (Amygdala) Pool	3.9
Lung ca. NCI-H526	0.0	Brain (cerebellum)	36.1
Lung ca. NCI-H23	7.4	Brain (fetal)	100.0
Lung ca. NCI-H460	5.4	Brain (Hippocampus) Pool	5.6
Lung ca. HOP-62	2.9	Cerebral Cortex Pool	5.6
Lung ca. NCI-H522	8.5	Brain (Substantia nigra) Pool	7.1
Liver	0.0	Brain (Thalamus) Pool	11.3
Fetal Liver	0.0	Brain (whole)	13.4
Liver ca. HepG2	0.8	Spinal Cord Pool	12.7
Kidney Pool	2.1	Adrenal Gland	0.0

Fetal Kidney	3.7	Pituitary gland Pool	0.0
Renal ca. 786-0	1.7	Salivary Gland	0.9
Renal ca. A498	0.7	Thyroid (female)	0.0
Renal ca. ACHN	1.9	Pancreatic ca. CAPAN2	2.3
Renal ca. UO-31	0.2	Pancreas Pool	2.6

Table AGD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3407, Run 165296462	Tissue Name	Rel. Exp.(%) Ag3407, Run 165296462
Secondary Th1 act	7.9	HUVEC IL-1beta	0.0
Secondary Th2 act	17.1	HUVEC IFN gamma	0.0
Secondary Tr1 act	40.1	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	4.4	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	7.0	HUVEC IL-11	0.0
Secondary Tr1 rest	11.7	Lung Microvascular EC none	0.0
Primary Th1 act	61.1	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	69.3	Microvascular Dermal EC none	0.0
Primary Tr1 act	90.8	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	20.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	42.6	Small airway epithelium none	3.0
Primary Tr1 rest	52.5	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	2.8	Coronary artery SMC rest	3.6
CD45RO CD4 lymphocyte act	14.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	5.8	Astrocytes rest	11.6
Secondary CD8 lymphocyte rest	18.9	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	22.2	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-	4.5	CCD1106	2.7

CD95 CH11		(Keratinocytes) none	
LAK cells rest	3.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	4.0	Liver cirrhosis	13.5
LAK cells IL-2+IL-12	5.7	Lupus kidney	4.1
LAK cells IL-2+IFN gamma	21.3	NCI-H292 none	9.0
LAK cells IL-2+ IL-18	6.7	NCI-H292 IL-4	14.8
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	3.5
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	5.0	NCI-H292 IFN gamma	5.5
Two Way MLR 5 day	2.3	HPAEC none	0.0
Two Way MLR 7 day	8.2	HPAEC TNF alpha + IL- 1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	2.8
PBMC PWM	21.3	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	20.4	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	2.8	Lung fibroblast IL-13	0.0
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	1.4
B lymphocytes CD40L and IL-4	19.8	Dermal fibroblast CCD1070 rest	34.4
EOL-1 dbcAMP	2.6	Dermal fibroblast CCD1070 TNF alpha	68.8
EOL-1 dbcAMP PMA/ionomycin	6.2	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	14.1
Dendritic cells anti- CD40	6.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	6.5	Colon	42.3
Macrophages rest	0.0	Lung	35.8
Macrophages LPS	0.0	Thymus	45.4
HUVEC none	0.0	Kidney	55.1
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3407 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3407 Highest expression of the CG59241-01 gene is seen in fetal brain (CT=31.3). Furthermore, low to moderate levels of expression is also observed in CNS cancer cell lines (CTs=32-34). The CG59241-01 gene codes for a putative amiloride-sensitive sodium channel. A similar amiloride-sensitive sodium channel was shown to be highly expressed in malignant glioblastoma multiforme tumors and to be a characteristic feature of malignant brain tumor cells (Ref.1). Therefore, therapeutic modulation of the activity of the protein encoded by this gene may be beneficial in the treatment of CNS cancer. Significant expression is also seen in a cluster of cell lines derived from brain, colon, breast, and ovarian cancers. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

In addition, this gene is expressed at low levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Bubien JK, Keeton DA, Fuller CM, Gillespie GY, Reddy AT, Mapstone TB, Benos DJ. (1999) Malignant human gliomas express an amiloride-sensitive Na⁺ conductance. Am J Physiol 276(6 Pt 1):C1405-10

Panel 4D Summary: Ag3407 Highest expression Of the CG59241-01 gene is detected in PWM treated B lymphocytes (CT=32). Similar expression is also detected in primary activated Th1, Th2 and Tr1 cells, as well as TNF alpha treated dermal fibroblast CCD1070 cells (CTs=32). Therefore, expression of this gene can be used to distinguish these samples from other samples in the panel. Furthermore, this gene is expressed in activated

lymphocytes. Likewise, no expression of this gene is seen in PBMC that contain normal B cells (CT=40), but it is induced when PBMC are treated with the pokeweed mitogen or PHA-L (CTs=34). In addition, the transcript is not seen in the B cell lymphoma Ramos regardless of stimulation. Therefore, the gene product could potentially be used

5 therapeutically in the treatment of Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, psoriasis and in other diseases in which T cells and B cells are activated.

In addition, low expression of this gene is also observed in normal colon, lung, thymus and kidney tissues. The CG59241-01 gene encodes an amiloride-sensitive sodium

10 channel. A similar channel, the amiloride-sensitive epithelial sodium channel (ENaC) constitutes the limiting step for sodium reabsorption in epithelial cells that line the distal nephron, distal colon, ducts of several exocrine glands and lung airways and plays an important role in pathophysiological and clinical conditions such as hypertension or lung edema. ENaC has been implicated in two genetic diseases, Liddle's syndrome and

15 pseudohypoaldosteronism (PHA-1) (Ref.1). Therefore, antibody or small molecule therapies designed with the protein encoded for by CG59241-01 gene could modulate kidney/colon/lung function and be important in the treatment of inflammatory or autoimmune diseases of these tissues in addition to hypertension, lung edema, Liddle's syndrom and PHA-1.

20 **Reference.**

1. Hummler E. (1998) Reversal of convention: from man to experimental animal in elucidating the function of the renal amiloride-sensitive sodium channel. Exp Nephrol 1998 Jul-Aug;6(4):265-71

AH. CG58602-01: FAD binding domain containing protein

25 Expression of gene CG58602-01 was assessed using the primer-probe set Ag3385, described in Table AHA. Results of the RTQ-PCR runs are shown in Tables AHB, AHC and AHD.

Table AHA. Probe Name Ag3385

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-tcatgaatccaggcaaagtg-3'	20	1427	499
Probe	TET-5'-ttagccccacaagttccctgactacgg-3'- TAMRA	26	1468	500
Reverse	5'-tggcatgaagaaaagttcca-3'	20	1503	501

Table AHB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3385, Run 210154892	Tissue Name	Rel. Exp.(%) Ag3385, Run 210154892
AD 1 Hippo	34.6	Control (Path) 3 Temporal Ctx	21.2
AD 2 Hippo	47.6	Control (Path) 4 Temporal Ctx	36.1
AD 3 Hippo	11.9	AD 1 Occipital Ctx	28.1
AD 4 Hippo	24.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	56.3	AD 3 Occipital Ctx	15.0
AD 6 Hippo	63.3	AD 4 Occipital Ctx	34.9
Control 2 Hippo	42.6	AD 5 Occipital Ctx	52.1
Control 4 Hippo	24.7	AD 6 Occipital Ctx	25.3
Control (Path) 3 Hippo	23.3	Control 1 Occipital Ctx	14.3
AD 1 Temporal Ctx	23.8	Control 2 Occipital Ctx	69.3
AD 2 Temporal Ctx	73.7	Control 3 Occipital Ctx	29.5
AD 3 Temporal Ctx	7.3	Control 4 Occipital Ctx	14.9
AD 4 Temporal Ctx	39.0	Control (Path) 1 Occipital Ctx	68.3
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	11.0
AD 5 Sup Temporal Ctx	55.5	Control (Path) 3 Occipital Ctx	8.9
AD 6 Inf Temporal Ctx	64.2	Control (Path) 4 Occipital Ctx	17.3
AD 6 Sup Temporal Ctx	54.0	Control 1 Parietal Ctx	32.8
Control 1 Temporal Ctx	23.8	Control 2 Parietal Ctx	62.0
Control 2 Temporal Ctx	50.3	Control 3 Parietal Ctx	33.4
Control 3 Temporal Ctx	38.4	Control (Path) 1 Parietal Ctx	70.7
Control 3	19.2	Control (Path) 2	31.4

Temporal Ctx		Parietal Ctx	
Control (Path) 1 Temporal Ctx	56.6	Control (Path) 3 Parietal Ctx	20.9
Control (Path) 2 Temporal Ctx	47.6	Control (Path) 4 Parietal Ctx	43.2

Table AHC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3385, Run 217043538	Tissue Name	Rel. Exp.(%) Ag3385, Run 217043538
Adipose	2.4	Renal ca. TK-10	3.5
Melanoma* Hs688(A).T	0.7	Bladder	6.6
Melanoma* Hs688(B).T	1.1	Gastric ca. (liver met.) NCI-N87	2.1
Melanoma* M14	0.9	Gastric ca. KATO III	0.9
Melanoma* LOXIMVI	1.3	Colon ca. SW-948	4.5
Melanoma* SK- MEL-5	2.2	Colon ca. SW480	0.8
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	1.3
Testis Pool	1.3	Colon ca. HT29	0.6
Prostate ca.* (bone met) PC-3	5.8	Colon ca. HCT-116	1.9
Prostate Pool	4.0	Colon ca. CaCo-2	28.5
Placenta	2.5	Colon cancer tissue	2.0
Uterus Pool	0.5	Colon ca. SW1116	0.9
Ovarian ca. OVCAR-3	1.1	Colon ca. Colo-205	3.5
Ovarian ca. SK- OV-3	3.7	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	0.2	Colon Pool	3.0
Ovarian ca. OVCAR-5	42.0	Small Intestine Pool	3.5
Ovarian ca. IGROV-1	8.0	Stomach Pool	1.8
Ovarian ca. OVCAR-8	2.7	Bone Marrow Pool	0.9
Ovary	3.3	Fetal Heart	12.9
Breast ca. MCF-7	10.3	Heart Pool	8.3
Breast ca. MDA- MB-231	3.0	Lymph Node Pool	3.5

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Breast ca. BT 549	1.3	Fetal Skeletal Muscle	2.6
Breast ca. T47D	100.0	Skeletal Muscle Pool	25.5
Breast ca. MDA-N	0.4	Spleen Pool	0.2
Breast Pool	3.1	Thymus Pool	2.7
Trachea	3.2	CNS cancer (glio/astro) U87-MG	4.0
Lung	2.9	CNS cancer (glio/astro) U-118-MG	1.3
Fetal Lung	3.0	CNS cancer (neuro;met) SK-N-AS	1.8
Lung ca. NCI-N417	0.2	CNS cancer (astro) SF-539	1.3
Lung ca. LX-1	1.1	CNS cancer (astro) SNB-75	0.9
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	5.0
Lung ca. SHP-77	3.1	CNS cancer (glio) SF-295	5.5
Lung ca. A549	4.3	Brain (Amygdala) Pool	5.5
Lung ca. NCI-H526	0.4	Brain (cerebellum)	13.5
Lung ca. NCI-H23	6.8	Brain (fetal)	5.6
Lung ca. NCI-H460	1.5	Brain (Hippocampus) Pool	5.2
Lung ca. HOP-62	0.1	Cerebral Cortex Pool	7.1
Lung ca. NCI-H522	3.6	Brain (Substantia nigra) Pool	11.5
Liver	13.6	Brain (Thalamus) Pool	7.2
Fetal Liver	12.0	Brain (whole)	7.2
Liver ca. HepG2	2.7	Spinal Cord Pool	4.8
Kidney Pool	6.2	Adrenal Gland	6.0
Fetal Kidney	4.0	Pituitary gland Pool	1.7
Renal ca. 786-0	0.2	Salivary Gland	6.6
Renal ca. A498	1.4	Thyroid (female)	5.2
Renal ca. ACHN	0.8	Pancreatic ca. CAPAN2	3.5
Renal ca. UO-31	0.9	Pancreas Pool	4.4

Table AHD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3385, Run 165296471	Tissue Name	Rel. Exp.(%) Ag3385, Run 165296471
Secondary Th1 act	1.2	HUVEC IL-1beta	0.0
Secondary Th2 act	3.6	HUVEC IFN gamma	3.7